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DT
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     15-DEC-2003 (Rel. 78, Last updated, Version 1)
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KW
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OC
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RN
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     Isogai T., Sugiyama T., Otsuki T., Wakamatsu A., Sato H., Ishii S.,
RA
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RA
     Tamechika I., Seki N., Yoshikawa T., Otsuka M., Nagahari K., Masuho Y.;
RT
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RL
     Patent number EP1347046-A/3981, 24-SEP-2003.
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     Research Association for Biotechnology (JP).
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     EQHKTESGYG SESSLRRHGS MVSLVSGASG YSATSTSSFK KGHSLREKLA EMETFRDILC
     RQVDTLQKYF DACADAVSKD ELQRDKVVED DEDDFPTTRS DGDFLHSTNG NKEKLFPHVT
     PKGINGIDPK GEAITFKATT AGILATLSHC IELMVKREDS WOKRLDKETE KKRRTEEAYK
     NAMTELKKKS HPGGPDYEEG PNSLINEEEF FDAVEAALDR QDKIEEQSQS EKVRLHWPTS
     LPSGDAPSSV GTHRFVQKPY SRSSSMSSID LVSASDDVHR FSSQVEEMVQ NHMTYSLQDV
     GGDANWQLVV EEGEMKVYRR EVEENGIVLD PLKATHAVKG VTGHEVCNYF WNVDVRNDWE
     TTIENPHVVE TLADNAIIIY QTHKRVWPAS QRDVLYLSVI RKIPALTEND PETWIVCNFS
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     VLRAVAKREY PKFLKRFTSY VQEKTAGKPI LF
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#### Remarks:

The complete document including Reference Tables and the Sequence Listing is available on CD-ROM from the European Patent Office, Vienna sub-office

#### (54) Full-length cDNA sequences

(57) Novel full-length cDNAs are provided. 2443 cDNA derived from human have been isolated. The full-length nucleotide sequences of the cDNA and amino acid sequences encoded by the nucleotide sequences have been determined. Because the cDNA of the present invention are full-length and contain the translation start site, they provide information useful for analyzing the functions of the polypeptide.

#### Description

#### FIELD OF THE INVENTION

[0001] The present invention relates to polynucleotides encoding novel polypeptides, polypeptides encoded by the polynucleotides, and new uses of these.

#### BACKGROUND OF THE INVENTION

[0002] Currently, the sequencing projects, the determination and analysis of the genomic DNA of various living organisms have been in progress all over the world. The whole genomic sequences of more than 40 species of prokaryotes, a lower eukaryote, yeast, a multicellular eukaryote, *C. elegans*, and a higher plants, arabidopsis, etc. are already determined. For human genome, presumably having 3 billion base pairs, the analysis was advanced under global cooperative organization, and a draft sequence was disclosed in 2001. Moreover, all the structures are to be clear and to be disclosed in 2002 - 2003. The aim of the determination of genomic sequence is to reveal the functions of all genes and their regulation and to understand living organisms as a network of interactions between genes, proteins, cells or individuals through deducing the information in a genome, which is a blueprint of the highly complicated living organisms. To understand living organisms by utilizing the genomic information from various species is not only important as an academic subject, but also socially significant from the viewpoint of industrial application.

[0003] However, determination of genomic sequences itself cannot identify the functions of all genes. For example, as for yeast, only the function of approximately half of the 6000 genes, which is predicted based on the genomic sequence was able to be deduced. On the other hand, the human genome has been estimated to contain about 30 000 40 000 genes. Further, 100,000 or more types of mRNAs are said to exist when variants produced by alternative splicing are taken into consideration. Therefore, it is desirable to establish "a high throughput analysis system of the gene functions" which allows us to identify rapidly and efficiently the functions of vast amounts of the genes obtained by the genomic sequencing.

[0004] Many genes in the eukaryotic genome are split by introns into multiple exons. Thus, it is difficult to predict correctly the structure of encoded protein solely based on genomic information. In contrast, cDNA, which is produced from mRNA that lacks introns, encodes a protein as a single continuous amino acid sequence and allows us to identify the primary structure of the protein easily. In human cDNA research, to date, more than three million ESTs (Expression Sequence Tags) are publicly available, and the ESTs presumably cover not less than 80% of all human genes.

[0005] The information of ESTs is utilized for analyzing the structure of human genome, or for predicting the exonregions of genomic sequences or their expression profile. However, many human ESTs have been derived from proximal regions to the 3'-end of cDNA, and information around the 5'-end of mRNA is extremely little. Among human cDNAs the number of the corresponding mRNAs whose encoding full-length protein sequences are deduced is approximately 13 000.

[0006] It is possible to identify the transcription start site of mRNA on the genomic sequence based on the 5'-end sequence of a full-length cDNA, and to analyze factors involved in the stability of mRNA that is contained in the cDNA, or in its regulation of expression at the translation stage. Also, since a full-length cDNA contains atgle codon, the translation start site in the 5'-region, it can be translated into a protein in a correct frame. Therefore, it is possible to produce a large amount of the protein encoded by the cDNA or to analyze biological activity of the expressed protein by utilizing an appropriate expression system. Thus, analysis of a full-length cDNA provides valuable information which complements the information from genome sequencing. Also, full-length cDNA clones that can be expressed are extremely valuable in empirical analysis of gene function and in industrial application.

[0007] Therefore, if a novel human full-length cDNA is isolated, it can be used for developing medicines for diseases in which the gene is involved. The protein encoded by the gene can be used as a drug by itself. Thus, it has great significance to obtain a full-length cDNA encoding a novel human protein.

[0008] In particular, human secretory proteins or membrane proteins would be useful by itself as a medicine like tissue plasminogen activator (TPA), or as a target of medicines like membrane receptors. In addition, genes for signal transduction-related proteins (protein kinases, etc.), glycoprotein-related proteins, transcription-related proteins, etc. are genes whose relationships to human diseases have been elucidated. Moreover, genes for disease-related proteins form a gene group rich in genes whose relationships to human diseases have been elucidated.

[0009] Therefore, it has great significance to isolate novel full-length cDNA clones of human, only few of which has been isolated. Especially, isolation of a novel cDNA clone encoding a secretory protein or membrane protein is desired since the protein itself would be useful as a medicine, and also the clones potentially include a gene involved in diseases. In addition, genes encoding proteins that are involved in signal transduction, glycoprotein, transcription, or diseases are expected to be useful as target molecules for therapy, or as medicines themselves. These genes form a gene group predicted to be strongly involved in diseases. Thus, identification of the full-length cDNA clones encoding those

proteins has great significance.

#### SUMMARY OF THE INVENTION

[0010] An objective of the present invention is to provide polynucleotides encoding novel polypeptides, polypeptides encoded by the polynucleotides, and novel usages of these.

[0011] The inventors have developed a method for efficiently cloning, from a cDNA library having very high fullness-ratio, a human full-length cDNA that is predicted to be a full-length cDNA clone, where the cDNA library is synthesized by an improved method (WO 01/04286) of the oligo-capping method (K. Maruyama and S. Sugano, Gene, 138: 171-174 (1994); Y. Suzuki et al., Gene, 200: 149-156 (1997)). Then, the nucleotide sequences of cDNA clones whose fullness ratio is high, obtained by this method, were determined mainly from their 5'-ends, and, if required; from 3'-ends.

[0012] Further, representative clones, which were estimated to be novel and full-length, among the clones obtained, were analyzed for their full-length nucleotide sequences. The determined full-length nucleotide sequences were analyzed by BLAST homology search of the databases shown below. Because the homology search of the present invention is carried out based on the information of full-length cDNAs including the entire coding regions, homology to every part of a polypeptide can be analyzed. Thus, in the present invention, the reliability of homology search has been greatly improved.

[1] SwissProt

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- (http://www.ebi.ac.uk/ebi\_docsSwissProt\_db/swisshome.html),
- [2] GenBank (http://www.ncbi.nlm.nih.gov/web/GenBank),
- [3] UniGene (Human) (http://www.ncbi.nlm.nih.gov/UniGene), and
- [4] nr (a protein database, which has been constructed by combining data of coding sequences (CDS) in nucleotide sequences deposited in GenBank, and data of SwissProt, PDB (http://www.rcsb.org/pdb/index.html), PIR (http://pir.georgetown.edu/pirwww/pirhome.shtml), and PRF (http://www.prf.or.jp/en/); overlapping sequences have been removed.)

[0013] Further, the gene expression profiles of cDNA clones whose full-length nucleotide sequence had been determined were studied by analyzing the large-scale cDNA database constructed based on the 5'-end nucleotide sequences of cDNAs obtained. In addition to the analysis for the expression profile by computer, the profiles of gene expression in living cells were also determined by PCR. The present inventors revealed the usefulness of the genes of the present invention based on these analysis results.

[0014] In the present invention, gene functions were revealed by the analysis of expression profiles *in silico* based on the information of full-length nucleotide sequences. The expression profiles used in the expression frequency analysis were studied based on the database containing sufficient amount of fragment sequence data. The expression frequency analysis was carried out by referring, for these expression profiles, to the full-length nucleotide sequences of many cDNA clones obtained in the present invention. Thus, a highly reliable analysis can be achieved by referring to the full-length nucleotide sequences of a wide variety of genes for the sufficiently large population for analysis (expression profiles). Namely, the results of expression frequency analysis using the full-length sequences of the present invention more precisely reflect the gene expression frequency in tissues and cells from which a certain cDNA library was derived. In other words, the information of full-length cDNA nucleotide sequence of the present invention made it possible to achieve the highly reliable expression frequency analysis.

[0015] The full-length cDNA clones of this invention were obtained by the method comprising the steps of [1] preparing libraries containing cDNAs with the high fullness ratio by oligo-capping, and [2] assembling 5'-end sequences and selecting one with the highest probability of completeness in length in the cluster formed (there are many clones longer in the 5'-end direction). However, the uses of primers designed based on the 5'- and 3'-erid sequences of polynucleotides provided by the present invention enable readily obtaining full-length cDNAs without such a special technique. The primer, which is designed to be used for obtaining cDNAs capable of being expressed, is not limited to the 5'- and 3'-end sequences of polynucleotide.

[0016] Specifically, the present invention relates to a polynucleotide selected from the group consisting of the following (a) to (g):

- (a) a polynucleotide comprising a protein-coding region of the nucleotide sequence of any one of SEQ ID NOs shown in Table 1:
- (b) a polynucleotide encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs shown in Table 1:
- (c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs shown in Table 1, wherein, in said amino acid sequence, one or more amino

acids have been substituted, deleted, inserted, and/or added, and wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide comprising the selected amino acid sequence;

- (d) a polynucleotide hybridizing under stringent conditions to a polynucleotide comprising the nucleotide sequence of any one of SEQ ID NOs shown in Table 1, wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide encoded by the selected nucleotide sequence;
- (e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotide according to any one of (a) to (d);
- (f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of (a); and
- (g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of (a).

[0017] The present invention also relates to a polypeptide encoded by the above-mentioned polynucleotide or a partial peptide thereof, an antibody binding to the polypeptide or the peptide, and a method for immunologically assaying the polypeptide or the peptide, which comprises the steps of contacting the polypeptide or the peptide with the antibody, and observing the binding between the two.

**[0018]** Furthermore, the present invention features a vector comprising the above-mentioned polynucleotide, a transformant carrying the polynucleotide or the vector, a transformant carrying the polynucleotide or the vector in an expressible manner, and a method for producing the polypeptide or the peptide, which comprises the steps of culturing the transformant and recovering an expression product.

[0019] Another feature of the present invention is an oligonucleotide comprising at least 15 nucleotides, said oligonucleotide comprising a nucleotide sequence complementary to the nucleotide sequence of any one of SEQ ID NOs: 1 to 2443 or to a complementary strand thereof. This oligonucleotide can be used as a primer for synthesizing the above-mentioned polynucleotide or used as a probe for detecting the polynucleotide. The present invention includes an antisense polynucleotide against the polynucleotide or a part thereof, and a method for detecting the polynucleotide, which comprises the following steps of:

- a) incubating a target polynucleotide with the oligonucleotide under hybridizable conditions, and
- b) detecting hybridization of the target polynucleotide with the oligonucleotide.

[0020] Still another feature of the present invention is a database of polynucleotides and/or polypeptides, said database comprising information on at least one of the nucleotide sequences of SEQ ID NOs: 1 to 2443 and/or on at least one of the amino acid sequences of SEQ ID NOs: 2444 to 4886.

[0021] Herein, "polynucleotide" is defined as a molecule, such as DNA and RNA, in which multiple nucleotides are polymerized. There are no limitations on the number of the polymerized nucleotides. In case that the polymer contains relatively low number of nucleotides, it is also described as an "oligonucleotide", which is included in the "polynucleotide" of the present invention. The polynucleotide or the oligonucleotide of the present invention can be a natural or chemically synthesized product. Alternatively, it can be synthesized using a template polynucleotide by an enzymatic reaction such as PCR. Furthermore, the polynucleotide of the present invention may be modified chemically. Moreover, not only a single-strand polynucleotide but also a double-strand polynucleotide is included in the present invention. In this specification, especially in claims, when the polynucleotide is described merely as "polynucleotide", it means not only a single-strand polynucleotide but also a double-strand polynucleotide. When it means double-strand polynucleotide, the nucleotide sequence of only one chain is indicated. However, based on the nucleotide sequence of a sense chain, the nucleotide sequence of the complementary strand thereof is essentially determined.

[0022] As used herein, an "isolated polynucleotide" is a polynucleotide the structure of which is not identical to that of any naturally occurring polynucleotide or to that of any fragment of a naturally occurring genomic polynucleotide spanning more than three separate genes. The term therefore includes, for example, (a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule in the genome of the organism in which it naturally occurs; (b) a polynucleotide incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion polypeptide. Specifically excluded from this definition are polynucleotides of DNA molecules present in mixtures of different (i) DNA molecules, (ii) transfected cells, or (iii) cell clones; e.g., as these occur in a DNA library such as a cDNA or genomic DNA library.

[0023] The term "substantially pure" as used herein in reference to a given protein or polypeptide means that the protein or polypeptide is substantially free from other biological macromolecules. For example, the substantially pure protein or polypeptide is at least 75%, 80%, 85%, 95%, or 99% pure by dry weight. Purity can be measured by any

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appropriate standard method known in the art, for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

[0024] All the cDNAs provided by the present invention are full-length cDNAs. The "full-length cDNA" herein means that the cDNA contains the ATG codon, which is the start point of translation therein. The untranslated regions upstream and downstream of the protein-coding region, both of which are naturally contained in natural mRNAs, are not indispensable. It is preferable that the full-length cDNAs of the present invention contain the stop codon.

#### BRIEF DESCRIPTION OF THE DRAWINGS

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[0025] Figure 1 shows the restriction map of the vector pME18SFL3.

#### DETAILED DESCRIPTION OF THE INVENTION

[0026] All the clones (2443 clones) of the present invention are novel and encode the full-length polypeptides. Further, all the clones are cDNAs with the high fullness ratio, which were obtained by oligo-capping method, and also clones which are not identical to any of known human mRNAs (namely, novel clones) selected by searching, for the 5'-end sequences. mRNA sequences with the annotation of "complete cds" in the GenBank and UniGene databases by using the BLAST homology search [S. F. Altschul, W. Gish, W. Miller, E. W. Myers & D. J. Lipman, J. Mol. Biol., 215: 403-410 (1990); W. Gish & D. J. States, Nature Genet., 3: 266-272 (1993)]; they are also clones that were assumed to have higher fullness ratio among the members in the cluster formed by assembling. Most of the clones assessed to have high fullness ratio in the cluster had the nucleotide sequences longer in the 5'-end direction.

[0027] All the full-length cDNAs of the present invention can be synthesized by a method such as PCR (Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons Section 6.1-6.4) using primer sets designed based on the 5'-end and 3'-end sequences or using primer sets of primers designed based on the 5'-end sequences and a primer of oligo dT sequence corresponding to poly A sequence. Table 1 contains the clone names of full-length cDNA of 2443 clones of the present invention, SEQ ID NOs of the full-length nucleotide sequences, CDS portions deduced from the full-length nucleotide sequences, and SEQ ID NOs of the translated amino acids. The positions of CDS are shown according to the rule of "DDBJ/EMBL/GenBank Feature Table Definition" (http://www.ncbi.nlm.nih.gov/collab/FT/index.html). The start position number corresponds to the first letter of "ATG" that is the nucleotide triplet encoding methionine: the termination position number corresponds to the third letter of the stop codon. These are indicated being flanked with the mark "..". However, with respect to the clones having no stop codon, the termination position is indicated by the mark ">" according to the above rule.

Table 1

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
3NB6910001910	1	301661	2444
3NB6920014080	2	80922	2445
3NB6920014590	3	1693	2446
ADIPS10000640	4	1271098	2447
ADIPS20004250	5	1702212	2448
ADRGL10001470	6	368829	2449
ADRGL20000640	7	5991345	2450
ADRGL20011190	8	61>2254	2451
ADRGL20012870	9	8271300	2452
ADRGL20013010	10	11271444	2453
ADRGL20013520	11	226837	2454
ADRGL20018300	12	3202233	2455
ADRGL20018540	13	55363	2456
ADRGL20028570	14	218976	2457
ADRGL20035850	· 15	55522	2458
ADRGL20044590	16	6921042	2459
ADRGL20048330	17	1892204	2460
ADRGL20061930	18	293>1899	2461
ADRGL20067670	19	108 512	2462

Table 1 (continued)

F	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
	Cione name	sequence	1 00111011 01 000	sequence
-	ADRGL20068170	20	217 615	2463
5	ADRGL20068460	21	576 1280	2464
	ADRGL20038430 ADRGL20073570	22	556 891	2465
	1	23	159 515	2466
	ADRGL20076360	23	418 1563	2467
10	ADRGL20078100	25	871 1368	2468
	ADRGL20083310		369 2168	2469
	ASTRO10001650	26	319 744	2470
	ASTRO20001410	27	1	2471
	ASTRO20005330	28	196 642	2472
15	ASTRO20008010	29	735 1169	2472
	ASTRO20012490	30	286 783	Į.
	ASTRO20027430	31	129 848	2474
	ASTRO20032120	32	860 1189	2475
	ASTRO20033160	33	139 1014	2476
20	ASTRO20055750	34	16 2007	2477
	ASTRO20058630	35	28 957	2478
	ASTRO20064750	36	1381 >2654	2479
	ASTRO20072210	37	274 >1868	2480
25	ASTRO20084250	38	35 1381	2481
20	ASTRO20100720	39	394714	2482
	ASTRO20105820	40	2051368	2483
	ASTRO20106150	41	1381811	2484
	ASTRO20108190	42 .	7912539	2485
30	ASTRO20111490	43	517921	2486
	ASTRO20114370	44	1451782	2487
	ASTRO20114610	45	53433	2488
	ASTRO20125520	46	16742456	2489
25	ASTRO20130500	47	152417	2490
35	ASTRO20136710	48	319657	2491
	ASTRO20138020	49	285 995	2492
	ASTRO20141350	50	394 1767	2493
	ASTRO20143630	51	103 1305	2494
40	ASTRO20145760	52	347 2008	2495
	ASTRO20152140	53	760 1233	2496
	ASTRO20155290	54	208 2298	2497
	ASTRO20166810	55	7381	2498
	ASTRO20168470	56	3341329	2499
45	ASTRO20173480	57	119724	2500
	ASTRO20181690	58	841967	2501
	ASTRO20190390	59	22822662	2502
	BEAST20004540	60	10221513	2503
<i>50</i> .	BGGI110000240	61	1231649	2504
	BGGI110001930	62	811307	2505
	BGGI120006160	63	6680	2506
	BLADE20003400	64	711876	2507
	BLADE20003890	65	555 2405	2508
55	BLADE20004630	66	58 405	2509
	BNGH420088500	67	2 1270	2510
	BRACE20003070	68	310 1563	2511
	B11A0120000070			

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	BRACE20006400	69	32 364	2512
	BRACE20011070	70	21 1553	2513
	BRACE20019540	71 .	538 993	2514
- 1	BRACE20027620	72 .	24 1289	2515
10	BRACE20037660	73	143 469	2516
	BRACE20038000	74	646 2187	2517
	BRACE20038470	· . 75	9631307	2518
	BRACE20038480	76	18382626	2519
	BRACE20038850 .	77	10991413	2520
15	BRACE20039040	78	12731671	2521
	BRACE20039440	79	216797	2522
	BRACE20039540	80	11531905	2523
	BRACE20050900	81	1151788	2524
	BRACE20051380	82	14331783	2525
20	BRACE20051690	83	380742	2526
	BRACE20052160	84	201024	2527
	BRACE20053280	85	7361524	2528
	BRACE20053480	86	24875	2529
25	BRACE20053630	87	81950	2530
	BRACE20054500	88	364669	2531
	BRACE20055180	89	156 656	2532
	BRACE20056810	90	338 940	2533
	BRACE20057190	91	1016 1660	2534
30	BRACE20057420	92	539 856	2535
	BRACE20057620	93	1226 1588	2536
	BRACE20057730	94	819 1592	2537
	BRACE20058580	95	146 1330	2538
35	BRACE20058810	96	40 345	2539
	BRACE20059370	97	192 1574	2540
	BRACE20060550	98	197 1687	2541
	BRACE20060720	99	220 618	2542
	BRACE20060840	100	37 927	2543
40	BRACE20060890	101	170 964	2544
	BRACE20061050	102	1130 1573	2545
	BRACE20061740	103	434 865	2546
	BRACE20062400	104	1310 1732	2547
<b>4</b> 5	BRACE20062640	105	278 2089	2548
. –	BRACE20062740	106	753 1151	2549
	BRACE20063630	107	414 800	2550
	BRACE20063780	108	11 892	2551
	BRACE20063800	109	70 435	2552
50 ·	BRACE20063930	110	1795 2433	2553
	BRACE20064880	111	365 1420	2554
	BRACE20067430	112	875 1189	2555
	BRACE20068590	113	260 1759	2556
55	BRACE20069090	114	1484 1960	2557
	BRACE20081720	115	1182 1565	2558
	BRACE20082950	116	1713 2018	2559
	BRACE20090440	117	58 444	2560

Table 1 (continued)

	Clone name	SEQ ID NO, of nucleotide	Position of CDS	SEQ ID NO. of amino acid
1		sequence		sequence
5	BRACE20096200	118	168 1130	2561
	BRACE20096540	119	43 729	2562
	BRACE20097320	120 、	51 509	2563
	BRACE20099570	121	3 425	2564
	BRACE20101700	122	579 968	2565
10	BRACE20101710	123	187 681	2566
	BRACE20106690	124	335 691	2567
	BRACE20106840	125	19 402	2568
	BRACE20107530	126	437 1063	2569 <sup>)</sup>
15	BRACE20108130	127	927 1229	2570
15	BRACE20108880	128	417 782	2571
	BRACE20109370	129	1197 1778	2572
	BRACE20109830	130	7471382	2573
	BRACE20111830	131	366 737	2574
20	BRACE20114780	132	515 886	2575
	BRACE20115450	133	399 764	2576
	BRACE20115920	134	41 937-	2577
	BRACE20116110	135	830 1150	2578
	BRACE20116460	136	84 509	2579
25	BRACE20118380	137	6571421	2580
	BRACE20121850	138	474. 857	2581
	BRACE20136240	139	111518	2582
	BRACE20141080	140	148534	2583
30	BRACE20142320	141	164499	2584
	BRACE20142570	142	591926	2585
	BRACE20147800	143	133513	2586
	BRACE20148210	144	11011541	2587
	BRACE20148240	145	7132128	2588
35	BRACE20150310	146	94408	2589
	BRACE20151320	147	1371189	2590
	BRACE20152870	148	207653	2591
	BRACE20153680	149	87956	2592
40	BRACE20154120	150	351989	2593
	BRACE20163150	151	6991085	2594
	BRACE20163350	152	4431597	2595
	BRACE20165830	153	401709	2596
	BRACE20171240	154	62439	2597
45	BRACE20172980	155	20445	2598
	BRACE20175870	156	67396	2599
	BRACE20177200	157	11781675	2600
	BRACE20179340	158	471171	2601
50 °	BRACE20185680	159	8801341	2602
	BRACE20188470	160	12472926	2603
	BRACE20190040	161	6464	2604
	BRACE20190440	162	3821287	2605
	BRACE20192440	163	11992062	2606
55	BRACE20195100	164	251736	2607
	BRACE20201570	165	6611056	2608
	BRACE20210140	166	248. 550	2609

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	BRACE20220300	167	10571392	2610
_	BRACE20223280	168	61976	2611
	BRACE20223330	169 .	972373	2612
	BRACE20224480	170	15681924	2613
	BRACE20224500	171	16742081	2614
10	BRACE20228480	172	12682176	2615
	BRACE20229280	173	239700	2616
	BRACE20230700	174	354752	2617
	BRACE20232840	175	792019	2618
15	BRACE20235400	176	213593	2619
	BRACE20237270	177	3494	2620
	BRACE20238000	178	135437	2621
	BRACE20240740	179	831546	2622
	BRACE20248260	180	6821533	2623
20	BRACE20253160	181	26559	2624
	BRACE20253330	182	2201041	2625
	BRACE20257100	183	1638 2021	2626
	BRACE20262930	184	256 681	2627
25	BRACE20262940	185	259 591	2628
10	BRACE20266750	186	58 1143	2629
	BRACE20267250	187	139 612	2630
	BRACE20269200	188	4 408	2631
	BRACE20269710	189	338 1063	2632
30	BRACE20273890	190	13651766	2633
	BRACE20274080	191	350 655	2634
	BRACE20276-130	192	232 >2028	2635
	BRACE20283920	193	7171025	2636
35	BRACE20284100	194	10261865	2637
	BRACE20286360	195	170727	2638
	BRACE20287410	196	603956	2639
	BRALZ20013500	197	215640	2640
	BRALZ20014450	198	6374	2641
40	BRALZ20017430	199	232747	2642
	BRALZ20018340	200	8791481	2643
	BRALZ20019660	201	180773	2644
	BRALZ20054710	202	1351223	2645
45	BRALZ20058880	203	1021607	2646
	BRALZ20059500	204	7221081	2647
	BRALZ20064740	205	24350	2648
	BRALZ20065600	206	25624	2649
	BRALZ20069760	207	14319	2650
50 °	BRALZ20073760	208	5761124	2651
	BRALZ20075450	209	7751200	2652
	BRALZ20075760	210	148726	2653
	BRALZ20077900	211	19002529	2654
55	BRALZ20077930	212	502077	2655
	BRALZ20080310	213	13042005	2656
	BRALZ20088690	214	104661	2657
	BRAMY100C1300	215	23522795	2658

Table 1 (continued)

ſ	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	BRAMY10001570	216	6961604	2659
	BRAMY20000520	217	3291204	2660
	BRAMY20000860	218	246548	2661
10	BRAMY200027	219	76 447	2662
	BRAMY20004110	220	145 540	2663
	BRAMY20011140	221	2661 3011	2664
	BRAMY20025840	222	1058 2002	2665
	BRAMY20039260	223	101 424	2666
	BRAMY20045240	224	662 1792	2667
15	BRAMY20054880	225	508 981	2668
,5	BRAMY20060920	226	110 439	2669
	BRAMY20063970	227	246 551	2670
	BRAMY20071850	228	178 705	2671
	BRAMY20102080	229	5131136	2672
20	BRAMY20103570	230	1141001	2673
	BRAMY20104640	231	3341410	2674
	BRAMY20110640	232	14001735	2675
	BRAMY20111960	233	534854	2676
25	BRAMY20112800	234	31606	2677
	BRAMY20116790	235	2348 2794	2678
	BRAMY20120910	236	182 976	2679
	BRAMY20121190	237	81 398	2680
	BRAMY20121620	238	51 1688	2681
30	BRAMY20124260	239	95 1759	2682
	BRAMY20134140	240	1 510	2683
	BRAMY20135900	241	4 1053	2684
	BRAMY20136210	242	1810 2145	2685
35	BRAMY20137560	243	2220 2795	2686
	BRAMY20144620	244	8921326	2687
	BRAMY20147540	245	147611	2688
	BRAMY20148130	246	2042138	2689
	BRAMY20152110	247	12571580	2690
40	BRAMY20153110	248	11763	2691
	BRAMY20157820	249	941740	2692
	BRAMY20160700	250	16862015	2693
	BRAMY20162510	251	1861757	2694
45	BRAMY20163250	252	96719	2695
	BRAMY20163270	253	5311010	2696
	BRAMY20167060	254	347865	2697 2698
	BRAMY20167710	255	900 1532	2699
	BRAMY20168920	256	91 1275	2700
50 °	BRAMY20170140	257	115 681 74 2179	2701
	BRAMY20174550	258	226 2025	2702
	BRAMY20178640	259	678 980	2703
	BRAMY20181220	260	208 738	2704
55	BRAMY20182730	261	213 653	2705
	BRAMY20183080	262 263	871 1548	2706
	BRAMY20184670	263	2087 2476	2707
	BRAMY20195090	204	2007 2470	

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	BRAMY20196000	265	50439	2708
	BRAMY20204450	266	34462	2709
	BRAMY20205740	267 .	177554	2710
	BRAMY20210400	268	131703	2711
	BRAMY20211390	269	14072303	2712
10	BRAMY20211420	270	1312407	2713
	BRAMY20213100	271	2452026	2714
	BRAMY20215230	272	207515	2715
	BRAMY20217460	273	6121217	2716
15	BRAMY20218250	274	1612167	2717
	BRAMY20218670	275	338652	2718
	BRAMY20229800	276	12701662	2719
	BRAMY20229840	277	10221678	2720
	BRAMY20230600	278	6141840	2721
20	BRAMY20231720	279	429773	2722
	BRAMY20240040	280	6932660	2723
	BRAMY20242470	281	15272243	2724
	BRAMY20245300	282	592482	2725
24	BRAMY20247110	283	3211382	2726
•	BRAMY20247280	284	611925	2727
	BRAMY20248490	285	17232079	2728
	BRAMY20250240	286	11791619	2729
	BRAMY20250320	287	18323	2730
<i>30</i>	BRAMY20252180	288	11501506	2731
	BRAMY20252720	289	5951113	2732
	BRAMY20260910	290	672646	2733
	BRAMY20261680	291	298 1041	2734
35	BRAMY20266850	292	26 685	2735
<b>3</b> 9	BRAMY20267130	293	235 708	2736
	BRAMY20268990	294	137 460	2737
	BRAMY20270730	295	124 2118	2738
	BHAMY20271400	296	177 >3011	2739
40	BRAMY20273960	297	48 1826	2740
	BRAMY20277140	298	1135 1485	2741
	BRAMY20277170	299	545 2221	2742
	BRAMY20280720	300	103 489	2743
45	BRAMY20284910	301	10591415	2744
	BRAMY20285160	302	14831977	2745
	BRAMY20285930	303	8111143	2746
	BRAMY20286820	304	14631777	2747
	BRAWH10000930	305	8431454	2748
50 ·	BRAWH20002320	306	162716	2749
	BRAWH20004600	307	661361	2750
	BRAWH20011710	308	2291872	2751
	BRAWH20012390	309	71562	2752
55	BRAWH20012410	310	291593	2753
در	BRAWH20014920	311	3531378	2754
	BRAWH20015350	312	12851641	2755
	BRAWH20015890	313	8061837	2756

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	BRAWH20016620	314	17212254	2757
	BRAWH20016660	315	511205	2758
	BRAWH20016860	316	548877	2759
	BRAWH20017010	317	155628	2760
	BRAWH20018730	318	561570	2761
10	BRAWH20028110	319	1231718	2762
	BRAWH20029630	320	9291276	2763
	BRAWH20030250	321	2641421	2764
	BRAWH20064050	322	2721591	2765
15	BRAWH20075700	323	3491407	2766
	BRAWH20096780	324	2721840	2767
	BRAWH20100690	325	14301849	2768
	BRAWH20101360	326	163852	2769
	BRAWH20103180	327	10811659	2770
20	BRAWH20103290	328	712626	2771
	BRAWH20105840	329	1391083	2772
	BRAWH20106180	330	628933	2773
	BRAWH20107540	331	.1540	2774
25	BRAWH20110660	332	156578	2775
20	BRAWH20110790	333	19942338	2776
	BRAWH20110960	334	741210	2777
	BRAWH20111550	335	569949	2778
	BRAWH20112940	336	8501968	2779
30	BRAWH20113430	337	135869	2780
	BRAWH20114000	338	721619	2781
	BRAWH20117950	339	4651568	2782
	BRAWH20118230	340	146565	2783
35	BRAWH20121640	341	981516	2784
	BRAWH20122580	342	104721	2785
	BRAWH20122770	343	1283 1612	2786
	BRAWH20125380	344	382 918	2787
	BRAWH20126190	345	154 459	2788
40	BRAWH20126980	346	222 686	2789
	BRAWH20128270	347	295 1020	2790
	BRAWH20132190	348	157 561	2791
	BRAWH20137480	349	273 1313	2792
45	BRAWH20138660	350	261 1376	2793
	BRAWH20139410	351	13 354	2794
	BRAWH20142340	352	99 413	2795
	BRAWH20147290	353	460 810	2796
	BRAWH20149340	354	442 1620	2797
50	BRAWH20155950	355	8 2074	2798
	BRAWH20158530	356	138 1136	2799
	BRAWH2016028	357	2093 2587	2800
	BRAWH20162690	358	33 1085	2801
55	BRAWH20164460	359	345 >2067	2802
	BRAWH20166790	360	224. 571	2803
	BRAWH20171030	361	152 1996	2804
	BRAWH20173050	362	1272 1604	2805

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	BRAWH20182060	363	1181740	2806
	BRAWH20185060	364	248607	2807
	BRCAN10001490	365 .	60452	2808
	BRCAN20003460	366	2391030	2809
10	BRCAN20006200	367	9081234	2810
	BRCAN20006390	368	252743	2811
	BRCAN20054490	369	3451067	2812
	BRCAN20060190	370	206595	2813
	BRCAN20064010	371	134685	2814
15	BRCAN20071190	372	1921586	2815
.5	BRCAN20091560	373	1902004	2816
	BRCAN20103740	374	207530	2817
	BRCAN20124080	375	1872079	2818
	BRCAN20126130	376	580897	2819
20	BRCAN20143700	377	14817	2820
	BRCAN20147880	378	121519	2821
	BRCAN20216690	379	66383 -	2822
	BRCAN20224720	380	5491544	2823
25	BRCAN20237240	381	23796	2824
25	BRCAN20263400	382	316729	2825
	BRCAN20273100	383	76468	2826
	BRCAN20273340	384	50352	2827
	BRCAN20273550	385	6521848	2828
30	BRCAN20273640	386	1311201	2829
	BRCAN20275130	387	374847	2830
	BRCAN20279700	388	23722839	2831
	BRCAN20280210	389	6441393	2832
25	BRCAN20280360	390	2651548	2833
35	BRCAN20280400	391	12801618	2834
	BRCAN20283190	392	4161321	2835
	BRCAN20283380	393	93533	2836
	BRCAN20284600	394	97549	2837
40	BRCAN20285450	395	118567	2838
	BRCOC10000870	396	186602	2839
	BRCOC20001860	397	10612179	2840
	BRCOC20004040	398	3831171	2841
45	BRCOC20004870	399	199 765	2842
43	BRCOC20006370	400	21 455	2843
	BRCOC20008160	401	166 >2490	2844
	BRCOC20008500	402	151 >2854	2845
	BRCOC20020850	403	1371 1820	2846
50 ·	BRCOC20021550	404	1121 2110	2847
	BRCOC20023230	405	682 1500	2848
	BRCOC20026640	406	148 516	2849
	BRCOC20027510	407	369 1088	2850
5 <i>6</i>	BRC0C20031000	408	207 581	2851
55	BRCOC20031250	409	7991122	2852
	BRCOC20031870	410	3751031	2853
	BRCOC20035130	411	171527	2854

Table 1 (continued)

Ī	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	BRCOC20037320	412	5473384	2855
_	BRCOC20037400	413	152493	2856
	BRCOC20041750	414	230535	2857
1	BRCOC20055420	415	991556	2858
	BRCOC20059510	416	199582	2859
10	BRCOC20074760	417	10>1918	2860
	BRCOC20077690	418	8671202	2861
	BRCOC20078640	419	8491208	2862
	BRCOC20090520	420	11571663	2863
15	BRCOC20091960	421	13711895	2864
13	BRCOC20093800	422	204590	2865
	BRCOC20099370	423	11890	2866
	BRCOC20101230	424	94810	2867
	BRCOC20105100	425	23932716	2868
20	BRC0C20107300	426	7091086	2869
	BRCOC20110100	427	369713	2870
	BRCOC20114180	428	167487	2871
	BRCOC20117690	429	152781	2872
24	BRCOC20119960	430	147500	2873
	BRC0C20121720	431	262983	2874
	BRC0020122290	432	92448	2875
	BRCOC20128130	433	1501364	2876
	BRCOC20134480	434	5871060	2877
30	BRCCC20135730	435	16032064	2878
	BRCOC20136750	436	28763229	2879
	BRC0C20144000	437	64459	2880
	BRCOC20147480	438	228578	2881
35	BRC0020148330	439	1691290	2882
35	BRC0020155970	440	111632	2883
	BRC0020158240	441	13572178	2884
	BRC0320176520	442	1851153	2885
	BHCOC20178270	443	2441257	2886
40	BRCOC20178560	444	651000	2887
	BRHIP10001290	445	8381731	2888
	BRHIP10001740	446	148594	2889
	BRHIP20000870	447	12351540	2890
45	BRHIP20001630	448	2871486	2891
	BRHIP20003120	449	1701951	2892
	BRHIP20005340	450	5971853	2893
	BRHIP20005530	451	30 1052	2894 2895
	BRHIP20096170	452	119 817	2896
50	BRHIP20096850	453	311 1582	2897
	BRHIP20103090	454	1345 1737	2898
	BRHIP20104440	455	166. 576 1056. 1466	2899
	BRHIP20105710	456	l control of the cont	2900
55	BRHIP20106100	457	314 1060 827 1528	2900
	BRHIP20107440	458	577 1083	2902
	BRHIP20110800	459	261 578	2903
	BRHIP20111200	460	201 378	1 2000

Table 1 (continued)

1	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
ļ		sequence		sequence
5	BRHIP20115080	461	7621751	2904
	BRHIP20115760	462	8771182	2905
	BRHIP20118380	463 、	2316	2906
	BRHIP20118910	464	82426	2907
1	BRHIP20119330	465	4202564	2908
10	BRHIP20121410	466	68505	2909
	BRHIP20123140	467	73432	2910
	BRHIP20129720	468	9341809	2911
	BRHIP20132860	469	1897	2912
15	BRHIP20135100	470	423743	2913
	BRHIP20137230	471	71 1180	2914
	BRHIP20139720	472	33 3254	2915
	BRHIP20140630	473	3521 3922	2916
	BRHIP20142850	474	259 612	2917
20	BRHIP20143730	475	229 1638	2918
	BRHIP20143860	476	1159 1638	2919
	BRHIP20149540	477	155 544	2920
	BRHIP20153560	478	1134 1445	2921
95	BRHIP20153600	479	40 675	2922
25	BRHIP20167880	480	183 656	2923
	BRHIP20169680	481	27347	2924
ł	BRHIP20169900	482	68502	2925
	BRHIP20170100	483	166936	2926
30	BRHIP20173150	484	494820	2927
	BRHIP20174040	485	712923	2928
	BRHIP20175420	486	3872	2929
	BRHIP20176420	487	9141756	2930
	BRHIP20179200	488	25322870	2931
35	BRHIP20180140	489	10281345	2932
	BRHIP20183690	490	1481620	2933
	BRHIP20186120	491	322723	2934
	BRHIP20186500	492	30893727	2935
40	BRHIP20189980	493	2471002	2936
	BRHIP20190070	494	65433	2937
	BRHIP20191490	495	19292270	2938
	BRHIP20191770	496	191502	2939
	BRHIP20191860	497	282 2084	2940
45	BRHIP20194940	498	119 1312	2941
	BRHIP20195890	499	1002 1376	2942
	BRHIP20196410	500	2371 2706	2943
	BRHIP20198190	501	2979 3407	2944
50 ·	BRHIP20205090	502	270 593	2945
	BRHIP20207430	503	370 687	2946
	BRHIP20207990	504	90 1628	2947
	BRHIP20208270	· 505	967 1353	2948
	BRHIP20208420	506	103 462	2949
55	BRHIP20208590	507	212607	2950
	BRHIP20214950	508	16372020	2951
	BRHIP20217620	509	27313087	2952

Table 1 (continued)

ſ	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
-		sequence		sequence
5	BRHIP20218580	510	19302589	2953
	BRHIP20222280	511	2691768	2954
	BRHIP20227080	512 、	16132011	2955
	BRHIP20230710	513	198554	2956
10	BRHIP20232290	514	110502	2957
	BRHIP20233090	515	17822105	2958
	BRHIP20234380	516	151079	2959
	BRHIP20236950	517	29>2580	2960
	BRHIP20238600	518	154729	2961
	BRHIP20238690	519	51383	2962
15	BRHIP20238880	520	132625	2963
	BRHIP20240460	521	21512540	2964
	BRHIP20243470	522	29293579	2965
	BRHIP20249110	523	1342887	2966
20	BRHIP20252450	524	123>3738	2967
	BRHIP20253660	525	2551031	2968
	BRHIP20254480	526	362994	2969
	BRHIP20277620	527	1241074	2970
25	BRHIP20283030	528	2194088	2971
25	BRHIP20284800	529	217606	2972
	BRHIP20285830	530	6111321	2973
	BRHIP20285930	531	105779	2974
	BRHIP30001110	532	17402294	2975
30	BRHIP30004570	533	189 1034	2976
	BRHIP30004880	534	191 2902	2977
	BRSSN10000920	535	1850 2215	2978
	BRSSN20003120	536	359 >2933	2979
<b>3</b> 5	BRSSN20006340	537	937 1401	2980
33	BRSSN20013420	538	111 2741	2981
	BRSSN20014260	539	167 1069	2982
	BRSSN20015030	540	105 458	2983
	BRSSN20015790	541	542 1639	2984
40	BRSSN20018690	542	110 463	2985
	BRSSN20021600	543	131497	2986
	BRSSN20028570	544	424726	2987
	BRSSN20038200	545	861555	2988
45	BRSSN20038410	546	187852	2989
	BRSSN20039370	547	9001628	2990
	BRSSN20043040	548	19592342	2991
	BRSSN20046570	549	18368	2992 2993
	BRSSN20046790	550	2531014	2993
50	BRSSN20046860	551	4061461	2995
	BRSSN20066110	552	7251165	2996
	BRSSN20097020	553	13522092	2997
	BRSSN20101100	554	18512330	2998
55	BRSSN20105870	555	83064	2999
	BRSSN20105960	556	183497 92415	3000
	BRSSN20108300	557	7331428	3001
	BRSSN20117990	558	7331420	550.

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	BRSSN20120810	559	7701687	3002
	BRSSN20121030	560	18890	3003
	BRSSN20137020	561 .	10971429	3004
	BRSSN20142940	562	14111803	3005
	BRSSN20146100	563	1812376	3006
10	BRSSN20151990	564	15401	3007
	BRSSN20152380	. 565	17418	3008
	BRSSN20159070	566	393728	3009
	BRSSN20159820	567	8671661	3010
15	BRSSN20169050	568	118636	3011
,,,	BRSSN20176820	569	131917	3012
	BRSSN20177570	570	3032651	3013
	BRSSN20187310	571	1631332	3014
	BRSTN10000830	572	216959	3015
20	BRSTN20000580	573	6171672	3016
	BRSTN20002200	574	159515	3017
	BRSTN20005360	575	431173	3018
	BRTHA20000570	576	641988	3019
25	BRTHA20004740	577	1921082	3020
25	BRTHA20046290	578	16572298	3021
	BRTHA20046390	579	191 571	3022
	BRTHA20046420	580	446 835	3023
	CD34C30001250	581	59 >3188	3024
30	CD34C30003140	582	458 2803	3025
	CD34C30004240	583	430 1290	3026
	CD34C30004940	584	970 1299	3027
	COLON10001350	585	18 1544	3028
35	COLON20043180	586	451 867	3029
33	COLON20093370	587	1261 1779	3030
	CTONG10000100	588	90 1118	3031
	CTONG10000220	589	191 847	3032
	CTONG10000620	590	94 2943	3033
40	CTONG10000930	591	18 2621	3034
	CTONG10000940	592	182 868	3035
	CTONG10001650	593	1916 2512	3036
	CTONG10002770	594	182 >3049	3037
45	CTONG20002180	595	90554	3038
43	CTONG20004690	596	301885	3039
	CTONG20009770	597	3213287	3040
	CTONG20014280	598	1761723	3041
	CTONG20027090	599	2802370	3042
50 ·	CTONG20028410	600	6002936	3043
	CTONG20038890	601	9611371	3044
	CTONG20049410	602	157669	3045
	CTONG20050280	603	1571944	3046
5.5	CTONG20052650	604	12101647	3047
55	CTONG20052900	605	130 1548	3048
	CTONG20075860	606	63 1391	3049
	CTONG20076130	607	11 994	3050

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
	·	sequence		sequence
5	CTONG20077790	608	270 635	3051
	CTONG20082690	609	75 896	3052
	CTONG20085950	610	905 2125	3053
	CTONG20091080	611	166 717	3054
	CTONG20091320	612	1223 1627	3055
10	CTONG20092570	613	690 1601	3056
	CTONG20092580	614	1555 1920	3057
	CTONG20092680	615	365823	3058
	CTONG20092700	616	224928	3059
15	CTONG20093950	617	2052388	3060
,5	CTONG20095270	618	11471611	3061
	CTONG20095290	619	312749	3062
	CTONG20095340	620	1092631	3063
	CTONG20096430	621	3111384	3064
20	CTONG20096750	622	7381184	3065
	CTONG20097660	623	133876	3066
	CTONG20098440	624	2061132	3067
	CTONG20099380	625	.1417 1806	3068
25	CTONG20099550	626	74 1939	3069
	CTONG20099630	627	99 2060	3070
	CTONG20100240	628	620 2155	3071
	CTONG20101480	629	13 411	3072
	CTONG20103480	630	30 356	3073
30	CTONG20105080	631	28 1260	3074
	CTONG20105660	632	75 674	3075
	CTONG20106230	633	2015 >3067	3076
	CTONG20106520	634	1693 3147	3077
35	CTONG20108210	635	234 1319	3078
	CTONG20114290	636	388 3225	3079
	CTONG20114740	637	1191 1832	3080
	CTONG20118150	638	144 2831	3081
	CTONG20118250	639	52 840	3082
40	CTONG20119200	640	2128 2637	3083
	CTONG20120770	641	29463341	3084
	CTONG20121010	642	1431732	3085
	CTONG20121580	643	97>2930	3086
45	CTONG20124010	644	2061369	3087
	CTONG20124220	645	1772477	3088
	CTONG20124470	646	7011237	3089
	CTONG20124730	647	8941280	3090
•	CTONG20125540	648	6161071	3091 3092
50 °	CTONG20125640	649	7561688	3092
	CTONG20126070	650	422843	3093
	CTONG20127450	651	22712642	3095
	CTONG20128430	652	3302180 9161479	3096
55	CTONG20128470	653	1183249	3097
	CTONG20129960	654	1183249	3098
	CTONG20131490	655 656	242>2879	3099
	CTONG20131560	000	242>2013	1 0000

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	CTONG2013220	657	11551598	3100
	CTONG20133390	658	6792304	3101
	CTONG20133480	659 、	86391	3102
	CTONG20133520	660	1282140	3103
	CTONG20136300	661	10781521	3104
10	CTONG20138030	662	30613396	3105
,	CTONG20139070	. 663	25082819	3106
	CTONG20139340	664	11821535	3107
	CTONG20139860	665	282169	3108
15	CTONG20140320	666	24542786	3109
,,,	CTONG20140580	667	74 1180	3110
	CTONG20141650	668	190 570	3111
	CTONG20143690	669	169 2583	3112
	CTONG20146300	670	1195 1674	3113
20	CTONG20146970	671	1201 1536	3114
	CTONG20147050	67.2	1304 1648	3115
	CTONG20149460	673	149 1942	3116
	CTONG20149950	674	42 371	3117
	CTONG20150910	675	792 1130	3118
25	CTONG20153300	676	755 2338	3119
	CTONG20153580	677	4881858	3120
	CTONG20155180	678	486>3005	3121
	CTONG20155400	679	19402458	3122
30	CTONG20156780	680	333104	3123
	CTONG20158040	681	1521297	3124
	CTONG20158150	682	662057	3125
	CTONG20158660	683	1712258	3126
	CTONG20159530	684	2311094	€127
35	CTONG20160560	685	79>2796	3128
	CTONG20161850	686	27734	3:29
	CTONG20162170	687	156734	3 <sup>-</sup> 30
	CTONG20163550	688	7721134	3131
40	CTONG20164990	689	13431753	3102
	CTONG20165050	690	15752018	3193
;	CTONG20186320	691	781595	3134
	CTONG20200310	692	22254	3138
	CTONG20265130	693	419892	3136
45	CTONG20267700	694	20462432	3137
	CTONG20273610	695	513923	3138.
	D3OST10001090	696	501462	3139
	D3OST10002670	697	77 853	3140
50 ·	D3OST10002700	698	84 461	3145
	D3OST20006180	699	148., 2259	3142
	D3OST20006540	700	140 442	3143
	D3OST20007340	701	369 1220	3144
	D3OST20013280	702	756 1118	3145
55	D3OST20024170	703	1373 1714	3146
	D3OST20024360	704	1984 2361	3147
	D3OST20024520	705	3 422	3148

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	D3OST20036070	706	122 1039	3149
	D3OST20037970	707	256 735	3150
	D3OST20038560	708 .	1976 2350	3151
10	D3OST30002580	709	1509 2957	3152
	D3OST30002910	710	1811 2248	3153
10	D6OST20003580	711	1760 2167	3154
	D6OST20004450	<sup>1</sup> . 712	1513 2547	3155
	D6OST20005070	713	28353398	3156
	D9OST20000310	714	239637	3157
15	D9OST20002780	715	6441360	3158
	D9OST20015470	71€	1871386	3159
	D9OST20023970	71 <sup></sup>	8721327	3160
	D9OST20026730	<b>71</b> .	1453159	3161
	D9OST20031370	71 :	6161251	3162
20	D9OST20033970	71. 3	241811	3163
	D9OST20035800	751	5241057	3164
	D9OST20035940	7/2 <b>2</b>	217867	3165
	D9OST20040180	<sup></sup> 23	1891127	3166
25	DFNES10000030	<sup></sup> 24	8971322	3167
	DFNES10001850	ÿ <b>2</b> 5	471899	3168
	DFNES20001530	726	26382	3169
	DFNES20010910	727	1591136	3170
	DFNES20014040	728	1481272	3171
30	DFNES20025880	729	10801415	3172
	DFNES20031920	730	6311104	3173
	DFNES20037420	731	1862090	3174
	DFNES20055270	732	159818	3175
35	DFNES20071130	733	2481156	3176
	DFNES20082800	734	258698	3177
	FCBBF10000240	735	5072942	3178
	FCBBF10000380	736	10241344	3179
	FCBBF10000630	737	5331654	3180
40	FCBBF10000770	738	561810	3181
	FCBBF10001150	739	3512555	3182
	FCBBF10001210	740	381066	3183
	FCBBF10001550	741	60653	3184
45	FCBBF10001710	742	3222133	3185
	FCBBF10001820	743	101032	3186
	FCBBF10002430	744	3491158	3187
	FCBBF10002700	745	189551	3188
	FCBBF10002800	746	4852818	3189
50 °	FCBBF10003220	747	479832	3190
	FCBBF10003670	748	1391266	3191
	FCBBF10003740	749	4072365	3192
	FCBBF10003760	750	10441358	3193
55	FCBBF10003770	751	242>3001	3194
	FCBBF10004120	752	142816	3195
	FC8BF10004370	753	4321511	3196
	FCBBF10005060	754	13402323	3197

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	FCBBF10005460	755	1792092	3198
	FCBBF10005500	756	15182123	3199
	FCBBF10005740	757 .	9541667	320(
	FCBBF20006780	758	356679	3201
	FCBBF20014270	759	49:.315	3202
10	FCBBF20023700	760	251589	3203
	FCBBF20032970	· . 761	8451186	3204
	FCBRF20035280	762	13393	3205
	FCBBF20042170	763	1861337	3206
15	FCBBF20042560	764	115576	3207
	FCBBF20049300	765	32631	3208
	FCBBF20051220	766	523948	3209
	FCBBF20054260	767	119535	3210
	FCBBF20056370	768	57704	3211
20	FCBBF20059090	769	9281245	3212
	FCBBF20064520	770	3681243	3213
	FCBBF20067810	771	681231	3214
	FCBBF20068820	772	74712	3215
25	FCBBF20071860	773	384911	3216
23	FCBBF20072650	774 ·	14711944	3217
	FCBBF20075560	775	7301086	3218
	FCBBF20076330	776	684998	3219
	FCBBF30001840	777	15031832	3220
30	FCBBF30007680	778	92117	3221
	FCBBF30008470	779	11571504	3222
	FCBBF30010810	780	1491483	3223
	FCBBF30012350	781	4191507	3224
<i>3</i> 5	FCBBF30012810	782	372>2409	3225
-	FCBBF30013770	783	3752795	3226
	FCBBF30015940	784	24>2507	3227
	FCBBF30016320	785	9901877	3228
	FCBBF30016570	786	574999	3229
40	FCBBF30018550	787	231>3402	3230
	FCBBF30019120	788	54398	3231
	FCBBF30024750	789	126560	3232
	FCBBF30025560	790	1711301	3233
45	FCBBF30028180	791	258830	3234
	FCBBF30033050	792	71089	3235
	FCBBF30039020	793	9552727	3236
	FCBBF30049550	794	222>4213	3237
	FCBBF30052160	795	2829 4214	3238
50 °	FCBBF3005-1440	796	33 2822	3239
	FCBBF30057290	797 ·	143 2068	3240
	FCBBF30062860	798	1135 >3256	3241
	FCBBF30070770	799	1049 2113	3242
55	FCBBF30071520	800	280 735	3243
	FCBBF30078290	801	280 1875	3244
	FCBBF30083620	802	125 1159	3245
	FCBBF30083820	803	298 774	3246

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5 ·	FCBBF30086440	804	192 863	3247
	FCBBF30090690	805	5451657	3248
	FCBBF30095260	806	204686	3249
	FCBBF30123470	807	10841614	3250
	FCBBF30129630	808	257973	3251
10	FCBBF30170590	809	13131672	3252
	FCBBF30172550	810	13501703	3253
	FCBBF30175310	811	1201280	3254
	FCBBF30178730	812	348833	3255
15	FCBBF30189490	813	19352468	3256
	FCBBF30190850	814	431560	3257
	FCBBF30195640	815	577>2751	3258
	FCBBF30199610	816	9721391	3259
	FCBBF30215060	817	42446	3260
20	FCBBF30225660	818	2312750	3261
	FCBBF30233680	819	28>4395	3262
	FCBBF30238870	820	5872761	3263
	FCBBF30240020	821	2481747	3264
25	FCBBF30240960	822	4651520	3265
	FCBBF30242250	823	271>2723	3266
	FCBBF30243640	824	339665	3267
	FCBBF30246230	825	18932357	3268
	FCBBF30246630	826	192070	3269
30	FCBBF30247930	827	5581187	3270
	FCBBF30250730	828	116>2647	3271
	FCBBF30251420	829	25902904	3272
	FCBBF30252520	830	27380	3273
35	FCBBF30252800	831	1391110	3274
	FCBBF30252850	832	451022	3275
	FCBBF30262360	833	51446	3276
	FCBBF30262510	834	362327	3277
	FCBBF30266780	835	20802382	3278
40	FCBBF30266920	836	5316	3279
	FCBBF30278630	837	492821	3280
	FCBBF30279030	838	16532447	3281
	FCBBF30281880	839	832221	3282
45	FCBBF30284720	840	230751	3283
	FCBBF30285280	841	185 3043	3284
	FCBBF40001420	842	364 681	3285
	FCBBF40001730	843	105 932	3286 3287
50 ·	FCBBF40005480 FEBRA10001880	844 845	119 589 4942236	3288
30	FEBRA10001900	846	6 389	3289
	FEBRA20002100	847	375 1064	3290
	FEBRA20002100	848	10 414	3290
	FEBRA20004620	849	297 1568	3292
55	FEBRA20007620	850	61 2400	3293
	FEBRA20009090	851	667 1032	3294
	FEBRA20010120	852	608 1216	3295
		J 302		1 2200

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	FEBRA20017050	853	1775 2197	3296
	FEBRA20018280	854	16 678	3297
	FEBRA20018690	855 、	664 981	3298
	FEBRA20024100	856	68 2659	3299
	FEBRA20025270	857	116 >2317	3300
10	FEBRA20025520	858	669 1133	3301
	FEBRA20026110	859	233 2692	3302
	FEBRA20026280	860	54 623	3303
	FEBRA20027810	861	155 2740	3304
15	FEBRA20029860	862	29 757	3305
	FEBRA20034360	863	1288 2013	3306
	FEBRA20034680	864	240 1955	3307
	FEBRA20037260	865	2376 2702	3308
	FEBRA20037500	866	10 1308	3309
20	FEBRA20040530	867	761407	3310
	FEBRA20042190	868	15901925	3311
	FEBRA20052910	869	11361486	3312
	FEBRA20060610	870	5991201	3313
25	FEBRA20072120	871	1062877	3314
	FEBRA20079310	872	23842806	3315
	FEBRA20080810	873	6791401	3316
	FEBRA20082010	874	1061779	3317
	FEBRA20082100	875	10421524	3318
30	FEBRA20086620	876	2151591	3319
	FEBRA20088360	877	29643521	3320
	FEBRA20090290	878	383823	3321
	FEBRA20092890	879	1982297	3322
35	FEBRA20093520	880	6511070	3323
	FEBRA20095140	881	264>2245	3324
	FEBRA20095880	882	18722186	3325
	FEBRA20097310	883	74 2101	3326
	FEBRA20098460	884	291 686	3327
40	FEBRA20111460	885	859 1221	3328
	FEBRA20113560	886	22 558	3329 3330
	FEBRA20125070	887	10 1002	3331
	FEBRA20130190	888	131 1192	3331
<b>45</b>	FEBRA20132740	889	770 1111 1664 2377	3333
	FEBRA20140100	890	1	3334
	FEBRA20144170	891	342 1976	3335
	FEBRA20145780	892	1262 1564 173 484	3336
	FEBRA20161120	893		3337
50 ·	FEBRA20166540	894 895	101 511 429 869	3338
	FEBRA20167390 FEBRA20171380	895	338 2002	3339
		897	125 2029	3340
	FEBRA20174410 FEBRA20176800	898	1320 1877	3341
55		899	36 533	3342
	FEBRA20184330 FEBRA20192420	900	2120 3799	3343
	FEBRA20195820	901	175 678	3344
•	- LDI IAZU 193020	] 301	1	1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	FEBRA2C195370	902	353 2032	3345
	FEBRA20195630	903	482 2359	3346
	FEBRA20197110	904	632 1222	3347
	FEBRA20204000	905	1958 2482	3348
	FEBRA20204060	906	366 728	3349
10	FEBRA20211710	907	282 929	3350
	FEBRA20214970	908	620 1264	3351
	FFBRA20215500	909	726 1256	3352
	FEBRA20216360	910	1398 1904	3353
15	FEBRA20222040	911	954 1391	3354
	FEBRA20223220	912	1254 1898	3355
	FEBRA20225040	913	131692	3356
	FEBRA20225010	914	14391933	3357
	FEBRA20229560	915	37381	3358
20	FEBRA20223630	916	184987	3359
	FEBRA20232850	917	7741193	3360
	FEBRA20233770	918	64636	3361
	FEBRA20235500	919	1206>2520	3362
25	FEBRA20237640	920	331933	3363
	FEHRT20003250	921	1731243	3364
	FELNG20002410	922	12571577	3365
	HCASM10000500	923	3001754	3366
	HCHON1 3001 760	924	2381182	3367
30	HCHON20000380	925	210644	3368
	HCHON20001560	926	5651611	3369
	HCHON20002260	927	6941389	3370
	HCHON20003220	928	23>2278	3371
35	HCHON20003440	929	1982>2519	3372
	HCHON20007380	930	1631248	3373
	HCHON20007510	931	1892636	3374
	HCHON20008150	932	204>2358	3375
	HCHON20008180	933	6711087	3376
40	HCHON20008320	934	1240>2284	3377
	HCHON20008980	935	578904	3378
	HCHON20009350	936	63422	3379
	HCHON20009560	937	16442489	3380
45	HCHON20010990	938	5311085	3381
	HCHON23011160	939	839 1156	3382
	HCHON20014970	940	302 2143	3383 3384
	HCHON20015230	941	950 1453	3385
. ·	HCHON23015350	942	647 >2887	3386
50 ·	HCHON20015980 HCHON20016040	944	100 1413 3 323	3387
	HCHON20016650	945	44 3418	3388
	HCHON20018630	945	1526 1978	3389
	HCHON23022470	947	1192 1614	3390
55	HCHON20035420	948	356 811	3391
	HCHON23036760	949	228647	3392
	HCHON23040020	950	2571288	3393
	1.0.1014230-0020			

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	HCHON20043590	951	263712	3394
	HCHON20059870	952	1982297	3395
	HCHON20064590	953	662063	3396
	HCHON20067220	954	313642	3397
	HCHON20067700	955	160591	3398
10	HCHON20068410	956	116>2811	3399
	HCHON20068710	957	335688	3400
	HCHON20074820	958	19735	3401
	HCHON20076500	959	17782473	3402
15	HCHON20086720	960	133864	3403
,,	HCHON20097490	961	14342819	3404
	HCHON20100740	962	1381277	3405
	HEART20003060	963	1091407	3406
	HEART20005410	964	302784	3407
20	HEART20017730	965	192064	3408
	HEART20021840	966	22507	3409
	HEART20025980	967	2931180	3410
	HEART20034320	968	312013	3411
	HEART20037810	969	8031108	3412
74	HEART20049400	970	178549	3413
	HEART20049410	971	44613	3414
	HEART20049800	972	15509	3415
	HEART20061950	973	1531961	3416
ж	HEART20063340	974	2201281	3417
	HEART20067870	975	256855	3418
	HEART20067890	976	3338	3419
	HEART20072310	977	471057	3420
	HEART20074430	978	205540	3421
35	HEART20077670	979	901223	3422
	HEART20083640	980	1921376	3423
	HEART2008-940	981	1501523	3424
	HEAHT20090000	982	1972116	3425
40	HEART20095990	983	5231077	3426
	HHDPC100C0650	984	9201531	3427
	HHDPC100C0830	985	110520	3428
	HHDPC200C1040	986	20802442	3429
	HHDPC200C6920	987	17582066	3430
45	HHDPC20014320	988	5526	3431
	HHDPC20030490	989	71529	3432
	HHDPC20031130	990	3692249	3433
	HHDPC20034390	991	94705	3434
50 ·	HHDPC20034720	992	167868	3435
	HHDPC20057420	993	44484	3436
	HHDPC20057940	994	1393	3437
	HHDPC20064600	995	2311493	3438
	HHDPC20068620	996	5151816	3439
55	HHDPC20084140	997	1632109	3440
	HHDPC20091140	998	160504	3441
	HHDPC20091780	999	491623	3442
	1.1101 020031700	1 000		

Table 1 (continued)

ſ	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
1		sequence		sequence
5	HHDPC20092080	1000	133702	3443
١ -	HHDPC20095280	1001	332745	3444
	HLUNG10000550	1002	7291058	3445
	HLUNG20016330	1003	86>1958	3446
	HLUNG20016770	1004	9191242	3447
10	HLUNG20017120	1005	6441144	3448
	HLUNG20023340	1006	2281181	3449
!	HLUNG20033780	1007	1562285	3450
	HLUNG20084390	1008	542997	3451
	IMR3220002430	1009	341176	3452
15	KIDNE20002520	1010	221593	3453
	KIDNE20003940	1011	1871986	3454
	KIDNE20006780	1012	164829	3455
	KIDNE20007210	1013	27350	3456
20	KIDNE20007770	1014	271415	3457
	KIDNE20008010	1015	127>1986	3458
	KIDNE20009470	1016	9>2664	3459
	KIDNE20011170	1017	347817	3460
05	KIDNE20011400	1018	17982334	3461
25	KIDNE20013730	1019	373777	3462
	KIDNE20017130	1020	2261740	3463
	KIDNE20018730	1021	35631	3464
	KIDNE20018970	1022	232546	3465
30	KIDNE20020150	1023	2151645	3466
	KIDNE20021680	1024	1401096	3467
	KIDNE20021910	1025	152018	3468
	KIDNE20021980	1026	15781910	3469
35	KIDNE20022620	1027	1122277	3470
33	KIDNE20024830	1028	1912>2715	3471
	KIDNE20027250	1029	359955	3472
	KIDNE20027950	1030	97543	3473
	KIDNE20028390	1031	31519	3474
40	KIDNE20028720	1032	701122	3475
	KIDNE20028830	1033	1071258	3476
	KIDNE20029800	1034	10561358	3477 3478
	KIDNE20067330	1035	9301865	3479
45	KIDNE20079440	1036	192539	3479
43	KIDNE20096280	1037	2661354	3480
	KIDNE20096470	1038	31639	3482
	KIDNE20100070	1039	4712204	3483
	KIDNE20100840	1040	167778	3484
50	KIDNE20101370	1041	9503	3485
	KIDNE20101510	1042	621795	3486
	KIDNE20102650	1043	3221614 7911501	3487
	KIDNE20102710	1044		3488
<i>5</i> 5	KIDNE20104300	1045	188>1957 55411	3489
	KIDNE20106740	1046	85399	3490
	KIDNE20107390	1047	180641	3491
	KIDNE20107500	1048	1,00041	

Table 1 (continued)

		·	continued)	
	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO, of amino acid
		sequence		sequence
5	KIDNE20107620	1049	2222213	3492
	KIDNE20109730	1050	571121	3493
	RIDNE20109890	1051 、	254>2578	3494
	KIDNE20112000	1052	430750	3495
	KIDNE20115080	1053	761092	3496
10	KIDNE20118580	1054	9621387	3497
	KIDNE20120090	1055	13341813	3498
	KIDNE20121880	1056	192866	3499
	KIDNE20122910	1057	1623.,2006	3500
15	KIDNE20124400	1058	5322499	3501
	KIDNE20125630	1059	67504	3502
	KIDNE20126010	1060	9911407	3503
	KIDNE20126130	1061	285701	3504
	KIDNE20127100	1062	2651944	3505
20	KIDNE20127450	1063	5701088	3506
	KIDNE20127750	1064	1751488	3507
	KIDNE20130450	1065	177512	3508
	KIDNE20131580	1066	1941912	3509
05	KIDNE20132180	1067	8941256	3510
25	KIDNE20137340	1068	8891710	3511
	KIDNE20138010	1069	15642046	3512
	KIDNE20141190	1070	71856	3513
	KIDNE20144890	1071	385738	3514
30	KIDNE20148900	1072	487981	3515
	KIDNE20163880	1073	3271364	3516
	KIDNE20180710	1074	379855	3517
	KIDNE20181660	1075	11091564	3518
_	KIDNE20182690	1076	5532019	3519
35	KIDNE20186780	1077	8371541	3520
	KIDNE20190740	1078	321653	3521
	LIVER10001260	1079	14131748	3522
	LIVER10004790	1080	1121113	3523
40	LIVER20002160	1081	791944	3524
	LIVER20011130	1082	8981569	3525
	LIVER20011910	1083	27425	3526
	LIVER20028420	1084	13051724	3527
	LIVER20035110	1085	551940	3528
45	LIVER20035680	1086	8731283	3529
	LIVER20038540	1087	6308	3530
	LIVER20045650	1088	23592886	3531
	LIVER20055200	1089	82618	3532
50 °	LIVER20055440	1090	16112240	3533
	LIVER20059810	1091	15971899	3534
	LIVER20062510	1092	631999	3535
	LIVER20064100	1093	279785	3536
	LIVER20064690	1094	1721161	3537
55	LIVER20075680	1095	25682939	3538
	LIVER20080530	1096	441426	3539
	LIVER20084730	1097	240788	3540
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Table 1 (continued)

Γ	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
-	ļ	sequence		sequence
5	LIVER20085800	1098	99416	3541
	LIVER20087060	1099	1402056	3542
-	LIVER20087510	1100 -	4781200	3543
Ì	LIVER20091180	1101	18374	3544
ŀ	MAMGL10000830	1102	401551	3545
10	MESAN10001260	1103	802137	3546
1	MESAN20004570	1104	354>2589	3547
	MESAN20014500	1105	781976	3548
	MESAN20025190	1106	16792323	3549
	MESAN20027090	1107	144653	3550
15	MESAN20029400	1108	210>2998	3551
	MESAN20031900	1109	1382348	3552
	MESAN20035290	1110	99797	3553
	MESAN20036460	1111	12031844	3554
20	MESAN20038510	1112	6391016	3555
,	MESAN20089360	1113	386802	3556
	MESAN20101140	1114	250504	3557
	MESAN20103120	1115	1431201	3558
	MESAN20106640	1116	71712	3559
25	MESAN20115970	1117	234644	3560
	MESAN20121130	1118	7942	3561
	MESAN20125860	1119	13961875	3562
	MESAN20127350	1120	2971724	3563
30	MESAN20130220	1121	1061626	3564
	MESAN20132110	1122	13632433	3565
	MESAN20136110	1123	1881582	3566
	MESAN20138450	1124	249647	3567
0.5	MESAN20139360	1125	195611	3568
<b>3</b> 5	MESAN20141920	1126	2502724	3569
	MESAN20152770	1127	64585	3570
	MESAN20153910	1128	141443	3571
	MESAN20154010	1129	24620	3572
40	MESAN20157080	1130	13361677	3573
	MESAN20161590	1131	7671081	3574
	MESAN20164090	1132	2732471	3575
	MESAN20171520	1133	103774	3576
16	MESAN20174170	1134	13751743	3577
45	MESAN20182090	1135	5>2440	3578
	MESAN20186700	1136	1333>3058	3579
	NESOP10001080	1137	1491489	3580
	NOVAR10000150	1138	14701895	3581
50	NOVAR10000910	1139	2471482	3582 3583
	NOVAR10001020	1140	136519	1
	NOVAR20000380	1141	422844	3584 3585
	NOVAR20003520	1142	8981377	3586
55	NT2NE20003740	1143	28555	3587
J	NT2NE20010050	1144	12401725	3588
	NT2NE20010210	1145	231626	3589
	NT2NE20010400	1146	9231546	1 3303

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleot tie	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	NT2NE20010490	1147	1051499	3590
	NT2NE20015240	1148	251646	3591
	NT2NE20021620	1149	7852266	3592
	NT2NE20043780	1150	8151285	3593
	NT2NE20053580	1151	9413	3594
10	NT2NE20068130	1152	2371601	3595
	NT2NE20072200	· . 1153	94855	3596
	NT2NE20074250	1154	9377	3597
	NT2NE20080170	1155	1292219	3598
15	NT2NE20089610	1156	19762329	3599 .
	NT2NE20089970	1157	150488	3600
	NT2NE20108540	1158	504806	3601
	NT2NE20110360	1159	44415	3602
	NT2NE20118960	1160	1972044	3603
20	NT2NE20122430	1161	14742016	3604
	NT2NE20124480	1162	135482	3605
	NT2NE20125050	1163	591462	3606
	NT2NE20130190	1164	7281438	3607
25	NT2NE20131890	1165	22762611	3608
	NT2NE20132170	1166	5851694	3609
	NT2NE20142210	1167	1772585	3610
	NT2NE20146810	1168	387707	3611
	NT2NE20152750	1169	190726	3612
30	NT2NE20155110	1170	486893	3613
	NT2NE20156260	1171	286633	3614
	NT2NE20157470	1172	2221199	3615
	NT2NE20158600	1173	348749	3616
35	NT2NE20159740	1174	<b>6</b> წ <b>664</b>	3617
	NT2NE20172590	1175	7991131	3618
	NT2NE20174800	1176	525860	3619
	NT2NE20174920	1177	5 <b>3</b> . 5 <b>38</b>	3620
	NT2NE20177520	1178	636 .2108	3621
40	NT2NE20181650	1179	496 1605	3622
	NT2NE20183760	1180	1087 .1548	3623
	NT2NE20184900	1181	2947 .>3371	3624
	NT2NE20187390	1182	170580	3625
45	NT2RI20001330	1183	841901	3626
	NT2RI20003480	1184	1661905	3627
	NT2RI20005750	1185	661088	3628
	NT2RI20009870	1186	1271053	3629
	NT2RI20022600	1187	10401621	3630
50	NT2RI20023160	1188	165947	3631
	NT2RI20023590	1189	6661058	3632
	NT2RI20023910	1190	5462945	3633
	NT2RI20025400	1191	315902	3634
55	NT2RI20025640	1192	9891650	3635
	NT2RI20028470	1193	1401297	3636 3637
	NT2RI20036670 NT2RI20040930	1194 1195	334852 3621075	3637 3638
	141211120040930	1133	3021073	3000

Table 1 (continued)

ſ	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO, of amino acid
5		sequence		sequence
	NT2RI20040990	1196	1242169	3639
	NT2RI20041880	1197	791368	3640
	NT2RI20046080	1198	36824	3641
10	NT2RI20048840	1199	3301349	3642
	NT2RI20050960	1200	2231701	3643
	NT2RI20054050	1201	1722154	3644
	NT2RI20055790	1202	4891178	3645
	NT2RI20056700	1203	1151491	3646
	NT2RI20069730	1204	6071209	3647
	NT2RI20076290	1205	1451197	3648
15	NT2RI20086220	1206	671068	3649
	NT2RI20091730	1207	113>2585	3650
	NT2RI20091940	1208	699118	3651
	NT2RI20198260	1209	70372	3652
20	NT2RI20203900	1210	176487	3653
	NT2RI20207030	1211	331181	3654
	NT2RI20216250	1212	8121312	3655
	NT2RI20240080	1213	1761090	3656
	NT2RI20244600	1214	1951010	3657
25	NT2RI20244960	1215	161595	3658
	NT2RI20250750	1216	263186	3659
	NT2RI20252550	1217	927. 1622	3660
	NT2RI20273230	1218	401215	3661
30	NT2RP60000770	1219	11472223	3662
	NT2RP60000850	1220	44. >2927	3663
	NT2RP70010740	1221	23 466	3664
	NT2RP70027380	1222	86 .3466	3665
25	NT2RP70032610	1223	10482514	3666
35	NT2RP70036880	1224	1 51491	3667
	NT2RP70037240	1225	2.212002	3668
	NT2RP70043480	1226	34. 1912	3669
	NT2RP70044280	1227	∴11506	3670
40	NT2RP70045590	1228	29877	3671
	NT2RP70056750	1229	1773578	3672
	NT2RP70062230	1230	3102748	3673 3674
	NT2RP70063950	1231	4993750	3675
45	NT2RP70072690	1232	11081545	3676
45	NT2RP70075240	1233	308814	3677
	NT2RP70077660	1234	20252441	3678
50	NT2RP70078420	1235	6222025	3679
	NT2RP70080850	1236	594003	3680
	NT2RP70081610	1237	41730	3681
	NT2RP70085440	1238	18562317	3682
	NT2RP70102350	1239	2251043	3683
	NT2RP70105210	1240	1321880	3684
<b>5</b> 5	NT2RP70110860	1241	8031129 271627	3685
55	NT2RP70111320	1242	7891112	3686
	NT2RP70122910	1243	10624	3687
	NT2RP70125160	1244	10024	

Table 1 (continued)

Clone name SEQ ID NO. of no sequence SEQ ID	sequence 372692 3688 109972 3689
5     NT2RP70130020     1245       NT2RP70133740     1246       NT2RP70134990     1247       NT2RP70137290     1248	372692 3688 109972 3689 24392 3690
NT2RP70133740 1246 NT2RP70134990 1247 NT2RP70137290 1248	109972 3689 24392 3690
NT2RP70134990 1247 NT2RP70137290 1248	24392 3690
NT2RP70137290 1248	
; I	10381 3691
NT2RP70137640 1249	
	315>2113 3692
<sup>10</sup> NT2RP70143480 1250	4821177 3693
NT2RP70147210 · . 1251	258566 3694
NT2RP70150800 1252	32445 3695
NT2RP70157890 1253	1701006 3696
15 NT2RP70159960 1254	308967 3697
NT2RP70169110 1255	123485 3698
NT2RP70175670 1256	89421 3699
NT2RP70179710 1257	942604 3700
NT2RP70181970 1258	59364 3701
20 NT2RP70188020 1259	380796 . 3702
NT2RP70188710 1260	4911024 3703
NT2RP70190640 1261	721880 3704
NT2RP70192730 1262	1801253 3705
NT2RP70194450 1263	10741901 3706
NT2RP70195430 1264	2011256 3707
NT2RP70198350 1265	131832 3708
NT2RP70203790 1266	2156>2479 3709
NTONG20009770 1267	1241947 3710
30 NTONG20013620 1268	17982325 3711
NTONG20015870 1269	651627 3712
NTONG20028070 1270	9545 3713
NTONG20029480 1271	3181898 3714
35 NTONG20029700 1272	2421693 3715
NTONG20046140 1273	3081108 3716
NTONG20048060 1274	14881961 3717
NTONG20049910 1275	47679 3718
NTONG20050620 1276	141521 3719
40 NTONG20050860 1277	59877 3720
NTONG20051530 1278	781697 3721
NTONG20052650 1279	84>2351 3722
NTONG20056570 1280	2261326 3723
NTONG20061870 1281	100996 3724
<sup>45</sup> NTONG20063010 1282	2191856 3725
NTONG20064400 1283	111330 3726
NTONG20064840 1284	15002447 3727
NTONG20065010 1285	156494 3728
50 NTONG20066460 1286	1211458 3729
NTONG20067090 1287	10461513 3730
NTONG20067830 1288	171006 3731
NTONG20070200 1289	3181418 3732
NTONG20070340 1290	2841228 3733
<sup>55</sup> NTONG20075220 1291	242>2591 3734
NTONG20076930 1292	261534 3735
NTONG20077560 1293	241567 3736

Table 1 (continued)

ſ	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	NTONG20083650	1294	2421711	3737
	NTONG20088620	1295	60>2536	3738
l	NTONG20090600	1296	5171134	3739
	NTONG20090680	1297	6731389	3740
10	NTONG20092290	1298	3071539	3741
	NTONG20092330	1299	2292235	3742
	OCBBF10000540	1300	8581916	3743
	OCBBF10001750	1301	2451144	3744
	OCBBF10001850	1302	4192233	3745
	OCBBF20005230	1303	56640	3746
15	OCBBF20006770	1304	292275	3747
	OCBBF20013890	1305	19782289	3748
	OCBBF20019380	1306	691364	3749
	OCBBF20019830	1307	3251536	3750
20	OCBBF20020150	1308	25072917	3751
	OCBBF20020830	1309	922869	3752
	OCBBF20022900	1310	881779	3753
	OCBBF20023570	1311	471276	3754
	OCBBF20026630	1312	18455	3755
25	OCBBF20028050	1313	1281108	3756
	OCBBF20028650	1314	7062286	3757
	OCBBF20029800	1315	334699	3758
	OCBBF20030280	1316	263898	3759
30	OCBBF20030910	1317	3831258	3760
	OCBBF20032460	1318	347805	3761
	OCBBF20035930	1319	65895	3762
	OCBBF20037440	1320	4131024	3763
	OCBBF20039250	1321	24821	3764
35	OCBBF20041680	1322	9671278	3765
	OCBBF20045330	1323	14071886	3766
	OCBBF20046120	1324	821641	3767
	OCBBF20046470	1325	4001137	3768
40	OCBBF20046690	1326	1561730	3769
	OCBBF20047570	1327	182577	3770
	OCBBF20048660	1328	292663	3771
	OCBBF20049300	1329	7212553	3772
	OCBBF20049840	1330	246>2607	3773
45	OCBBF20050770	1331	724>2679	3774
	OCBBF20051610	1332	41493	3775
50 .	OCBBF20053430	1333	5862478	3776
	OCBBF20053490	1334	7361068	3777
	OCBBF20053730	1335	872090	3778
	OCBBP20054200	1336	315869	3779
	OCBBF20054760	1337	1951016	3780
	OCBBF20059560	1338	224>3045	3781
	OCBBF20060300	1339	13892171	3782
	OCBBF20061720	1340	7111139	3783
	OCBBF20062140	1341	444749	3784
	OCBBF20062410	1342	19202240	3785

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	OC3B=20063320	1343	145519	3786
	OC3B=20066390	1344	21592713	3787
	OC3B=20068490	1345 、	152702	3788
	OC3BF20071210	1346	20293486	3789
	OC3B=20071840	1347	45:.1670	3790
10	OC38=20071960	1348	12941698	3791
	OC3BF20072240	1349	3351432	3792
	OC38=20072320	1350	17492087	3793
	OC3BF20073540	1351	561132	3794
15	OC3B=20074140	1352	81>3793	3795
,,	OC3BF20076220	1353	15522013	3796
	OC3BF20078920	1354	8491340	3797
	OC3BF20079310	1355	2401349	3798
	OC3B=20079460	1356	122099	3799
20	OC3B=20080050	1357	1592150	3800
	OC3B=20080410	1358	1221672	3801
	OC3BF20081380	1359	7421140	3802
	OC3BF20082830	1360	1391209	3803
25	OC3BF20084660	1361	741621	3804
25	OCBBF20085200	1362	6591207	3805
	OC3BF20086400	1363	63797	3806
	OC3BF20086910	1364	5412304	3807
	OC3BF20087010	1365	325633	3808
30	OCBBF20088140	1366	1575. 1916	3809
	OC3B=20088220	1367	25052915	3810
	OCBBF20091150	1368	256648	3811
	OCBB=20074240	1369	821122	3812
26	OCBBF20097720	1370	471815	3813
35	OCBBF20100400	1371	4073043	3814
	OC3BF20103130	1372	1141439	3815
	OC3B=20104040	1373	310612	3816
	OCBB-20105570	1374	24042874	3817
10	OC3BF20107090	1375	1271935	3818
	OC3BF20107920	1376	16922018	3819
	OC3BF20108190	1377	2781591	3820
	OC3BF20108430	1378	8321851	3821
	OC3BF20108580	1379	11522354	3822
45	OC3B220108630	1380	2491133	3823
	OC38F20109310	1381	342355	3824
	OC38F20111770	1382	291629	3825
	OCBB=20116850	1383	1172354	3826
50 ·	OCBBF20118970	1384	361855	3827
	OCBBF20120390	1385	1292282	3828
	OC3BF20121390	1386	5242254	3829
	OCBB=20122620	1387	9901544	3830
	OC3B=20124360	1388	12231951	3831
55	OCBBF20125530	1389	3792310	3832
	OC3B-20126780	1390	12701599	3833
	OC3B=20127040	1391	1772327	3834

Table 1 (continued)

1		SEC ID NO. of publication	Position of CDS	SEQ ID NO. of amino acid
	Clone name	SEQ ID NO. of nucleotide sequence	Fosition of ODO	sequence
	0000000107110	1392	10181530	3835
5	OCBBP20127140	1393	103>2362	3836
	OCBBF20127550	1394	1181311	3837
	OCBBF20128120		378>3283	3838
	OCBBF20129360	1395 1396	132452	3839
10	OCBBF20130110		25272892	3840
,,	OCBBF20130910	1397	11723331	3841
	OCBBF20132850	1398	1	3842
	OCBBF20139260	1399	7722592	3843
	OCBBF20140640	1400	241894	3844
15	OCBBF20140890	1401	39>4369	3845
	OCBBF20145760	1402	8941757	i
	OCBBF20148280	1403	871787	3846
	OCBBF20148730	1404	501855	3847
	OCBBF20149280	1405	13852035	3848
20	OCBBF20151150	1406	1352216	3849
	OCBBF20153340	1407	135>2621	3850
	OCBBF20153350	1408	16161942	3851
	OCBBF20155060	1409	1023245	3852
25	OCBBF20164050	1410	50370	3853
	OCBBF20164670	1411	401077	3854
	OCBBF20170690	1412	159503	3855
	OCBBF20173060	1413	63383	3856
	OCBBF20173250	1414	315692	3857
30	OCBBF20173980	1415	2621857	3858
	OCBBF20178150	1416	12452231	3859
	OCBBP20178880	1417	27403207	3860
	OCBBP20178990	1418	13281819	3861
25	OCBBF20180120	1419	2181780	3862
35	OCBBF20180840	1420	11691540	3863
	OCBBF20186870	1421	12781736	3864
	OCBBF20188730	1422	320766	3865
	OCBBF20189560	1423	15122165	3866
40	PANCR10000910	1424	1219>1943	3867
	PEBLM10000240	1425	306674	3868
	PEBLM10000710	1426	17191940	3869
	PEBLM20013120	1427	26952	3870
	PEBLM20024320	1428	6121406	3871
45	PEBLM20024550	1429	11791499	3872
	PEBLM20040150	1430	17312165	3873
	PEBLM20042900	1431	226>2439	3874
	PEBLM20044520	1432	9221974	3875
50 .	PEBLM20052820	1433	411782	3876
-	PEBLM20060310	1434	1731>2083	3877
	PEBLM20060360	1435	58330	3878
	PEBLM20060490	1436	431892	3879
	PEBLM20071880	1437	497814	3880
55	PEBLM20072960	1438	1281093	3881
	PEBLM20074370	1439	60458	3882
	PEBLM20075980	1440	531153	3883
	, 252,425075550	1		

Table 1 (continued)

		lable 1 (c		
	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	PEBLM20078320	1441	51672	3884
	PEBLM20085760	1442	122763	3885
	PERIC10000250	1443 .	6891516	3886
	PERIC20002140	1444	1511239	3887
	PERIC20003860	1445	33359	3888
10	PERIC20003870	1446	402817	3889
	PERIC20004220	1447	1301935	3890
	PERIC20004780	1448	132956	3891
	PLACE50000660	1449	3292527	3892
15	PLACE60003480	1450	35877	3893
.,	PLACE60004630	1451	216533	3894
	PLACE60060420	1452	34246	3895
	PLACE60079250	1453	336>3307	3896
	PLACE60086400	1454	279764	3897
20	PLACE60119750	1455	28570	3898
	PLACE60121080	1456	7691182	3899
	PLACE60136500	1457	19002241	3900
	PLACE60136720	1458	782519	3901
0.5	PLACE60138830	1459	7501202	3902
25	PLACE60153220	1460	247561	3903
	PLACE60155130	1461	8331171	3904
	PLACE60161600	1462	771099	3905
	PLACE60169420	1463	1651097	3906
30	PLACE60177140	1464	13212190	3907
	PLACE60181070	1465	13551708	3908
	PLACE60187690	1466	16061941	3909
	PLACE60188340	1467	4301224	3910
	PROST10003220	1468	187933	3911
35	PROST10004800	1469	87419	3912
	PROST20005050	1470	6731164	3913
	PROST20005670	1471	1132>2293	3914
	PROST20021010	1472	612926	3915
40	PROST20024890	1473	14514	3916
	PROST20029270	1474	10161363	3917
	PROST20047270	1475	13002250	3918
	PROST20047390	1476	1632283	3919
	PROST20050670	1477	16222074	3920
45	PROST20052280	1478	326634	3921
	PROST20057930	1479	237>2116	3922
	PROST20059040	1480	10471355	3923
	PROST20066880	1481	19372521	3924
50 ·	PROST20079500	1482	8631957	3925
	PROST20083600	1483	2091087	3926
	PROST20087700	1484	4811287	3927
	PROST20097950	1485	91405	3928
	PROST20100460	1486	631796	3929
55	PROST20104000	1487	10592012	3930
	PROST20107820	1488	3041524	3931
	PROST20111050	1489	7721281	3932
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Table 1 (continued)

ſ	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
	1	sequence		sequence
5	PROST20112970	1490	66671	3933
	PROST20114390	1491	12911749	3934
ł	PROST20115600	1492	4339	3935
	PROST20120050	1493	176589	3936
1	PROST20120160	1494	283597	3937
10	PROST20121900	1495	68385	3938
	PROST20123530	1496	16192044	3939
ļ	PROST20127400	1497	11561524	3940
	PROST20127800	1498	9422120	3941
15	PROST20130530	1499	4161588	3942
'	PROST20132600	1500	14472040	3943
i	PROST20133270	1501	2529	3944
	PROST20144220	1502	10111367	·3945
	PROST20146010	1503	2981953	3946
20	PROST20149160	1504	16771991	3947
	PROST20149250	1505	6351201	3948
	PROST20151240	1506	300938	3949
	PROST20152460	1507	15422084	3950
05	PROST20153320	1508	184540	3951
25	PROST20159240	1509	286612	3952
	PROST20161950	1510	90716	3953
	PROST20164440	1511	25703004	3954
	PROST20166680	1512	53874	3955
30	PROST20168290	1513	17572143	3956
	PROST20169800	1514	1681763	3957
	PROST20170980	1515	281245	3958
	PROST20171280	1516	3061493	3959
35	PROST20175290	1517	15382323	3960
33	PROST20176170	1518	9982053	3961
	PROST20178360	1519	72566	3962
	PROST20185830	1520	12002015	3963
	PROST20189770	1521	2192018	3964
40	PROST20191640	1522	3181229	3965
	PUAEN10000850	1523	1212040	3966
	PUAEN20003740	1524	104409	3967
	PUAEN20011880	1525	282028	3968
45	PUAEN20015260	1526	141881	3969
	PUAEN20015860	1527	711846	3970
	PUAEN20018820	1528	411870	3971
	PUAFN20025680	1529	6671584	3972
	PUAEN20027580	1530	36512	3973 3974
50	PUAEN20030180	1531	127978	3975
	PUAEN20040670	1532	3262644	3975
	PUAEN20044000	1533	541957	3977
	PUAEN20045110	1534	335886	3977
55	PUAEN20045250	1535	3351054	3979
	PUAEN20051100	1536	2281319	3980
	PUAEN20052470	1537	16992046 2952553	3981
	PUAEN20055020	1538	2952555	1 3301

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
ĺ		sequence		sequence
5	PUAEN20078980	1539	6989	3982
	PUAEN20081230	1540	62469	3983
	PUAEN20083140	1541	1041687	3984
	PUAEN20085150	1542	167502	3985
	PUAEN20108240	1543	21993	3986
10	RECTM10001410	1544	4261631	3987
	RECTM20003490	1545	8761193	3988
	RECTM20005100	1546	1491273	3989
	SALGL10001710	1547	2711722	3990
15	SKMUS20001980	1548	751034	3991
	SKMUS20003610	1549	86910	3992
	SKMUS20007010	1550	24977	3993
İ	SKMUS20007800	1551	708>1835	3994
	SKMUS20011640	1552	16408	3995
20	SKMUS20012010	1553	3001019	3996
	SKMUS20016220	1554	801267	3997
	SKMUS20018230	1555	98442 ·	3998
	SKMUS20018500	1556	2731172	3999
.,,	SKMUS20020840	1557	791014	4000
	SKMUS20021530	1558	4322135	4001
	SKMUS20024750	1559	2011208	4002
	SKMUS20028210	1560	358753	4003
	SKMUS20028400	1561	18644	4004
30	SKMUS20029200	1562	1741130	4005
	SKMUS20031680	1563	171485	4006
	SKMUS20046670	1564	234617	4007
	SKMUS20048970	1565	1041132	4008
35	SKMU320049030	1566	1911096	4009
	SKMUS20077400	1567	170772	4010
	SKMUS20084740	1568	83>1516	4011
	SKNM020006220	1569	11761856	4012
	SKNSH20008190	1570	4902289	4013
40	SKNSH20020540	1571	21842924	4014
	SKNSH20028660	1572	192581	4015
	SKNSH20031740	1573	120563	4016
	SKNSH20034660	1574	562996	4017
45	SKNSH20051940	1575	10061488	4018
	SKNSH20062340	1576	85453	4019
	SKNSH20063040	1577	91768	4020
	SKNSH20080430	1578	81524	4021
	SKNSH20087770	1579	107>1808	4022
50 Î	SKNSH20089400	1580	341092	4023
	SKNSH20091970	1581	181489	4024
	SMINT20001760	1582	2671706	4025
	SMINT20005410	1583	138557	4026
55	SMINT20008240	1584	11231500	4027
33	SMINT20009840	1585	31750	4028
	SMINT20011140	1586	12541664	4029
	SMINT20011580	1587	131811	4030

Table 1 (continued)

F	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
1	Clone hame	sequence		sequence
-	SMINT20011990	1588	132512	4031
5	SMINT20013480	1589	87686	4032
į	SMINT20014580	1590	57410	4033
1	SMINT20014580 SMINT20015590	1591	13751818	4034
	SMINT20013390 SMINT20022020	1592	133726	4035
10	SMINT20022020	1593	8901345	4036
	SMINT20023200 SMINT20024570	1594	18522370	4037
	SMINT20024370 SMINT20026890	1595	5412790	4038
	SMINT20028820	1596	12401749	4039
	SMINT20028820	1597	236 1282	4040
15	SMINT20029780 SMINT20033170	1598	539 931	4041
	_	1599	20 778	4042
	SMINT20033400 SMINT20035690	1600	11 1411	4043
		1601	39 1169	4044
20	SMINT20040860 SMINT20042990	1602	397 750	4045
		1603	109588	4046
	SMINT20047810	1604	99641	4047
	SMINT20049090 SMINT20050750	1605	101907	4048
	SMINT20050750	1606	561513	4049
25	1	1607	12511598	4050
	SMINT20053300 SMINT20053870	1608	85894	4051
	SMINT20055870	1609	356754	4052
	SMINT20058210 SMINT20058000	1610	200565	4053
30	SMINT20058000 SMINT20060780	1611	18554	4054
30	SMINT20065960	1612	8591314	4055
	SMINT20068910	1613	136.,1026	4056
	SMINT20088010	1614	2121183	4057
	SMINT20071400 SMINT20073650	1615	591549	4058
35	SMINT20076470	1616	16781983	4059
	SMINT20080540	1617	12801606	4060
	SMINT20089170	1618	54530	4061
	SMINT20092330	1619	169858	4062
40	SMINT20092720	1620	16402293	4063
40	SMINT20095050	1621	7331107	4064
	SMINT20098320	1622	112465	4065
	SMINT20100680	1623	237614	4066
	SMINT20101440	1624	1872109	4067
45	SMINT20102780	1625	261642	4068
	SMINT20103690	1626	208960	4069
	SMINT20105000	1627	194514	4070
	SMINT20105330	1628	15802020	4071
50 ·	SMINT20106290	1629	5011802	4072
50	SMINT20106720	1630	801498	4073
	SMINT20108530	1631	185523	4074
	SMINT20109970	1632	1444>1974	4075
	SMINT20110330	1633	13982222	4076
55	SMINT20110660	1634	11081500	4077
	SMINT20112730	1635	801564	4078
	SMINT20115880	1636	6791746	4079
	0	<u>_1</u>		

Table 1 (continued)

	Table 1 (continued)			
	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	SMINT20121220	1637	263>1798	4080
	SMINT20121950	1638	6443	4081
	SMINT20122850	1639	454777	4082
	SMINT20122910	1640	15162094	4083
	SMINT20127350	1641	6221449	4084
10	SMINT20127930	1642	671554	4085
	SMINT20130320	1643	1782601	4086
	SMINT20131810	1644	5831257	4087
	SMINT20132280	1645	293655	4088
15	SMINT20136130	1646	12911752	4089
	SMINT20138900	1647	871439	4090
	SMINT20144430	1648	54647	4091
	SMINT20144800	1649	1711394	4092
	SMINT20144890	1650	209520	4093
20	SMINT20152940	1651	386985	4094
	SMINT20153260	1652	1351838	4095
:	SMINT20153530	1653	11861524	4096
	SMINT20154540	1654	1071339	4097
25	SMINT20155180	1655	20763	4098
23	SMINT20157450	1656	6691118	4099
	SMINT20158100	1657	30587	4100
	SMINT20161220	1658	3971977	4101
	SMINT20162860	1659	36494	4102
30	SMINT20163960	1660	6651036	4103
	SMINT20164400	1661	125706	4104
	SMINT20164770	1662	529870	4105
	SMINT20168570	1663	15932069	4106
35	SMINT20173190	1664	251829	4107
35	SMINT20173240	1665	253582	4108
	SMINT20174360	1666	9781733	4109
	SMINT20177360	1667	172771	. 4110
	SMINT20178550	1668	51692	4111
40	SMINT20179740	1669	781865	4112
	SMINT20183530	1670	11302530	4113
	SMINT20190170	1671	801567	4114
	SMINT20191420	1672	491365	4115
<b>4</b> 5	SMINT20191530	1673	402040	4116
<b>→</b> 3	SMINT20192000	1674	49435	4117
	SPLEN10000830	1675	1586 2053	4118
	SPLEN20000640	1676	27 755	4119
	SPLEN20002220	1677	87 434	4120
50 ·	SPLEN20003070	1678	684 1046	4121
	SPLEN20006070	1679	78 2837	4122
	SPLEN20008390	1680	375 2378	4123
	SPLEN20008740	1681	66 1547	4124
	SPLEN20008820	1682	31 1872	4125
55	SPLEN20011410	1683	199 2394	4126
	SPLEN20013540	1684	978 1310	4127
	SPLEN20016260	1685	9061748	4128
1				

Table 1 (continued)

ſ	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
l	Ciono name	sequence	, 33	sequence
_ }	SPLEN20019450	1686	180680	4129
5	SPLEN20020070	1687	65451	4130
l	SPLEN20021660	1688	130771	4131
	SPLEN20022230	1689	1331026	4132
	SPLEN20023140	1690	11531605	4133
10	SPLEN20026950	1691	8553383	4134
	SPLEN20027440	1692	292488	4135
	SPLEN20029310	1693	70585	4136
	SPLEN20031600	1694	16582083	4137
	SPLEN20032040	1695	357746	4138
15	SPLEN20032190	1696	441785	4139
	SPLEN20033960	1697	161026	4140
-	SPLEN20039240	1698	11771929	4141
	SPLEN20040600	1699	60368	4142
20	SPLEN20054290	1700	1872421	4143
	SPLEN20034230 SPLEN20076530	1701	254586	4144
	SPLEN20077500	1702	791941	4145
	SPLEN20079260	1703	5351506	4146
	SPLEN20079510	1704	1880>2197	4147
.74	SPLEN20084600	1705	13 1878	4148
	SPLEN20095410	1706	816 1541	4149
	SPLEN20095550	1707	193 >2558	4150
	SPLEN20095810	1708	248 670	4151
<i>3</i> 0	SPLEN20097330	1709	1448 1849	4152
	SPLEN20099700	1710	91 >3025	4153
	SPLEN20101190	1711	18642250	4154
	SPLEN20103950	1712	25507	4155
	SPLEN20106250	1713	295711	4156
35	SPLEN20117660	1714	6621099	4157
	SPLEN20118300	1715	3321486	4158
	SPLEN20119810	1716	5261644	4159
	SPLEN20121750	1717	4641021	4160
40	SPLEN20126190	1718	2742688	4161
	SPLEN20128000	1719	961664	4162
	SPLEN20129610	1720	207557	4163
	SPLEN20140800	1721	3872144	4164
	SPLEN20141360	1722	491799	4165
45	SPLEN20141990	1723	443745	4166
	SPLEN20142100	1724	301996	4167
	SPLEN20143180	1725	50448	4168
	SPLEN20144520	1726	20022463	4169
50	SPLEN20145720	1727	1205>1939	4170
	SPLEN20146450	1728	362862	4171
	SPLEN20146690	1729	19662550	4172
	SPLEN20147110	1730	3132067	4173
	SPLEN20147390	1731	1691479	4174
55	SPLEN20149110	1732	2769	4175
	SPLEN20149190	1733	26364	4176
	SPLEN20149240	1734	7872490	4177

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	SPLEN20150940	1735	792385	4178
	SPLEN20151210	1736	661715	4179
	SPLEN20152610	1737	9861453	4180
	SPLEN20152760	1738	284628	4181
	SPLEN20157300	1739	426728	4182
10	SPLEN20157880	1740	35769	4183
	SPLEN20158900	• . 1741	16432032	4184
	SPLEN20158990	1742	8431172	4185
	SPLEN20160450	1743	5521115	4186
15	SPLEN20160690	1744	7341099	4187
.5	SPLEN20160980	1745	124456	4188
	SPLEN20162680	1746	6462007	4189
	SPLEN20163560	1747	862173	4190
	SPLEN20165310	1748	801492	4191
20	SPLEN20166270	1749	11341814	4192
	SPLEN20167200	1750	223570	4193
	SPLEN20169220	1751	160576	4194
	SPLEN20169720	1752	722492	4195
25	SPLEN20170310	1753	1251039	4196
25	SPLEN20171210	1754	7837	4197
	SPLEN20171470	1755	412272	4198
	SPLEN20171890	1756	13121716	4199
	SPLEN20172120	1757	138 500	4200
30	SPLEN20173510	1758	235 1785	4201
	SPLEN20174260	1759	99 428	4202
	SPLEN20176200	1760	36 431	4203
	SPLEN20179180	1761	173 1201	4204
35	SPLEN20179810	1762	1374 3224	4205
33	SPLEN20181810	1763	641 1183	4206
	SPLEN20186430	1764	80 979	4207
	SPLEN20193110	1765	1744 2118	4208
	SPLEN20194050	1766	1351 2331	4209
40	SPLEN20198110	1767	1260 1562	4210
	SPLEN20204170	1768	202 594	4211
	SPLEN20211220	1769	601 1500	4212
	SPLEN20211570	1770	174 521	4213
45	SPLEN20211940	1771	241 1155	4214
	SPLEN20212730	1772	979 1830	4215
	SPLEN20212950	1773	283 2055	4216
	SPLEN20213830	1774	137 460	4217
	SPLEN20214400	1775	28 387	4218
50	SPLEN20214580	1776	300 602	4219
	SPLEN20222270	1777	241 927	4220
	SPLEN20225220	1778	672 1199	4221
	SPLEN20242320	1779	136 522	4222
<i>55</i>	SPLEN20242730	1780	2343 2732	4223
<i>J</i> J	SPLEN20243830	1781	197 556	4224
	SPLEN20245300	1782	945 1529	4225
	SPLEN20249560	1783	8891584	4226

Table 1 (continued)

ſ	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	SPLEN20250170	1784	4573012	4227
,	SPLEN20250390	1785	13271788	4228
	SPLEN20252190	1786	14132609	4229
	SPLEN20261440	1787	511894	4230
	SPLEN20264110	1788	11951662	4231
10	SPLEN20267650	1789	391331	4232
	SPLEN20273950	1790	6081222	4233
	SPLEN20279950	1791	18742518	4234
	SPLEN20280660	1792	12861612	4235
	SPLEN20283650	1793	13621	4236
15	SPLEN20284240	1794	2821175	4237
	SPLEN20292950	1795	92456	4238
	SPLEN20293800	1796	73858	4239
	SPLEN20303970	1797	7781104	4240
20	SPLEN20304950	1798	71011	4241
	SPLEN20305620	1799	13561853	4242
	SPLEN20329240	1800	5361	4243
	STOMA20001830	1801	811574	4244
	STOMA20005390	1802	591567	4245
25	STOMA20005670	1803	811478	4246
	STOMA20006400	1804	801687	4247
	STOMA20006780	1805	411975	4248
	STOMA20006860	1806	12721988	4249
<i>30</i>	STOMA20008880	1807	1121485	4250
	STOMA20010250	1808	66419	4251
	STOMA20013890	1809	21512486	4252
	STOMA20026880	1810	548874	4253
35	STOMA20032890	1811	17102600	4254
33	STOMA20034770	1812	811583	4255
	STOMA20036460	1813	311772	4256
	STOMA20046680	1814	7681154	4257
	STOMA20048520	1815	160663	4258
40	STOMA20048840	1816	9361487	4259
	STOMA20051200	1817	140619	4260
	STOMA20056640	1818	49555	4261
	STOMA20056670	1819	811556	4262
45	STOMA20057820	1820	601226	4263
43	STOMA20062130	1821	35427	4264
	STOMA20062290	1822	289693	4265
	STOMA20063250	1823	109438	4266 4267
	STOMA20063980	1824	97480	4268
50	STOMA20064470	1825	781118	4269
	STOMA20067800	1826	35397	4270
	STOMA20069040	1827	364792	4270
	STOMA20072690	1828	351701 311 784	4272
55	STOMA20076800	1829		4273
30	STOMA20077450	1830	780 2300 59 1735	4274
	STOMA20080500	1831	80 1564	4275
	STOMA20083610	1832	1 80 1304	1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	STOMA20086140	1833	201 746	4276
	STOMA20088380	1834	48 1535	4277
	STOMA20092530	1835	80 1501	4278
	STOMA20092560	1836	68 439	4279
	STOMA20092890	1837	105 1223	4280
10	SYNOV20001520	1838	25 735	4281
	SYNOV20001730	1839	561480	4282
	SYNOV20002510	1840	791629	4283
	SYNOV20002790	1841	591480	4284
15	SYNOV20002970	1842	561471	4285
,5	SYNOV20003970	1843	357881	4286
	SYNOV20004260	1844	801489	4287
	SYNOV20007000	1845	551485	4288
	SYNOV20008240	1846	611494	4289
20	SYNOV20009230	1847	401515	4290
	SYNOV20010880	1848	611479	4291
	SYNOV20011110	1849	561468	4292
	SYNOV20013000	1850	301433	4293
	SYNOV20013560	1851	791494	4294
25	SYNOV20013900	1852	811499	4295
	SYNOV20017080	1853	4661905	4296
	SYNOV30001840	1854	1462443	4297
	TBAES20000590	1855	1697 >2237	4298
30	TBAES20002550	1856	16 1896	4299
	TBAES20003150	1857	42 1064	4300
	TBAES20003770	1858	117 3437	4301
	TCOLN20001390	1859	237 1106	4302
25	TESOP20000900	1860	110 448	4303
35	TESOP20003120	1861	42 929	4304
	TESOP20004000	1862	295 1125	4305
	TESOP20005270	1863	568 921	4306
	TESOP20005690	1864	230 574	4307
40	TESTI10000940	1865	1271752	4308
	TESTI20001000	1866	129944	4309
	TESTI20001170	1867	1071291	4310
	TESTI20001720	1868	204722	4311
	TESTI20002720	1869	92>2187	4312
45	TESTI20002780	1870	8211471	4313
	TESTI20004890	1871	1401231	4314
	TESTI20011200	1872	16151968	4315
	TESTI20017950	1873	622023	4316
50	TESTI20018230	1874	5061024	4317
	TESTI20023510	1875	. 1001935	4318
	TESTI20029930	1876	5971847	4319
	TESTI20030310	1877	13621757	4320
	TESTI20030890	1878	17362167	4321
<i>55</i>	TESTI20031270	1879	8201332	4322
	TESTI20031810	1880	2351926	4323
	TESTI20035960	1881	801327	4324

Table 1 (continued)

	Clone name	SEQ ID NO, of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	TESTI20036380	1882	1252110	4325
	TESTI20037560	1883	161986	4326
ì	TESTI20038270	1884	42347	4327
	TESTI20039400	1885	631430	4328
j	TESTI20041690	1886	1942320	4329
10	TESTI20044230	1887	761308	4330
	TESTI20044310	1888	3071899	4331
	TESTI20046750	1889	56871	4332
	TESTI20057750	1890	154495	4333
15	TEST120060400	1891	1021754	4334
"	TESTI20061110	1892	1021574	4335
1	TEST120063830	1893	1861793	4336
	TESTI20066670	1894	3451823	4337
	TESTI20066770	1895	8671937	4338
20	TESTI20067200	1896	251149	4339
1	TESTI20076850	1897	8641307	4340
	TESTI20082330	1898	122249	4341
1	TESTI20083200	1899	80967	4342
05	TESTI20083940	1900	601973	4343
25	TESTI20086210	1901	651465	4344
	TESTI20087620	1902	1162191	4345
	TESTI20088220	1903	3182435	4346
	TESTI20094020	1904	3411885	4347
30	TESTI20094120	1905	4021184	4348
	TESTI20094230	1906	13972158	4349
	TESTI20094470	1907	4281540	4350
	TESTI20098350	1908	1371849	4351
25	TESTI20098530	1909	220564	4352
35	TESTI20102800	1910	278640	4353
	TESTI20105720	1911	1542 1901	4354
	TESTI20108720	1912	101 1123	4355
	TESTI20110280	1913	212 1396	4356
40	TESTI20112940	1914	579 899	4357
	TESTI20114070	1915	1575 1937	4358
	TESTI20116650	1916	43 387	4359
	TESTI20116830	1917	825 1208	4360
45	TESTI20121550	1918	191 1900	4361
73	TESTI20122310	1919	149 826	4362
	TESTI20123080	1920	432 767	4363
	TESTI20123560	1921	249>816	4364
	TESTI20127760	1922	1491141	4365
50 ·	TESTI20128350	1923	178591	4366
	TESTI20129150	1924	241969	4367
	TESTI20129220	1925	366773	4368
	TESTI20130010	1926	8661420	4369
55	TESTI20130120	1927	119748	4370
55	TESTI20135660	1928	9611374	4371
	TESTI20136100	1929	71406	4372
	TESTI20136710	1930	14>1826	4373

Table 1 (continued)

	<u> </u>	Table 1 (C		<del></del>
	Ctone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	ESTI20136990	1931	19032292	4374
	TEST120137370	1932	37339	4375
	TEST120137570	1933	181561	4376
	TESTI20143240	1934	486908	4377
	TESTI20143390	1935	52.:1068	4378
10	TESTI20143520	1936	9701332	4379
	TESTI20148000	1937	2502004	4380
	TESTI20152460	1938	2221499	4381
	TEST120155900	1939	10951499	4382
15	TESTI20156100	1940	311200	4383
	TESTI20157100	1941	4811149	4384
	TESTI20157520	1942	55>1880	4385
	TESTI20159140	1943	424>1611	4386
	TESTI20161970	1944	1381658	4387
20	TESTI20164100	1945	60470	4388
	TESTI20168480	1946	911341	4389
	TESTI20168530	1947	12191608	4390
	TESTI20168960	1948	37570	4391
25	TESTI20169960	1949	8011139	4392
23	TESTI20170350	1950	11061429	4393
	TESTI20171020	1951	11>2194	4394
	TESTI20178160	1952	10841452	4395
	TESTI20179320	1953	191664	4396
30	TESTI20183370	1954	190870	4397
	TESTI20184620	1955	1232417	4398
	TESTI20185650	1956	751904	4399
	TESTI20185810	1957	243 587	4400
35	TESTI20189410	1958	16 >1759	4401
33	TESTI20192280	1959	10 906	4402
	TESTI20192800	1960	193 >2366	4403
	TESTI20193360	1961	66 854	4404
	TESTI20194300	1962	70 576	4405
40	TESTI20194810	1963	78473	4406
	TESTI20197940	1964	771>1987	4407
	TESTI20199170	1965	244558	4408
	TESTI20199750	1966	921957	4409
	TEST120200260	1967	307846	4410
45	TESTI20200710	1968	1901749	4411
	TEST120202550	1969	551299	4412
	TESTI20203440	1970	11091600	4413
	TEST120204450	1971	4171916	4414
50 .	TESTI20208400	1972	10271782	4415
	TEST120208710	1973	702046	4416
	TESTI20209460	1974	10351400	4417
	TESTI20209810	1975	8721405	4418
	TESTI20209990	1976	106549	4419
55	TESTI2021116C	1977	6271424	4420
	TEST120211220	1978	15611944	4421
	TESTI20211240	1979	150>1469	4422
	TESTI20211240	1979	150>1469	4422

Table 1 (continued)

Г	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid	
	Olone Hamo	sequence		sequence	l
_ }	TESTI20213150	1980	3801303	4423	ĺ
5	TESTI20213580	1981	338697	4424	
	TESTI20214250	1982	46933	4425	
l	TESTI20215990	1983	428 2635	4426	
	TESTI20216370	1984	572 1195	4427	
10	TESTI20220100	1985	539 1264	4428	
	TESTI20220650	1986	164 481	4429	
	TESTI20224620	1987	221 532	4430	
ļ	TESTI20226230	1988	335 >1500	4431	
	TESTI20226490	1989	1044 1367	4432	1
15	TESTI20229600	1990	342 2669	4433	
	TESTI20230250	1991	1310 1693	4434	
	TEST120230850	1992	246 2567	4435	-
	TESTI20231920	1993	949 1392	4436	
20	TESTI20231940	1994	382 975	4437	
	TESTI20232140	1995	26 1237	4438	
	TESTI20234140	1996	182 1738	4439	1
	TESTI20234270	1997	334 642	4440	1
	TESTI20234360	1998	23 460	4441	
25	TESTI20237520	1999	1721734	4442	
	TEST120238000	2000	9781322	4443	
	TESTI20238610	2001	1501373	4444	
	TESTI20239470	2002	1322294	4445	
30	TESTI20239510	2003	7011333	4446	
	TESTI20240090	2004	101179	4447	
	TESTI20241530	2005	5941985	4448	
	TESTI20241920	2006	13091632	4449	
25	TESTI20242830	2007	422306	4450	
35	TESTI20242990	2008	9681330	4451	
	TESTI20244190	2009	801630	4452	
	TESTI20244760	2010	12581647	4453	
	TESTI20249990	2011	6981960	4454	
40	TESTI20254220	2012	811376	4455	
	TESTI20254540	2013	9971830	4456	-
	TESTI20254860	2014	205>2004	4457	
	TESTI20255820	2015	1201565	4458	
<b>4</b> 5	TESTI20258460	2016	371212	4459	
43	TESTI20262330	2017	9281521	4460	
	TESTI20262910	2018	3351336	4461 4462	
	TESTI20265250	2019	17512095	4462	1
	TESTI20265370	2020	46378	4464	
50	TESTI20265970	2021	2581961	4465	
	TESTI20266740	2022	881203	4466	
	TESTI20269570	2023	6431047	4467	
	TESTI20271850	2024	202504	4468	
55	TESTI20272060	2025	13793253	4469	
33	TESTI20272390	2026	123767	4470	
	TESTI20272960	2027	9821932 98583	4471	-
	TESTI20275030	2028	30303	1-7.	

Table 1 (continued)

- 1	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	TESTI20275620	2029	1508 1840	4472
	TESTI20277360	2030	298 1704	4473
	TESTI20278200	2031	48 698	4474
	TESTI20278400	2032	70 >1856	4475
	TESTI20280980	2033	619 1071	4476
10	TESTI20282540	2034	310 1356	4477
	TESTI20284880	2035	683 1114	4478
	TESTI20285830	2036	494 853	4479
	TESTI20288110	2037	234 899	4480
15	TESTI20288910	2038	51 965	4481
	TESTI20289850	2039	198 698	4482
	TESTI20291310	2040	106 2034	4483
	TESTI20291620	2041	1611 2021	4484
	TESTI20291960	2042	809 1921	4485
20	TESTI20294700	2043	898 1236	4486
	TESTI20297850	2044	1 837	4487
	TESTI20301360	2045	114 506	4488
	TESTI20303220	2046	288 2711	4489
25	TESTI20303360	2047	767 2050	4490
20	TESTI20303420	2048	34 768	4491
	TESTI20305540	2049	97 2949	4492
	TESTI20305560	2050	49 582	4493
	TESTI20307540	2051	88 513	4494
30	TESTI20307700	2052	32 412	4495
	TESTI20308600	2053	72 1307	4496
	TESTI20309170	2054	722 2233	4497
	TESTI20310070	2055	2052097	4498
35	TESTI20311290	2056	9401398	4499
	TESTI20314180	2057	10731744	4500
	TESTI20316870	2058	25813	4501
	TESTI20317600	2059	1071420	4502
	TESTI20318090	2060	10121644	4503
40	TESTI20319190	2061	3841481	4504
	TESTI20320440	2062	2001861	4505
	TESTI20320670	2063	2591257	4506
	TESTI20326810	2064	8321377	4507
45	TESTI20327680	2065	1351730	4508
	TESTI20327740	2066	132518	4509
	TESTI20328280	2067	872135	4510
	TESTI20330310	2068	3151307	4511
	TESTI20332420	2069	6821461	4512 4513
50 ·	TEST120333000	2070	3661586	4513 4514
	TEST120333950	2071	76 1500	4515
	TEST120334410	2072	167 1630	4515 4516
	TEST120335050	2073	340 1389	I i
55	TEST/20335200	2074	612 968	4517 4518
	TEST/20336410	2075	17 325 40 384	4519
	TESTI20337100	2076 2077	322 642	4519
	TESTI20342430	20//	322 042	-020

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	TESTI20343070	2078	530 2563	4521
	TESTI20343570	2079	900 1568	4522
	TESTI20345060	2080	15 1382	4523
	TESTI20347180	2081	3710	4524
	TESTI20347300	2082	623931	4525
10	TESTI20347740	2083	1001599	4526
	TESTI20347770	2084	37351	4527
	TESTI20351830	2085	9191773	4528
4	TESTI20352620	2086	182907	4529
15	TESTI20355020	2087	81651	4530
	TESTI20357750	2088	547951	4531
	TESTI20357930	2089	11481498	4532
	TESTI20357960	2090	363725	4533
	TESTI20358980	2091	851332	4534
20	TESTI20361140	2092	8011514	4535
	TESTI20366910	2093	51396	4536
	TESTI20367360	2094	324629	4537
	TESTI20368330	2095	201 1856	4538
25	TESTI20369130	2096	243611	4539
2.5	TESTI20369220	2097	118441	4540
	TESTI20369650	2098	6332204	4541
	TESTI20369690	2099	3061208	4542
	TEST120370020	2100	3461830	4543
30	TESTI20370550	2101	160462	4544
	TESTI20370810	2102	2232334	4545
	TESTI20371030	2103	2091180	4546
	TESTI20371060	2104	1401177	4547
35	TESTI20373820	2105	2371109	4548
33	TESTI20375340	2106	3871559	4549
	TESTI20377230	2107	5741314	4550
	TESTI203/8190	2108	3801795	4551
	TESTI20378450	2109	489>2419	4552
40	TEST120380650	2110	9611272	4553
	TESTI20381040	2111	3391394	4554
	TEST120382750	2112	11591797	4555
	TEST120383880	2113	419988	4556
45	TEST120385960	2114	6841637	4557
	TEST120386230	2115	7481059	4558
	TESTI20386440	2116	185514	4559
	TESTI20388580	2117	405788	4560
	TESTI20390260	2118	142522	4561
50	TESTI20390410	2119	16041969	4562
	TESTI20391130	2120	1852224	4563
	TEST120391210	2121	12591801	4564
	TESTI20391770	2122	2371634	4565
55	TESTI20392090	2123	405881	4566
	TEST/20392250	2124	10571941	4567
	TEST120392270	2125	3161185	4568
	TESTI20392760	2126	3062279	4569

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	TESTI20393530	2127	1941198	4570
	TESTI20396130	2128	338682	4571
	TESTI20397760	2129 、	3711129	4572
	TESTI20400940	2130	2312705	4573
	TESTI20401020	2131	5831281	4574
10	TESTI20401280	2132	53379	4575
	TESTI20401430	. 2133	340651	4576
	TESTI20404240	2134	11101550	4577
	TESTI20406420	2135	1861340	4578
15	TESTI20408150	2136	195752	4579
	TESTI20408970	2137	247 1170	4580
	TESTI20409440	2138	17 337	4581
	TESTI20409890	2139	120 1082	4582
	TESTI20413300	2140	66 503	4583
20	TESTI20415170	2141	45 419	4584
	TESTI20415640	21.42	1 324	4585
	TESTI20416640	2143	1092 1574	4586
	*ESTI20417300	2144	107 1807	4587
.24	TESTI20419560	2145	5 331	4588
	TEST120420520	2146	334 2139	4589
	TESTI20421490	2147	2188,. 2628	4590
	TEST(20422540	2148	974 2149	4591
	TEST(20423020	2149	252 >1770	4592
30	TEST120424000	2150	339 842	4593
	TESTI20424730	2151	928 1263	4594
	TEST(20425070	2152	1145 1726	4595
	TEST120427830	2153	42380	4596
35	TEST120428060	2154	230598	4597
33	TEST120429280	2155	9251551	4598
	TEST120429580	2156	9701458	4599
	TESTI20432750	2157	561399	4600
	ES1120432820	2158	181232	4601
40	TEST120433130	2159	247549	4602
	TESTI20436560	2160	1031578	4603
	TESTI20438570	2161	12521719	4604
	TEST120438560	2162	22272622	4605
45	TESTI20441940	2163	6131596	4606
	TEST120442760	2164	82>2054	4607
	TEST120443090	2165	2011019	4608
	TESTI20444130	2166	79417	4609
	TESTI20444180	2167	26547	4610
50	TESTI20447540	2168	184516	4611
	TESTI20449200	2169	6721766	4612
	TESTI20451710	2170	429731	4613
	TESTI20451990	2171	2102264	4614
55	TEST120455090	2172	4891268	4615
	TESTI20455620	2173	1101351	4616
	TESTI20456110	2174	41191	4617
	TESTI20458190	2175	235579	4618

Table 1 (continued)

ſ	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	TESTI20463520	2176	9981402	4619
	TESTI20463580	2177	5772037	4620
	TESTI20465350	2178	3171258	4621
	TESTI20465520	2179	535 1026	4622
	TESTI20465690	2180	214 1074	4623
10	TESTI20467210	2181	435 1613	4624
	TESTI20467320	2182	951 1922	4625
1	TESTI20467970	2183	332 1690	4626
	TESTI20468630	2184	380 688	4627
15	TESTI20471410	2185	97 1464	4628
15	TESTI20471470	2186	31 369	4629
	TESTI20471530	2187	2264 2641	4630
	TESTI20472120	2188	517 876	4631
	TESTI20473420	2189	140607	4632
20	TESTI20473830	2190	9511532	4633
	TESTI20477920	2191	13871860	4634
	TESTI20478010	2192	169558	4635
	TEST120478180	2193	428754	4636
0.5	TESTI20478850	2194	9491323	4637
25	TESTI20479300	2195	6631205	4638
	THYMU10005360	2196	48899	4639
	THYMU10005540	2197	841508	4640
	THYMU20000570	2198	216728	4641
3 <b>0</b>	THYMU20011950	2199	45 626	4642
	THYMU20015210	2200	1003 1314	4643
	THYMU20018190	2201	336 758	4644
	THYMU20023380	2202	1426 1728	4645
25	THYMU20027560	2203	63 602	4646
35	THYMU20029100	2204	215 928	4647
	THYMU20032870	2205	1042 1404	4648
	THYMU20039810	2206	54 2204	4649
	THYMU20045120	2207	66 425	4650
40	THYMU20058070	2208	984 1388	4651
	THYMU20061700	2209	40435	4652
	THYMU20066100	2210	188814	4653
	THYMU20070360	2211	13331635	4654
45	THYMU20075320	2212	11861767	4655
43	THYMU20081490	2213	127>2055	4656
	THYMU20095960	2214	304945	4657
	THYMU20100410	2215	219 1415	4658
	THYMU20101610	2216	1087 1446	4659
50	THYMU20101920	2217	765 1310	4660
	THYMU20105190	2218	850 1713	4661
	THYMU20106710	2219	89 493	4662
	THYMU20108310	2220	97 642	4663
55	THYMU20111180	2221	33 1367	4664
55	THYMU20111420	2222	914 1303	4665
	THYMU20111830	2223	38 796	4666
	THYMU20114470	2224	122 502	4667

Table 1 (continued)

		rable i (C	continuea)	
	Clone name	SEQ ID NO, of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	THYMU20115850	2225	15001805	4668
3	THYMU20118060	2226	355687	4669
	THYMU20118520	2227 •	220567	4670
	THYMU20119390	2228	118525	4671
	THYMU20122730	2229	3431140	4672
10	THYMU20126900	2230	1631446	4673
	THYMU20128070	2231	2349	4674
	THYMU20128260	2232	76411	4675
	THYMU20130890	2233	221757	4676
	THYMU20141670	2234	1961152	4677
15	THYMU20142040	2235	24653	4678
}	THYMU20142970	2236	4951499	4679
	THYMU20143270	2237	5241549	4680
	THYMU20147770	2238	801501	4681
20	THYMU20153160	2239	13031920	4682
	THYMU20158250	2240	117488	4683
	THYMU20159430	2241	791581	4684
	THYMU20161640	2242	110679	4685
	THYMU20162190	2243	299646	4686
25	THYMU20169680	2244	718. 1395	4687
	THYMU20172150	2245	375956	4688
	THYMU20173980	2246	355813	4689
	THYMU20180280	2247	13521699	4690
30	THYMU20186390	2248	4611495	4691
	THYMU20186730	2249	194535	4692
	THYMU20187720	2250	284661	4693
	THYMU20193640	2251	6591165	4694
	THYMU20193840	2252	257955	4695
35	THYMU20194420	2253	10801403	4696
	THYMU20195990	2254	344673	4697
	THYMU20201980	2255	10942023	4698
	THYMU20202890	2256	9352188	4699
40	THYMU20204160	2257	6541199	4700
••	THYMU20204180	2258	65385	4701
	THYMU20208300	2259	144542	4702
	THYMU20208500	2260	1932061	4703
	THYMU20215090	2261	862 1380	4704
45	THYMU20215970	2262	1004 1552	4705
	THYMU20216840	2263	605 2074	4706
	THYMU2022890	2264	1896 2198	4707
	THYMU20226600	2265	246 1232	4708
50 ·	THYMU20228540	2266	109 426	4709
55	THYMU20229220	2267	259 894	4710
	THYMU20232090	2268	111 539	4711
	THYMU20232090	2269	357 674	4712
	THYMU20239000	2270	44 1672	4713
55	THYMU20239430	2271	656 982	4714
	THYMU20240710	2272	680 2077	4715
	THYMU20241210	2273	77 511	4716
	11110020241210	CLI U	1 ,,	11.10

Table 1 (continued)

	Clone name	SEQ ID NO, of nucleotide	Position of CDS	SEQ ID NO. of amino acid
		sequence		sequence
5	THYMU20241850	2274	63 890	4717
	THYMU20246840	2275	110 415	4718
	THYMU20247480	2276 -	4 1176	4719
	THYMU20250420	2277	222 707	4720
_	THYMU20251890	2278	1433 1777	4721
10	THYMU20253250	2279	713 1540	4722
	THYMU20255570	2280	882 1550	4723
	THYMU20255720	2281	88 645	4724
	THYMU20259090	2282	1763 2092	4725
15	THYMU20265300	2283	60 1949	4726
	THYMU20271250	2284	681., 1628	4727
	THYMU20272490	2285	174 560	4728
	THYMU20277390	2286	930 1541	4729
	THYMU20279750	2287	716 1114	4730
20	THYMU20283790	2288	253 804	4731
	THYMU20284120	2289	178 525	4732
	THYMU20286290	2290	287 1981	4733
	THYMU20286320	2291	1214 1594	4734
.25	TKIDN10000010	2292	386 838	4735
	TKIDN20004640	2293	549 1172	4736
	TKIDN20005210	2294	294 1133	4737
	TKIDN20030590	2295	143 1558	4738
	TKIDN20030620	2296	25 531	4739
<i>3</i> 0	TKIDN20047480	2297	1038 1460	4740
	TOVAR20004760	2298	675 1454	4741
	TOVAR20005750	2299	348 713	4742
	TRACH20002870	2300	77 613	4743
35	TRACH20003590	2301	244 1773	4744
	TRACH20005020	2302	75 1463	4745
	TRACH20005400	2303	57 728	4746
	*RACH2000/020	2304	271 1830	4747
	*HACH20016210	2305	1221132	4748
40	RACH20019960	2306	112 1410	4749
	*RACH20027840	2307	61384	4750
	RACH20028030	2308	1611441	4751
	*RACH20029540	2309	14101859	4752
45	TRACH20032720	2310	8301354	4753
	TRACH20033230	2311	5602110	4754
	TRACH20034840	2312	1985>3328	4755
	TRACH20037360	2313	1309	4756
	TRACH20041830	2314	4241035	4757
50	TRACH20042920	2315	771540	4758
	TRACH20048450	2316	5111845	4759
	TRACH20050040	2317	70594	4760
	TRACH20056980	2318	4051055	4761
55	TRACH20057690	2319	14481993	4762
	TRACH20060150	2320	3329	4763
	TRACH20067620 TRACH20068660	2321 2322	166603 63890	4764 4765
	717012000000	2322	05,.650	4765

Table 1 (continued)

	<del></del>	Table 1 (C	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	
	Clone name	SEQ ID NO, of nucleotide	Position of CDS	SEQ ID NO, of amino acid
		sequence		sequence
5	TRACH20068700	2323	1441811	4766
	TRACH20069180	2324	631625	4767
	TRACH20076740	2325 `	7791669	4768
	TRACH20076760	2326	17372183	4769
	TRACH20077540	2327	18592455	4770
10	TRACH20079690	2328	1442144	4771
	TRACH20082780	<b>2329</b>	16752103	4772
	TRACH20084720	2330	381819	4773
	TRACH20085400	2331	2232346	4774
15	TRACH20085830	2332	411567	4775
	TRACH20091230	2333	16602067	4776
	TRACH20092680	2334	56457	4777
	TRACH20096610	2335	417935	4778
	TRACH20099340	2336	156494	4779
20	TRACH20105870	2337	14182176	4780
	TRACH20107710	2338	13474	4781
	TRACH20109650	2339	14211849	4782
	TRACH20111130	2340	15481937	4783
05	TRACH20115740	2341	507893	4784
25	TRACH20118940	2342	17812083	4785
	TRACH20121380	2343	795 1808	4786
	TRACH20128110	2344	1233 1796	4787
	TRACH20128230	2345	80 1657	4788
30	TRACH20134950	2346	675 1001	4789
	TRACH20135520	2347	425 2335	4790
	TRACH20136710	2348	42 545	4791
	TRACH20139820	2349	1630 1998	4792
	TRACH20140820	2350	196 738	4793
35	TRACH20141240	2351	270 875	4794
	TRACH20145440	2352	243 1511	4795
	TRACH20147250	2353	834 1196	4796
	TRACH20149970	2354	124 1776	4797
40	TRACH20153810	2355	216 635	4798
	TRACH20154860	2356	3 1439	4799
	TRACH20162860	2357	98 364	4800
	TRACH20163170	2358	267 1028	4801
	TRACH20164980	2359	6572165	4802
45	TRACH20167220	2360	9862422	4803
	TRACH20168350	2361	200589	4804
	TRACH20169800	2362	19222359	4805
	TRACH20180840	2363	12881593	4806
50 ·	TRACH20183170	2364	10292252	4807
	TRACH20184490	2365	2141596	4808
	TRACH20187180	2366	13221639	4809
	TRACH20190240	2367	16242313	4810
	TSTOM10001860	2368	961859	4811
<i>55</i>	TSTOM20001390	2369	2411671	4812
	TSTOM20001390	2370	1031245	4813
	TSTOM20003180	2371	3701626	4814
	131010120005690	23/1	3701020	40 l 4

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
	Cione name	sequence	Position of CDS	sequence
_	TUTER20002830	2372	172930	4815
5	UMVEN10001560	2373	130669	4816
	UMVEN10001860	2374	198>2048	4817
	UMVEN20000690	2375	61118	4818
	UMVEN20003540	2376	4519	4819
10	UTERU20000740	2377	20622400	4820
	UTERU20004240	2378	38385	4821
	UTERU20006290	2379	101406	4822
	UTERU20006960	2380	106555	4823
	UTERU20020010	2381	54431	4824
15	UTERU20022940	2382	7351232	4825
	UTERU20030570	2383	1841737	4826
	UTERU20040610	2384	92409	4827
	UTERU20046640	2385	152699	4828
20	UTERU20046980	2386	216926	4829
	UTERU20050690	2387	619924	4830
	UTERU20054460	2388	557>2294	4831
	UTERU20055330	2389	45632	4832
	UTERU20055480	2390	921765	4833
25	UTERU20055930	2391	90869	4834
	UTERU20056010	2392	65484	4835
	UTERU20059050	2393	8091459	4836
	UTERU20061030	2393	9941389	4837
30	UTERU20064000	2395	153479	4838
-	UTERU20064860	2396	261780	4839
	UTERU20065930	2397	372097	4840
	UTERU20067050	2398	641952	4841
	UTERU20068990	2399	9451319	4842
35	UTERU20070040	2400	36383	4843
	UTERU20070810	2401	7611219	4844
	UTERU20076390	2402	71499	4845
	UTERU20081300	2403	20632464	4846
40	UTERU20084260	2404	4941321	4847
	UTERU20094350	2405	293 802	4848
	UTERU20095380	2406	872 1213	4849
	UTERU20095400	2407	737 1456	4850
	UTERU20097760	2408	1232 1759	4851
45	UTERU20099720	2409	201 746	4852
	UTERU20101240	2410	210 602	4853
	UTERU20114100	2411	538 963	4854
	UTERU20115740	2412	469 933	4855
50	UTERU20116570	2413	327 1694	4856
	UTERU20118110	2414	87 485	4857
	UTERU20118970	2415	229549	4858
	UTERU20119060	2416	11922436	4859
	UTERU20119680	2417	6761185	4860
<i>55</i>	UTERU20120310	2418	681066	4861
	UTERU20124070	2419	368733	4862
	UTERU20126880	2420	5241045	4863
				<u> </u>

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide	Position of CDS	SEQ ID NO. of amino acid
	sequence		sequence
UTERU20134910	2421	10701489	4864
UTERU20135860	2422	6761965	4865
UTERU20143980	2423	68370	4866
UTERU20144640	2424	2311148	4867
UTERU20145480	2425	1722193	4868
UTERU20146310	2426	1141580	4869
UTERU20146680	2427	5241045	4870
UTERU20150870	2428	47499	4871
UTERU20151980	2429	220981	4872
UTERU20158300	2430	342686	4873
UTERU20158800	2431	1611318	4874
UTERU20161570	2432	2951209	4875
UTERU20164260	2433	54890	4876
UTERU20168220	2434	8351530	4877
UTERU20176130	2435	271184	4878
UTERU20176320	2436	1081364	4879
UTERU20178100	2437	21782528	4880
UTERU20179880	2438	1722379	4881
UTERU20183640	2439	22892828	4882
UTERU20185230	2440	1251927	4883
UTERU20186740	2441	851 1156	4884
UTERU20188110	2442	125 1135	4885
UTERU20188810	2443	84 389	4886

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[0028] Namely, primers used to synthesize polynucleotides can be designed based on the nucleotide sequences of polynucleotides of the present invention shown in SEQ ID NOs in the above Table 1. When one intends to synthesize full-length cDNAs, an oligo dT primer can be used as the 3'-end primer. The length of the primers is usually 15-100 bp, and favorably between 15-35 bp. In case of LA PCR, which is described below, the primer length of 25-35 bp may provide a good result.

[0029] A method to design a primer that enables a specific amplification based on the aimed nucleotide sequence is known to those skilled in the art (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4). In designing a primer based on the 5'-end sequence, the primer is designed so as that, in principle, the amplification products will include the translation start site. Accordingly, for example, when the 5'-end primer is designed based on the nucleotide sequence of 5' untranslated region (5'UTR), any part of the 5'-end, which ensures the specificity to the cDNA of interest, can be selected as the primer.

[0030] When synthesizing a full-length cDNA, the target nucleotide sequence to be amplified can extend to several thousand bp in some cDNA. However, it is possible to amplify such a long nucleotides by using such as LA PCR (Long and Accurate PCR). It is advantageous to use LA PCR when synthesizing long DNA. In LA PCR, in which a special DNA polymerase having 3'-> 5' exonuclease activity is used, misincorporated nucleotides can be removed. Accordingly, accurate synthesis of the complementary strand can be achieved even with a long nucleotide sequence. By using LA PCR, it is reported that amplification of a nucleotide with 20 kb longer can be achieved under desirable conditions (Takeshi Hayashi (1996) Jikken-Igaku Bessatsu, "Advanced Technologies in PCR" Youdo-sha).

[0031] A template DNA for synthesizing the full-length cDNA of the present invention can be obtained by using cDNA libraries that are prepared by various methods. The full-length cDNA clones of the present invention are clones with high probability of completeness in length, which were obtained by the method comprising the steps of [1] preparing libraries containing cDNAs with the very high fullness ratio by oligo-capping, and [2] assembling the 5'-end sequences and selecting one with the highest probability of completeness in length in the cluster formed (there are many clones longer in the 5'-end direction).

[0032] However, the uses of primers designed based on the full-length nucleotide sequences provided by the present invention enable easily obtaining full-length cDNAs without such a special technique.

[0033] The problem with the cDNA libraries prepared by the known methods or commercially available is that mRNA

contained in the libraries has very low fullness ratio. Thus, it is difficult to screen full-length cDNA clone directly from the library using ordinary cloning methods. The present invention has revealed a nucleotide sequence of novel full-length cDNA. If a full-length nucleotide sequence is provided, it is possible to synthesize a target full-length cDNA by using enzymatic reactions such as PCR. In particular, a full-length-enriched cDNA library, synthesized by methods such as oligo-capping, is desirable to synthesize a full-length cDNA with more reliability.

[0034] The 5'-end sequence of the full-length cDNA clones of the invention can be used to isolate the regulatory element of transcription including the promoter on the genome. A rough draft of the human genome (analysis of human genomic sequence with lower accuracy), which covers 90% of the genome, has been reported (Nature, Vol.409, 814-823, 2001), and by the year 2003, analysis of the entire human genomic sequence is going to be finished. However, it is hard to analyze with software the transcription start sites on the human genome, in which long introns exist. By contrast, it is easy to specify the transcription start site on the genomic sequence using the nucleotide sequence which includes the 5'-end of the full-length cDNA clone of the present invention, and thus it is easy to obtain the genomic region involved in transcription regulation, which includes the promoter that is contained in the upstream of the transcription start site.

[0035] The polypeptide encoded by the full-length cDNA of the invention can be prepared as a recombinant polypeptide or as a natural polypeptide. For example, the recombinant polypeptide can be prepared by inserting the polynucleotide encoding the polypeptide of the invention into a vector, introducing the vector into an appropriate host cell and purifying the polypeptide expressed within the transformed host cell, as described below. In contrast, the natural polypeptide can be prepared, for example, by utilizing an affinity column to which an antibody against the polypeptide of the invention (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 16.1-16.19) is attached. The antibody used for affinity purification may be either a polyclonal antibody, or a monoclonal antibody. Alternatively, *in vitro* translation (See, for example, "On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system." Dasso M.C., and Jackson R.J. (1989) Nucleic Acids Res. 17: 3129-3144) may be used for preparing the polypeptide of the invention.

[0036] Polypeptides functionally equivalent to the polypeptides of the present invention can be prepared based on the activities, which were clarified in the above-mentioned manner, of the polypeptides of the present invention. Using the biological activity possessed by the polypeptide of the invention as an index, it is possible to verify whether or not a particular polypeptide is functionally equivalent to the polypeptide of the invention by examining whether or not the polypeptide has said activity.

[0037] Polypeptides functionally equivalent to the polypeptides of the present invention can be prepared by those skilled in the art, for example, by using a method for introducing mutations into an amino acid sequence of a polypeptide (for example, site-directed mutagenesis (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 8.1-8.5). Besides, such polypeptides can be generated by spontaneous mutations. The present invention also includes a polypeptide comprising the amino acid sequence shown in Table 1 in which one or more amino acids are substituted, deleted, inserted, and/or added, as long as the polypeptides have the equivalent functions to those of the polypeptides identified in the present Examples described later.

[0038] There are no limitations on the number and sites of amino acid mutations, as long as the polypeptides maintain the functions thereof. The number of mutations typically corresponds to 30% or less, or 20% or less, or 10% or less, preferably 5% or less, or 3% or less of the total amino acids, more preferably 2% or less or 1% or less of the total amino acids. Alternatively, herein, substitution of one or more amino acids includes substitution of several amino acids. As used herein, the term "several amino acids" means, for example, 5 amino acids, preferably 4 or 3 amino acids, more preferably 2 amino acids, and further preferably 1 amino acid.

[0039] From the viewpoint of maintaining the polypeptide function, it is preferable that a substituted amino acid has a similar property to that of the original amino acid. For example, Ala, Val, Leu, Ile, Pro, Met, Phe and Trp are assumed to have similar properties to one another because they are all classified into a group of non-polar amino acids. Similarly, substitution can be performed among non-charged amino acid such as Gly, Ser, Thr, Cys, Tyr, Asn, and Gln, acidic amino acids such as Asp and Glu, and basic amino acids such as Lys, Arg, and His.

[0040] In addition, polypeptides functionally equivalent to the polypeptides of the present invention can be isolated by using techniques of hybridization or gene amplification known to those skilled in the art. Specifically, using the hybridization technique (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)), those skilled in the art can usually isolate a polynucleotide highly homologous to the polynucleotide encoding the polypeptide identified in the present Example based on the identified nucleotide sequence (Table 1) or a portion thereof and obtain the functionally equivalent polypeptide from the isolated polynucleotide. The present invention include polypeptides encoded by the polynucleotides hybridizing with the polynucleotides encoding the polypeptides identified in the present Example, as long as the polypeptides are functionally equivalent to the polypeptides identified in the present Example. Organisms from which the functionally equivalent polypeptides are isolated are illustrated by vertebrates such as human, mouse, rat, rabbit, pig and bovine, but are not limited to these animals.

[0041] Washing conditions of hybridization for the isolation of polynucleotides encoding the functionally equivalent

polypeptides are usually "1x SSC, 0.1% SDS, 37°C"; more stringent conditions are "0.5x SSC, 0.1% SDS, 42°C"; and still more stringent conditions are "0.1x SSC, 0.1% SDS, 65°C". Alternatively, the following conditions can be given as hybridization conditions of the present invention. Namely, conditions in which the hybridization is done at "6x SSC, 40% Formamide, 25°C", and the washing at "1x SSC, 55°C" can be given. More preferable conditions are those in which the hybridization is done at "6x SSC, 40% Formamide, 37°C", and the washing at "0.2x SSC, 55°C". Even more preferable are those in which the hybridization is done at "6x SSC, 50% Formamide, 37°C", and the washing at "0.1x SSC, 62°C". The more stringent the conditions of hybridization are, the more frequently the polynucleotides highly homologous to the probe sequence are isolated. Therefore, it is preferable to conduct hybridization under stringent conditions. Examples of stringent conditions in the present invention are, washing conditions of "0.5x SSC, 0.1% SDS, 42°C", or alternatively, hybridization conditions of "6x SSC, 40% Formamide, 37°C", and the washing at "0.2x SSC, 55°C".

[0042] One skilled in the art can suitably select various conditions, such as dilution ratios of SSC. formamide concentrations, and temperatures to accomplish a similar stringency.

[0043] However, the above-mentioned combinations of SSC, SDS and temperature conditions are indicated just as examples. Those skilled in the art can select the hybridization conditions with similar stringency to those mentioned above by properly combining the above-mentioned or other factors (for example, probe concentration, probe length and duration of hybridization reaction) that determines the stringency of hybridization.

[0044] The amino acid sequences of polypeptides isolated by using the hybridization techniques usually have high identity to those of the polypeptides of the present invention, which are shown in Table 1. The present invention encompasses a polynucleotide comprising a nucleotide sequence that has a high identity to the nucleotide sequence of claim 1 (a). Furthermore, the present invention encompasses a peptide, or polypeptide comprising an amino acid sequence that has a high identity to the amino acid sequence encoded by the polynucleotide of claim 1 (b). The term "high identity" indicates sequence identity of at least 40% or more; preferably 60% or more; and more preferably 70% or more. Alternatively, more preferable is identity of 90% or more, or 93% or more, or 95% or more, furthermore, 97% or more, or 99% or more. The identity can be determined by using the BLAST search algorithm.

[0045] As used herein, "percent identity" of amino acid sequences or nucleic acids is determined using the algorithm BLAST of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol.215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN program, for example, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, for example, score = 50, wordlength = 3. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs are used. See http://www.ncbi.nlm.nih.gov.

[0046] With the gene amplification technique (PCR) (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.1-6.4)) using primers designed based on the nucleotide sequence (Table 1) or a portion thereof identified in the present Example, it is possible to isolate a polynucleotide fragment highly homologous to the polynucleotide sequence or a portion thereof and to obtain functionally equivalent polypeptide to a particular polypeptide identified in the present Example based on the isolated polynucleotide fragment.

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[0047] The present invention also provides a polynucleotide containing at least 15 nucleotides complementary to a polynucleotide comprising a nucleotide sequence of SEQ ID NOs shown in Table 1 or the complementary strand thereof. Herein, the term "complementary strand" is defined as one strand of a double strand DNA composed of A:T and G:C base pair to the other strand. Also, "complementary" is defined as not only those completely matching within a continuous region of at least 15 nucleotides, but also having a identity of at least 70%, favorably 80% or higher, more favorably 90% or higher, and most favorably 95% or higher within that region. The identity may be determined using the algorithm described herein.

[0048] Such a polynucleotide includes probes and primers used for the detection and amplification of a polynucleotide encoding the inventive polypeptide. When used as a primer, the polynucleotide usually comprises 15 to 100 bp, and preferably of 15 to 35 bp. When used as a probe, the polynucleotide comprises the whole or a part of the sequence of a polynucleotide of the invention, and comprises at least 15 bp. When used as primers, such polynucleotides are complementary at the 3'-end, and restriction enzyme recognition sequences or tags can be added to the 5'-end.

[0049] Furthermore, polynucleotides of the present invention include an antisense polynucleotide for suppressing the expression of a polypeptide of the invention, which comprises an amino acid sequence of SEQ ID NOs shown in Table 1. To exert an antisense effect, an antisense polynucleotide has at least 15 bp or more, for example 50 bp or more, preferably 100 bp or more, and more preferably 500 bp or more, and usually has 3000 bp or less, and preferably 2000 bp or less. Antisense polynucleotides can be used in the gene therapy of diseases caused by abnormalities of the polypeptides of the invention (abnormal function or abnormal expression). An antisense polynucleotide can be prepared, for example, by the phosphorothioate method ("Physicochemical properties of phosphorothioate oligodeoxynucleotides." Stein (1988) Nucleic Acids Res. 16: 3209-3221) based on the sequence information of polynucleotide encoding a polypeptide of the invention (for example, the nucleotide sequences of SEQ ID NO: 1 to 2443).

[0050] The polynucleotides or antisense polynucleotides of the present invention can be used in, for example, gene

therapy. As target diseases, for example, cancers or various inflammatory diseases may be preferable. These molecules can be used for gene therapy, for example, by administrating them to patients by the *in vivo* or *ex vivo* method using virus vectors such as retrovirus vectors, adenovirus vectors, and adeno-related virus vectors, or non-virus vectors such as liposomes.

[0051] The present invention also includes a partial peptide of the polypeptides of the invention. The partial peptide comprises a polypeptide generated as a result that a signal peptide has been removed from a secretory protein. If the polypeptide of the present invention has an activity as a receptor or a ligand, the partial peptide may function as a competitive inhibitor of the polypeptide and may bind to the receptor (or ligand). In addition, the present invention includes an antigen peptide for raising antibodies. For the peptides to be specific for the polypeptide of the invention, the peptides comprise at least 7 amino acids, preferably 8 amino acids or more, more preferably 9 amino acids or more, and even more preferably 10 amino acids or more. The peptide can be used for preparing antibodies against the polypeptide of the invention, or competitive inhibitors of them, and also screening for a receptor that binds to the polypeptide of the invention. The partial peptides of the invention can be produced, for example, by genetic engineering methods, known methods for synthesizing peptides, or digesting the polypeptide of the invention with an appropriate peptidase.

[0052] The present invention also relates to a vector into which a polynucleotide of the invention is inserted. The vector of the invention is not limited as long as it contains the inserted polynucleotide stably. For example, if *E. coli* is used as a host, vectors such as pBluescript vector (Stratagene) are preferable as a cloning vector. To produce the polypeptide of the invention, expression vectors are especially useful. Any expression vector can be used as long as it is capable of expressing the polypeptide *in vitro*, in *E. coli*, in cultured cells, or *in vivo*. For example, pBEST vector (Promega) is preferable for *in vitro* expression, pET vector (Invitrogen) for *E. coli*, pME18S-FL3 vector (GenBank Accession No. AB009864) for cultured cells, and pME18S vector (Mol. Cell. Biol. (1988) 8: 466-472) for *in vivo* expression. To insert the polynucleotide of the invention, ligation utilizing restriction sites can be perfermed according to the standard method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

[0053] Recently, the technique of GATEWAY<sup>TM</sup> system (Invitrogen), which is an expression vector construction system for polypeptide expression, has been developed (Experimental Medicine, Vol. 18, No. 19 (December), p2716-2717, 2000). This system includes two types of site-specific recombinases (BP CLONASE<sup>TM</sup> and LR CLONASE<sup>TM</sup>) derived from lambda phage and uses BP CLONASE<sup>TM</sup>-specific recombination sites for an Entry Vector and LR CLONASE<sup>TM</sup>-specific recombination sites for an Entry Vector and LR CLONASE<sup>TM</sup>-specific recombination sites for a Destination Vector, which may comprise a tag useful for polypeptide purification. With this system, an expression vector can be obtained by using homologous recombination.

[0054] First, a polynucleotide fragment of interest is inserted into the entry vector using the first recombination. Then, the secondary recombination is allowed to take place between the entry vector, where the polynucleotide fragment of interest has been inserted, and the destination vector. Thus, the expression vector can be prepared rapidly and highly efficiently. With the above-mentioned typical method using restriction enzyme and ligase reactions, the step of expression vector construction and expression of polypeptide of interest takes about 7 to 10 days. However, with the GATE-WAY<sup>TM</sup> system, the polypeptide of interest can be expressed and prepared in only 3 to 4 days. Thus, the system ensures a high-throughput functional analysis for expressed polypeptides (http://biotech.nikkeibp.co.jp/netlink/lto/gate-way/).

[0055] The present invention also relates to a transformant carrying the vector of the invention. Any cell can be used as a host into which the vector of the invention is inserted, and various kinds of host cells can be used depending on the purposes. For strong expression of the polypeptide in eukaryotic cells, COS cells or CHO cells can be used, for example.

[0056] Introduction of the vector into host cells can be performed, for example, by calcium phosphate precipitation method, electroporation method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 9.1-9.9), lipofectamine method (GIBCO-BRL), or microinjection method, etc.

[0057] Further, a polynucleotide containing at least 15 nucleotides comprising a nucleotide sequence of any one of the polynucleotides comprising the nucleotide sequences of SEQ ID NOs shown in Table 1 or the complementary strand thereof can be used not only as a primer for synthesizing full-length cDNAs but also for testing and diagnosing the abnormalities of the polypeptide encoded by the full-length cDNA of the present invention. For example, by utilizing polymerase chain reaction (genomic DNA-PCR, or RT-PCR) using the polynucleotide of the invention as a primer, polynucleotide encoding the polypeptide of the invention can be amplified. It is also possible to obtain the regulatory region of expression in the 5'-upstream by using PCR or hybridization since the transcription start site within the genomic sequence can be easily specified based on the 5'-end sequence of the full-length cDNA. The obtained genomic region can be used for detection and/or diagnosis of the abnormality of the sequence by RFLP analysis, SSCP, or sequencing. Especially, in the case where expression of the mRNA of the present invention varies according to a specific disease, analysis of the amount of expression of the mRNA using the polynucleotide of the present invention as a probe or a primer enables detection and diagnosis of the disease.

[0058] The present invention also relates to antibodies that bind to the polypeptide of the invention. There are no

limitations in the form of the antibodies of the invention. They include polyclonal antibodies, monoclonal antibodies, or their portions that can bind to an antigen. They also include antibodies of all classes. Furthermore, special antibodies such as humanized antibodies and chimeric antibodies are also included.

[0059] The polyclonal antibody of the invention can be obtained according to the standard method by synthesizing an oligopeptide corresponding to the amino acid sequence and immunizing rabbits with the peptide (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.12-11.13). The monoclonal antibody of the invention can be obtained according to the standard method by purifying the polypeptide expressed in *E. coli*, immunizing mice with the polypeptide, and producing a hybridoma cell by fusing the spleen cells and myeloma cells (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

[0060] The antibody binding to the polypeptide of the present invention can be used for purification of the polypeptide of the invention, and also for detection and/or diagnosis of the abnormalities of the expression and structure of the polypeptide. Specifically, polypeptides can be extracted, for example, from tissues, blood, or cells, and the polypeptide of the invention is detected by Western blotting, immunoprecipitation, or ELISA, etc. for the above purpose.

[0061] Furthermore, the antibody binding to the polypeptide of the present invention can be utilized for treating the diseases that associates with the polypeptide of the invention. If the antibodies are used for treating patients, human antibodies, humanized antibodies, or chimeric antibodies are preferable in terms of their low antigenicity. The human antibodies can be prepared by immunizing a mouse whose immune system is replaced with that of human (e.g., see "Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice" Mendez, M.J. et al. (1997) Nat. Genet. 15: 146-156). The humanized antibodies can be prepared by recombination of the hypervariable region of a monoclonal antibody (Methods in Enzymology (1991) 203: 99-121).

[0062] A cDNA of the present invention encodes, for example, an amino acid sequence of a protein that is predicted to have the following function. The use of the amino acid sequences of the polypeptides encoded by the cDNAs of the present invention enables predicting that the polypeptides have the following functions. It can be predict, from the results of homology search of SwissProt, GenBank, UniGene, or nr, that these polypeptides have such functions. Specifically, for instance, as shown in Examples, searching for a known gene or polypeptide that is homologous to the partial sequence of the full-length cDNA of the invention (2443 clone) and referring the function of the gene and of the polypeptide encoded by the gene make it possible to predict the function of the polypeptide encoded by the cDNA of the invention. In this way, each of 1216 clones out of the 2443 full-length cDNA clones of the invention was predicted to encode a polypeptide that was classified into the following categories.

Secretory and/or membrane protein (632 clones)

Glycoprotein-related protein (128 clones)

Signal transduction-related protein (84 clones)

Transcription-related protein (144 clones)

Disease-related protein (387 clones)

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Enzyme and/or metabolism-related protein (206 clones)

Cell division- and/or cell proliferation-related protein (33 clones)

Cytoskeleton-related protein (75 clones)

Nuclear protein and/or RNA synthesis-related protein (65 clones)

Protein synthesis- and/or transport-related protein (62 clones)

Cellular defense-related protein (15 clones)

Development and/or differentiation-related protein (13 clones)

DNA- and/or RNA-binding protein (174 clones)

ATP- and/or GTP-binding protein (68 clones)

[0063] The functions of the polypeptides encoded by the cDNAs of the present invention can be predicted by assessing the presence of signal sequence, transmembrane region, nuclear translocation signal, glycosylation signal, phosphorylation site, and zinc finger motif, SH3 domain, etc. in the amino acid sequences. The programs, PSORT (Nakai K., and Kanehisa M. (1992) Genomics 14: 897-911), SOSUI (Hirokawa T. et al. (1998) Bioinformatics 14: 378-379) (Mitsui Knowledge Industry), and MEMSAT (Jones D.T., Taylor W.R., and Thornton J.M. (1994) Biochemistry 33: 3038-3049) can be used to predict the existence of the signal sequence or transmembrane region. Alternatively, a partial amino acid sequence of the polypeptide is fused with another polypeptide such as GFP, the fusion polypeptide is transfected into cultured cells, and the localization is analyzed to predict the function of the original polypeptide.

[0064] Based on the determined nucleotide sequences of the full-length cDNAs obtained in the present invention, it is possible to predict more detailed functions of the polypeptides encoded by the cDNA clones, for example, by searching the databases such as GenBank, Swiss-Prot, UniGene, and nr for homologies of the cDNAs; or by searching the amino acid sequences deduced from the full-length cDNAs for signal sequences by using software programs such as PSORT, for transmembrane regions by using software programs such as SOSUI or for motifs by using software pro-

grams such as Pfam (http://www.sanger.ac.uk/Software/Pfam/index.shtml) and PROSITE (http://www.expasy.ch/prosite/) As a matter of course, the functions are often predictable by using partial sequence information (preferably 300 nucleotides or more) instead of the full-length nucleotide sequences. However, the result of the prediction by using partial nucleotide sequence does not always agree with the result obtained by using full-length nucleotide sequence, and thus it is needless to say that the prediction of function is preferably performed based on the full-length nucleotide sequences.

[0065] GenBank Swiss-Prot, UniGene and nr databases were searched for homologies of the full-length nucleotide sequences of the 2443 clones (see Example 6). The amino acid sequences deduced from the full-length nucleotide sequences were searched for functional domains by PSORT, SOSUI and Pfam. Prediction of functions of polypeptides encoded by the clones and the categorization thereof were performed based on these results obtained. The categorization was carried out by the following method.

[1] Firstly, the cDNA clones were classified into the above-mentioned 14 functional categories based on the results of annotation-based categorization (using the keywords in the case of Swiss-Prot hit data; using Definition or Reference information in the case of GenBank. UniGene, or nr hit data), and the signal sequence search of the ceduced ORFs by PSORT and the transmembrane region search by SOSUI.

[2] Secondly clones which had been unassignable to the categories by the method of [1] were searched for functional comains and/or motifs by Pfam. Based on the results, the clones were additionally classified into the above-mentioned 14 types of categories when they had a functional domain and/or motif assignable to any one of the categories

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[0066] The following 632 clones presumably belong to secretory and/or membrane proteins. ADIPS10000640 ADRGL10001470, ADRGL20013520. ADRGL20018540, ADRGL20035850, ASTRO20001410, ASTRO20C05330 ASTRO20033160, ASTRO20055750. ASTRO20058630, ASTRO20190390, BEAST20004540, BGGi110000240 BNGH420088500, BRACE20006400. BRACE20038000, BRACE20038470, BRACE20039040, BRACE20039540 BRACE20051380, BRACE20053630. BRACE20059370, BRACE20060550, BRACE20061050, BRACE20063530 BRACE20067430, BRACE20069090. BRACE20081720, BRACE20101700, BRACE20101710, BRACE20116110 BRACE20147800, BRACE20153680. BRACE20163350, BRACE20179340, BRACE20188470, BRACE20195100 BRACE20201570, BRACE20210140. BRACE20224480, BRACE20224500, BRACE20228480, BRACE20232340 BRACE20238000, BRACE20273890, BRACE20274080, BRALZ20013500, BRALZ20054710, BRALZ20054740 BRALZ20069760, BRALZ20073760. BRALZ20077930. BRAMY20000860, BRAMY20002770, BRAMY20025840 BRAMY20039260, BRAMY20060920. BRAMY20063970, BRAMY20111960, BRAMY20112800, BRAMY20124260 BRAMY20134140, BRAMY20135900. BRAMY20136210, BRAMY20144620, BRAMY20152110, BRAMY20174550 BRAMY20181220, BRAMY20195090. BRAMY20211390, BRAMY20211420, BRAMY20215230, BRAMY20218250 BRAMY20218670, BRAMY20229800. BRAMY20231720, BRAMY20247280. BRAMY20252180, BRAMY20273960 BRAMY20277170, BRAMY20284910. BRAMY20285160, BRAWH20015350, BRAWH20015890, BRAWH20016863 BRAWH20018730, BRAWH20030250. BRAWH20064050, BRAWH20110790, BRAWH20112940, BRAWH20117950 BRAWH20118230, BRAWH20121640, BRAWH20122580, BRAWH20132190, BRCAN20064010, BRCAN20071190 BRCAN20091560, BRCAN20103740, BRCAN20224720, BRCAN20273550, BRCAN20280360, BRCAN20285450 BRCOC10000870, BRCOC20004040, BRCOC20006370, BRCOC20041750, BRCOC20077690, BRCOC20078640 BRCOC20090520, BRCOC20101230, BRCOC20107300, BRCOC20114180, BRCOC20121720, BRCOC20:34480 BRCOC20136750, BRHIP10001290, BRHIP20000870, BRHIP20003120, BRHIP20103090, BRHIP20111200 BRHIP20118380, BRHIP20118910, BRHIP20121410, BRHIP20135100, BRHIP20174040, BRHIP20179200 BRHIP20183690, BRHIP20191490, BRHIP20191770, BRHIP20198190, BRHIP20207430, BRHIP20208270 BRHIP20208590, BRHIP20217620, BRHIP20233090, BRHIP20234380, BRHIP20238880, BRHIP20283036 BRHIP30004570, BRSSN20003120, BRSSN20043040, BRSSN20066110, BRSSN20120810, BRSSN20137020 BRSSN20142940, BRSSN20146100, BRSSN20151990, BRSSN20169050, BRSTN20002200, BRTHA2000474C BRTHA20046290, BRTHA20046420, COLON10001350, COLON20093370, CTONG10000100, CTONG10000940 CTONG10001650, CTONG20004690, CTONG20009770, CTONG20092570. CTONG20092580, CTONG20095340 CTONG20099380, CTONG20103480, CTONG20105080, CTONG20114740, CTONG20119200, CTONG20120770 CTONG20124730, CTONG20131490, CTONG20132220, CTONG20133480. CTONG20139340, CTONG20149950 CTONG20155400, CTONG20158660, CTONG20159530, CTONG20161850, CTONG20267700, D3OST1000109C D3OST20036070 D3OST20038560, D3OST30002580, D6OST20005070, D9OST20002780, D9OST2001547C D9OST20023970, D9OST20026730, D9OST20035940, D9OST20040180, DFNES20025880, FCBBF10000240 FCBBF10000380, FCBBF10001150, FCBBF10001210, FCBBF10001550, FCBBF10002430, FCBBF10002700 FCBBF10003220, FCBBF10003760, FCBBF10005460, FCBBF10005740, FCBBF20032970, FCBBF20042560 FCB8F20049300; FCBBF20051220, FCBBF30008470, ECBBF30024750, FCBBF30078290, FCBBF30083620 FCBEF30086440, FCBBF30090690, FCBBF30095260, FCBBF30123470, FCBBF30172550,

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UTERU20135860, UTERU20144640, UTERU20158300, UTERU20158800, UTERU20161570; UTERU20178100,
UTERU20183640, UTERU20186740
[0067] The following 128 clones presumably belong to glycoprotein-related proteins.
ADIPS10000640, BRACE20059370, BRACE20163350, BRAMY20277170, BRAMY20285160, BRAWH20064050,
BRAWH20112940, BRAWH20117950, BRAWH20118230, BRCAN20103740, BRCOC20004040, BRCOC20006370,
BRHIP10001290, BRHIP20103090, BRHIP20283030, BRHIP30004570, BRSSN20003120, BRSSN20146100,
BRTHA20046290, COLON10001350, CTONG20159530, D9OST20023970 D9OST20040180 FCBBF10001150;
FCBBF20049300, FCBBF30024750, FCBBF30083620, FCBBF30190850, FCBBF30238870, FEBRA20086620,
FEBRA20092890, HCHON20015980, HCHON20016040, HCHON20064590, HCHON20086720, HCHON20100740,
HEART20003060, HHDPC20014320, HHDPC20068620, HHDPC20092080, KIDNE20003940, KIDNE20007770,
KIDNE20101510, LIVER20064690, MESAN20125860, NT2NE20118960, NT2NE20157470, NT2NE20177520,
NT2RI20003480, NT2RI20056700, NT2RP70192730, NTONG20051530, NTONG20076930, OCBBF20107090,
OCBBF20108630, OCBBF20120390, OCBBF20145760, OCBBF20155060, PLACE60177140, SMINT20050750,
SMINT20073650. SMINT20105330, SMINT20106720. SMINT20112730, SMINT20127930, SMINT20153260,
SMINT20179740. SMINT20190170, SPLEN20021660, SPLEN20142100, SPLEN20157880, SPLEN20165310,
SPLEN20179810, SPLEN20186430, STOMA20001830, STOMA20005390, STOMA20005670, STOMA20006400,
STOMA20008880, STOMA20034770, STOMA20056640, STOMA20056670, STOMA20083610, STOMA20088380,
STOMA20092530, SYNOV20001520, SYNOV20001730, SYNOV20002510, SYNOV20002790. SYNOV20002970,
SYNOV20004260. SYNOV20007000, SYNOV20008240, SYNOV20009230, SYNOV20010880, SYNOV20011110,
SYNOV20013000, SYNOV20013560, SYNOV20013900, TESOP20004000, TESTI20136100, TESTI20216370,
TESTI20244190. TESTI20254860, TESTI20303220, TESTI20335200, TESTI20352620, TESTI20358980,
TESTI20442760. TESTI20449200. TESTI20455090, THYMU10005360, THYMU10005540, THYMU20147770,
THYMU20159430, THYMU20241850, TRACH20016210, TRACH20050040, TRACH20067620, TRACH20069180,
 TRACH20076740, TRACH20128230, UTERU20046980, UTERU20064860, UTERU20144640, UTERU20158800,
 UTERU20161570, UTERU20183640
 [0068] The following 84 clones presumably belong to signal transduction-related proteins.
 ASTRO20108190, BRACE20115920, BRACE20154120, BRACE20177200, BRACE20237270, BRAMY20104640,
 BRAMY20242470, BRAMY20271400, BRAWH20016620, BRAWH20103290, BRAWH20149340, BRCOC20021550,
 BRCOC20091960, BRHIP20189980, BRHIP20218580, BRHIP20238600, BRSSN20038200, CD34C30004240,
 CTONG20118150, CTONG20127450, CTONG20200310, FCBBF30012350, FCBBF40001730, FEBRA10001880,
 FEBRA20004620, FEBRA20132740, FEBRA20144170, FEHRT20003250, HCHON20007510, HLUNG20033780,
 IMR3220002430, KIDNE20008010, KIDNE20102710, KIDNE20107620, NT2NE20080170, NT2NE20181650,
 NT2RP70027380, NT2RP70036880, NT2RP70063950, NT2RP70078420, NT2RP70159960, NTONG20046140,
 NTONG20056570, OCBBF20028050, OCBBF20053430, OCBBF20054760, OCBBF20124360, OCBBF20127140,
 OCBBF20149280, OCBBF20173980, PEBLM20013120, PEBLM20085760, PROST20161950, PUAEN20015260,
 PUAEN20015860. PUAEN20083140, SMINT20028820, SMINT20049090, SMINT20110660, SPLEN20011410,
 SPLEN20121750, SPLEN20170310, SPLEN20181810, SPLEN20222270, SPLEN20250170, SPLEN20283650,
 TESTI20035960, TESTI20288910, TESTI20305540, TESTI20326810, TESTI20369650, TESTI20392250,
 TESTI20416640, TESTI20432750. TESTI20467320, THYMU20169680, THYMU20172150, THYMU20201980,
 THYMU20202890, TKIDN20004640, TKIDN20047480, TRACH20057690, UMVEN10001860, UTERU20146310
 [0069] The following 144 clones presumably belong to transcription-related proteins.
 3NB6920014590, ADIPS20004250, ASTRO20008010, ASTRO20168470, BLADE20003400, BLADE20003890,
 BRACE20060890, BRACE20068590, BRACE20257100, BRAMY20210400, BRAMY20260910, BRAMY20270730,
 BRAWH20028110, BRAWH20075700, BRAWH20096780, BRCAN20280210, BRCOC20144000, BRCOC20178270,
 BRHIP20005340, BRHIP20096170, BRHIP20119330, BRHIP20191860, BRHIP20195890, BRHIP202222280,
 BRSSN20039370, BRSSN20046790, BRSSN20176820, CTONG20050280, CTONG20075860, CTONG20085950,
 CTONG20091080, CTONG20092700, CTONG20121010, CTONG20124220, CTONG20133390, CTONG20133520,
 D9OST20033970, FCBBF10001710, FCBBF10004370, FCBBF20059090, FCBBF20068820, FCBBF30007680,
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FCBBF30010810, FCBBF30018550, FCBBF30025560, FCBBF30057290, FCBBF30083820, FCBBF30129630,
FCBBF30240960, FCBBF30246230, FEBRA20018690, FEBRA20026110, FEBRA20034680, FEBRA20040530,
FEBRA20082010. FEBRA20171380. FEBRA20195820. FEBRA20233770, HCHON20008320. HCHON20009560,
HCHON20035130, HHDPC10000830, HHDPC20030490, HHDPC20031130, KIDNE20027250, KIDNE20027950,
KIDNE20182690, LIVER20055440, NT2NE20010490, NT2NE20089970, NT2NE20142210, NT2NE20184900,
NT2RP60000770, NT2RP70043480, NT2RP70063950, NT2RP70102350, NT2RP70157890, NTONG20070200,
OCBBF10001850, OCBBF20020830, OCBBF20037440, OCBBF20046120, OCBBF20049300, OCBBF20054200,
OCBBF20066390, OCBBF20071840, OCBBF20080410, OCBBF20108190, OCBBF20125530, OCBBF20148280,
PEBLM20060360, PEBLM20078320, PERIC20003870, PROST10003220, PROST20047390, PROST20066880,
PROST20185830, PROST20189770, PROST20191640, SKNSH20008190, SMINT20001760, SMINT20028820,
SMINT20130320. SMINT20144800, SPLEN20026950, SPLEN20054290, SPLEN20079260, SPLEN20095410,
SPLEN20117660, SPLEN20140800, SPLEN20147390, SPLEN20160450, SPLEN20162680, SPLEN20243830,
SPLEN20250170, SPLEN20252190, SPLEN20267650, STOMA20032890, STOMA20063250, TESTI20039400.
TESTI20041690, TESTI20067200, TESTI20088220, TESTI20130010, TESTI20156100, TESTI20230850,
TESTI20318090, TESTI20320670, TESTI20378190, TESTI20385960, TESTI20409890, TESTI20420620,
TESTI20432820, TESTI20456110, THYMU20247480, TRACH20079690, TRACH20154860, TRACH20163170.
TRACH20164980, TRACH20184490, UTERU20099720, UTERU20116570, UTERU20145480, UTERU20176130
[0070] The following 387 clones presumably belong to disease-related proteins.
ADIPS20004250, ADRGL10001470, ADRGL20011190, ADRGL20018300, ADRGL20035850, ADRGL20078100,
ASTRO10001650, ASTRO20008010, ASTRO20027430, ASTRO20106150, ASTRO20108190, ASTRO20168470,
BLADE20003400, BLADE20003890, BRACE20038480, BRACE20039540, BRACE20059370, BRACE20108130,
BRACE20108880, BRACE20115920, BRACE20116460, BRACE20232840, BRACE20248260, BRACE20253330,
BRACE20284100, BRALZ20013500, BRALZ20017430, BRALZ20018340, BRAMY20000520, BRAMY20025840,
BRAMY20120910, BRAMY20134140, BRAMY20135900, BRAMY20162510, BRAMY20174550. BRAMY20210400.
BRAMY20211390, BRAMY20242470, BRAMY20245300, BRAMY20266850, BRAMY20285160, BRAWH20016620,
BRAWH20028110, BRAWH20064050, BRAWH20096780, BRAWH20110960, BRAWH20113430, BRAWH20114000,
BRAWH20118230, BRAWH20121640, BRAWH20128270, BRAWH20137480, BRCAN20103740, BRCAN20224720,
BRCAN20279700, BRCAN20280210, BRCAN20283190, BRCOC20001860, BRCOC20006370, BRCOC20027510,
BRCOC20055420, BRCOC20099370, BRCOC20178270, BRCOC20178560, BRHIP20003120, BRHIP20005340,
BRHIP20174040, BRHIP20176420, BRHIP20191490, BRHIP20191860, BRHIP20194940, BRHIP20195890,
BRHIP20222280. BRHIP20249110. BRHIP20285930, BRHIP30004880. BRSSN20013420. BRSSN20038200.
BRSSN20039370. BRSSN20046790, BRSSN20066110, BRSSN20101100, BRSSN20120810, BRSSN20187310,
BRTHA20046290, CD34C30004240, COLON10001350, CTONG20004690, CTONG20052650, CTONG20099550,
CTONG20124220, CTONG20125640, CTONG20128430, CTONG20131560, CTONG20133390, CTONG20153300,
CTONG20153580, CTONG20158040, CTONG20159530, D6OST20003580 D9OST20023970 DFNES20001530,
DFNES20037420, FCBBF10001210, FCBBF10001710, FCBBF10003770, FCBBF20059090, FCBBF20064520.
FCBBF30068820, FCBBF30010810, FCBBF30024750, FCBBF30025560, FCBBF30039020, FCBBF30049550,
FCBBF30057290, FCBBF30083620, FCBBF30129630, FCBBF30190850, FCBBF30238870, FCBBF30240960,
FCBBF30243640, FCBBF30279030, FCBBF30281880. FCBBF40001730, FEBRA10001880, FEBRA20004620,
FEBRA20010120, FEBRA20018690, FEBRA20082010, FEBRA20097310, FEBRA20130190, FEBRA20132740,
FEBRA20144170, FEBRA20195820, FEBRA20233220, FEBRA20233770, FEBRA20235500, FEHRT20003250,
HCHON10001760, HCHON20007380, HCHON20008320, HCHON20009560, HCHON20015230. HCHON20015980,
HCHON20016040, HCHON20035130, HCHON20036420, HCHON20064590, HCHON20067700. HCHON20086720,
HCHON20100740, HEART2003060, HEART20017730, HEART20025980, HEART20049410, HHDPC20014320,
HHDPC20030490. HHDPC20084140. HHDPC20091140, HHDPC20091780, HHDPC20092080. HLUNG20033780,
IMR3220002430, KIDNE20007770, KIDNE20020150, KIDNE20021680, KIDNE20022620, KIDNE20024830,
KIDNE20027950, KIDNE20101370, KIDNE20101510, KIDNE20182690, LIVER20002160. LIVER20055200,
LIVER20055440, LIVER20059810, LIVER20064690, MESAN20101140, MESAN20125860, MESAN20130220,
MESAN20154010, MESAN20174170, NOVAR10000910, NT2NE20010490, NT2NE20118960, NT2NE20157470,
NT2RI20040990, NT2RI20041880, NT2RI20048840, NT2RI20050960, NT2RI20240080, NT2RP60000770,
NT2RP70027380, NT2RP70032610, NT2RP70037240, NT2RP70192730, NT2RP70198350, NTONG20013620,
NTONG20015870, NTONG20028070, NTONG20067830, NTONG20070200, NTONG20090600. NTONG20092330,
OCBBF2006770, OCBBF20037440, OCBBF20046120, OCBBF20049300, OCBBF20053490, OCBBF20053730,
OCBBF20054760, OCBBF20071840, OCBBF20072240, OCBBF20078920, OCBBF20108430, OCBBF20108580,
OCBBF20127140, OCBBF20129360, OCBBF20145760, OCBBF20153350, OCBBF20173980, OCBBF20178880,
PEBLM10000710, PEBLM20013120, PERIC10000250. PLACE60060420, PLACE60177140, PROST20100460,
PROST20159240, PROST20169800, PROST20176170, PUAEN20018820, PUAEN20030180, PUAEN20055020,
PUAEN20083140, SKMUS20018230, SKMUS20018500, SKMUS20021530, SKMUS20024750, SKMUS20029200,
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SKMUS20048970, SKMUS20049030, SKNSH20008190, SKNSH20089400, SMINT20001760, SMINT20026890,
SMINT20028820, SMINT20050750, SMINT20073650, SMINT20105330, SMINT20112730, SMINT20121220,
SMINT20127350. SMINT20127930, SMINT20136130, SMINT20138900, SMINT20153260, SMINT20155180,
SMINT20179740. SMINT20190170, SMINT20191420, SPLEN20006070, SPLEN20011410, SPLEN20026950,
SPLEN20027440, SPLEN20039240, SPLEN20079260, SPLEN20095410, SPLEN20146450, SPLEN20147390,
SPLEN20151210, SPLEN20160450, SPLEN20170310, SPLEN20179180, SPLEN20186430, SPLEN20212730,
SPLEN20243830. SPLEN20245300. SPLEN20250390. SPLEN20252190. SPLEN20267650. SPLEN20305620.
STOMA20001830, STOMA20005390, STOMA20008880, STOMA20010250, STOMA20034770. STOMA20046680,
STOMA20056670, STOMA20064470, STOMA20077450, STOMA20080500, STOMA20083610, STOMA20088380,
SYNOV20001520, SYNOV20001730, SYNOV20002790, SYNOV20002970, SYNOV20007000. SYNOV20008240,
SYNOV20009230, SYNOV20010880, SYNOV20011110, TBAES20003770, TESOP20004000, TESOP20005270,
                                                             TESTI20116830,
TESTI20031270, TESTI20036380, TESTI20044310,
                                             TESTI20067200,
                                                                            TESTI20121550,
TESTI20156100,
               TESTI20168480,
                              TESTI20208400,
                                             TESTI20215990,
                                                             TESTI20231940,
                                                                            TESTI20234360,
               TESTI20238610,
TESTI20237520,
                              TESTI20239510,
                                             TESTI20249990,
                                                             TESTI20266740,
                                                                             TESTI20316870,
TESTI20318090,
               TESTI20335050,
                                             TESTI20343570,
                              TESTI20335200,
                                                             TESTI20352620,
                                                                            TESTI20368330,
              TESTI20385960,
TESTI20369650,
                              TESTI20392250,
                                             TESTI20400940,
                                                             TESTI20404240,
                                                                            TESTI20420620.
              TESTI20438570,
                                            TESTI20442760,
TESTI20436560.
                              TESTI20441940.
                                                             TESTI20443090.
                                                                            TESTI20449200:
TESTI20455090, TESTI20455620, TESTI20456110, TESTI20463580,
                                                             TESTI20465350,
                                                                            TESTI20465690,
TESTI20467210, THYMU20122730, THYMU20126900, THYMU20130890, THYMU20159430, THYMU20169680.,
THYMU20172150, THYMU20180280, THYMU20193640, THYMU20209590, THYMU20232090, THYMU20247480,
TKIDN1000010. TKIDN2004640, TKIDN20047480, TRACH20016210, TRACH20019960, TRACH20050040,
TRACH20057690. TRACH20067620, TRACH20077540, TRACH20079690, TRACH20096610, TRACH20105870,
TRACH20121380. TRACH20154860, TRACH20162860, TRACH20163170, TRACH20164980, TRACH20190240,
TSTOM20005690. TUTER20002830, UTERU20030570, UTERU20116570, UTERU20144640, UTERU20151980,
UTERU20158800. UTERU20183640, UTERU20185230
[0071] The following 206 clones presumably belong to the category of enzymes and/or metabolism-related proteins.
3NB6910001910, ADRGL10001470, ADRGL20035850, ADRGL20078100, ASTRO20105820, ASTRO20106150,
ASTRO20130500 ASTRO20145760, BRACE20027620, BRACE20038000, BRACE20062640, BRACE20096200,
BRACF20107530 BRACE20108130, BRACE20108880, BRACE20116460, BRACE20148240, BRACE20185680,
BRACE20253160. BRALZ20017430, BRALZ20018340, BRAMY20104640, BRAMY20134140, BRAMY20153110,
BRAMY20213100. BRAMY20252720, BRAWH20016620, BRAWH20105840, BRAWH20112940, BRAWH20114000.
BRAWH20117950 BRAWH20125380, BRAWH20132190, BRAWH20171030, BRCAN20054490, BRCAN20224720,
BRCAN20280360. BRCAN20283190, BRCAN20283380, BRCOC20001860, BRCOC20031250, BRCOC20055420,
BRCOC20091960, BRCOC20144000, BRHIP10001290, BRHIP20005530, BRHIP20096850, BRHIP20103090,
BRHIP20174040. BRHIP20249110, BRSSN20013420, BRSSN20015790, BRSSN20120810, BRSSN20146100,
CTONG20095340 CTONG20106520, CTONG20118250, CTONG20127450, CTONG20140580, CTONG20153300,
CTONG20*58040 D3OST20006180, D6OST20003580, DFNES20031920, DFNES20071130, FCBBF10001820,
FCBBF10003670 FCBBF30012350, FCBBF30012810, FCBBF30175310, FCBBF30243640, FEBRA10001880,
FEBRA20007620, FEBRA20130190, FEBRA20144170, FEBRA20167390, FEBRA20196630, FEHRT20003250,
HCHON10001760. HCHON20003220, HCHON20015350, HEART20034320, HEART20090000, HHDPC20014320,
KIDNE20002520. KIDNE20008010, KIDNE20021680, KIDNE20022620, KIDNE20028390, KIDNE20028720,
KIDNE20107620 LIVER20059810, MESAN20154010, NT2NE20118960, NT2NE20157470, NT2RI20005750,
N12HI20244600. NT2RI20273230, NT2RP70032610, NT2RP70045590, NT2RP70192730, NT2RP70195430,
N1ONG20009770. NTONG20013620, NTONG20046140, OCBBF20028650, OCBBF20030910, OCBBF20046690,
OCBBF20050770. OCBBF20053430, OCBBF20053490, OCBBF20053730, OCBBF20054760, OCBBF20078920,
OCBBF20124360. OCBBF20129360, OCBBF20178880, PEBLM20044520, PEBLM20052820, PEBLM20060490,
PERIC10000250. PLACE50000660, PROST20083600, PROST20169800, PUAEN20015260, PUAEN20030180,
SKMJS20018230. SMINT20028820, SMINT20049090, SMINT20102780, SMINT20105330, SMINT20106290,
SMINT20110660. SMINT20152940, SMINT20191420, SMINT20191530, SPLEN20021660, SPLEN20026950,
SPLEN20121750. SPLEN20145720, SPLEN20149240, SPLEN20150940, SPLEN20151210, SPLEN20173510,
SPLEN20212730. SPLEN20250390. SPLEN20305620, STOMA20006860, STOMA20077450. TBAES20002550,
TBAES20003150, TESOP20004000, TESOP20005270, TESTI20001000, TESTI20002720, TESTI20002780,
TESTI20060400. TESTI20066670, TESTI20082330, TESTI20083200, TESTI20108720, TESTI20116830,
TESTI20143390. TESTI20148000. TESTI20216370, TESTI20232140, TESTI20234360,
                                                                             TEST120237520.
               TESTI20266740, TESTI20314180, TESTI20334410, TESTI20343570,
                                                                             TESTI20352620.
TESTI20239510.
                                                              TESTI20375340.
               TESTI20366910, TESTI20368330,
                                                                             TESTI20397760,
                                              TESTI20369650.
TEST120355020.
               TESTI20432750, TESTI20463580, TESTI20465350,
                                                             TESTI20471410,
                                                                             TESTI20473830.
TESTI20416640.
THYMU20023380, THYMU20111830, THYMU20126900, THYMU20169680, THYMU20202890, TKIDN20004640,
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TKIDN20047480, TRACH20003590, TRACH20016210, TRACH20019960, TRACH20041830, TRACH20057690, TRACH20067620, TRACH20084720, TRACH20085830, TRACH20162860, UTERU20064860, UTERU20144640, UTERU20146310, UTERU20151980

[0072] The following 33 clones presumably belong to the category of cell division- and/or cell proliferation-related proteins

BRALZ20077900, BRAMY20135900, BRAWH20002320, BRAWH20128270, BRCAN20071190. BRCAN20273640, BRHIP20096170, CTONG10000940, CTONG20124220, FCBBF30247930, FEBRA20113560, HCASM10000500, HCHON20097490, MESAN20025190, NT2RI20050960, OCBBF20039250, OCBBF20054760, OCBBF20072240, SMINT20051610. SPLEN20147110, SPLEN20284240, TESOP20005690, TESTI20234360, TESTI20305540, TESTI20332420, TESTI20335050, TESTI20368330, TESTI20392760, TESTI20400940, THYMU20161640, TKIDN20047480, UTERU20097760, UTERU20185230

[0073] The following 75 clones presumably belong to the category of cytoskeleton-related proteins.

ADRGL20011190, ADRGL20018300, ASTRO10001650, ASTRO20055750, BRACE20003070, BRACE20059370, BRACE20163350, BRAMY20121620, BRAMY20157820, BRAMY20242470, BRAWH20028110, BRAWH20137480, BRCAN20003460, BRCOC2008160, BRCOC20059510, BRHIP20115080, BRHIP20137230, BRHIP20167880, BRHIP202883030, BRHIP20285830, BRSSN20187310, CTONG10002770, CTONG20052900, CTONG20121580, FCBBF10001150, FCBBF30013770, FCBBF30015940, FCBBF30049550, FEBRA20024100, FEBRA20237640, HCHON20015980, HCHON20068410, HEART20017730, HEART20025980, HEART20061950, HEART20077670, HLUNG20016330, KIDNE20118580, MESAN20004570, NT2RI20040990, NT2RI20041880, NT2RP70037240, NT2RP70062230, NTONG20015870, NTONG20056570, NTONG20067830, NTONG20090600, OCBBF20107090, OCBBF20155060, PLACE60079250, PUAEN20040670, SKMUS20001980, SKMUS20016220, SKMUS20048970, SKMUS20049030, SMINT20024570, SMINT20026890, SMINT20121220, SMINT20138900, SPLEN20006070, SPLEN20027440, SPLEN20142100, TESTI20063830, TESTI20094230, TESTI20278400, TESTI20371030, TESTI20436560. TESTI20455090, THYMU20105190, THYMU20172150, THYMU20209590, TRACH20096610, UMVEN10001560, UTERU20116570

[0074] The following 65 clones presumably belong to the category of nuclear proteins and/or RNA synthesis-related proteins.

BRACE20057190, BRACE20064880, BRACE20248260, BRACE20253160, BRAMY20000520, BRAMY20120910, BRAWH20113430, BRAWH20171030, BRCAN10001490, BRCAN20283190, BRCOC20037320, BRCOC20178560, BRHIP20106100, BRHIP20176420, BRHIP20243470, BRSSN20101100, CTONG20114290, CTONG20125540, CTONG20131560, CTONG20140580, DFNES20001530, FCBBF20064520, FEBRA20007620, FEBRA20010120, FEBRA20097310, FEBRA20144170, FEBRA20174410, FEBRA20215500, IMR3220002430, MESAN20101140, NT2RI20273230, OCBBF20028650, OCBBF20030910, OCBBF20078920, PROST20104000, PUAEN20018820, SKMUS20007010, SMINT20127350, SMINT20177360, SMINT20191530, SPLEN20008740, SPLEN20146450, STOMA20046680, TESTI20082330, TESTI20094470, TESTI20121550, TESTI20208400, TESTI20234360, TESTI20237520, TESTI20249990, TESTI20334410, TESTI20355020, TESTI20368330, TESTI20392760, TESTI20408970, TESTI20436560, TESTI20438570, TESTI20443090, THYMU20193640, THYMU20202890, THYMU20241210, TRACH20096610, TUTER20002830, UTERU20151980, UTERU20176320

[0075] The following 62 clones presumably belong to the category of protein synthesis- and/or protein transport-

3NB6910001910, ASTRO20106150, ASTRO20130500, ASTRO20141350, BRACE20038480, BRACE20052160, BRACE20057620, BRACE20106840, BRACE20172980, BRACE20192440, BRAWH20110960, BRCOC20037320, BRHIP20005530, BRSSN20120810, BRSTN20005360, CTONG20009770, CTONG20114290, CTONG20125640, CTONG20153300, D6OST20003580 DFNES20037420, FCBBF30012810, FEBRA20080810, HCHON20064590, HHDPC20014320, HHDPC20084140, HLUNG20017120, LIVER20064690, NT2NE20132170, NT2NE20157470, NT2RP70133740, NTONG20009770, NTONG20075220, NTONG20076930, OCBBF20030910, OCBBF20035930, OCBBF20153340, PLACE60060420, SMINT20152940, SPLEN20008740, SPLEN20103950, SPLEN20118300, SPLEN20212730, SPLEN20250390, STOMA20077450, TBAES20002550, TESOP20004000, TESTI20239510, TESTI20278400, TESTI20314180, TESTI20463580, THYMU20111830, THYMU20122730, THYMU20130890, THYMU20232090, TKIDN10000010, TRACH20084720, TRACH20105870, TRACH20139820, TRACH20149970, UTERU20120310, UTERU20188110

[0076] The following 15 clones presumably belong to the category of cellular defense-related proteins. BRCOC20144000, CTONG20092680, KIDNE20020150, LIVER20002160, NT2RI20050960, NT2RP70045590,

OCBBF20128120, PLACE60003480, SKNSH20089400, SMINT20106290, SPLEN20039240, TESTI20001000, TESTI20455620, TRACH20028030, UTERU20176320

[0077] The following 13 clones presumably belong to the category of development and/or differentiation-related proteins

3NB6920014590, BRAMY20211390, CTONG20091080, CTONG20121010, FCBBF30024750, KIDNE20027250,

NT2NE20142210, OCBBF20054200, PROST10003220, SKMUS20007010, SPLEN20179810, STOMA20063250, TESTI20291960 [0078] The following 174 clones presumably belong to the category of DNA- and/or RNA-binding proteins. 3NB6920014590, ADIPS20004250, ASTRO2008010, ASTRO20168470, BLADE20003400, BLADE20003890, BRACE20057620, BRACE20060890, BRACE20064880, BRACE20068590, BRACE20248260, BRACE20253160, BRAMY20000520, BRAMY20213100, BRAMY20260910, BRAMY20270730, BRAWH20028110, BRAWH20075700, BRAWH20096780, BRAWH20113430, BRCAN10001490, BRCAN20280210, BRCAN20283190, BRCOC20144000, BRCOC20178270, BRCOC20178560, BRHIP20005340, BRHIP20106100, BRHIP20119330, BRHIP20153600, BRHIP20176420, BRHIP20191860, BRHIP20195890, BRHIP20222280, BRSSN20039370, BRSSN20046790, BRSSN20176820, CTONG20050280, CTONG20075860, CTONG20085950, CTONG20091080, CTONG20092700, CTONG20121010, CTONG20124220, CTONG20125540, CTONG20133390, CTONG20133520, CTONG20140580, CTONG20156780. D9OST20033970 FCBBF10001710, FCBBF10004370, FCBBF20059090, FCBBF20064520, FCBBF20068820, FCBBF30007680, FCBBF30010810, FCBBF30018550, FCBBF30025560, FCBBF30057290, FCBBF30083820, FCBBF30129630, FCBBF30240960. FCBBF30246230, FEBRA20010120, FEBRA20018690, FEBRA20026110, FEBRA20034680, FEBRA20040530, FEBRA20082010, FEBRA20097310, FEBRA20171380, FEBRA20195820, FEBRA20196630, FEBRA20233770, HCHON20008320, HCHON20009560, HCHON20035130, HHDPC10000830, HHDPC20031130, KIDNE20017130, KIDNE20027250, KIDNE20027950, KIDNE20107390, KIDNE20182690, LIVER20055440, MESAN20101140, NT2NE20010490, NT2NE20089970, NT2NE20142210, NT2NE20184900, NT2RP60000770, NT2RP70044280, NT2RP70102350, NT2RP70157890, NTONG20070200, OCBBF10001850, OCBBF20020830, OCBBF20037440, OCBBF20046120, OCBBF20049300. OCBBF20066390, OCBBF20071840, OCBBF20078920, OCBBF20080410, OCBBF20108190, OCBBF20125530, OCBBF20148280, PEBLM20060360, PEBLM20060490, PEBLM20078320, PERIC10000250, PROST10003220, PROST20047390, PROST20066880, PROST20185830, PROST20189770, PROST20191640, PUAEN20018820, SKNSH20008190, SKNSH20089400, SMINT20001760, SMINT20127350, SMINT20144800, SMINT20177360, SMINT20191530, SPLEN20054290, SPLEN20079260, SPLEN20095410, SPLEN20140800, SPLEN20147390, SPLEN20160450, SPLEN20252190, SPLEN20267650, STOMA20010250, STOMA20032890, STOMA20046680, STOMA20063250, TESTI20039400, TESTI20067200, TESTI20088220, TESTI20094470, TESTI20121550, TESTI20130010. TESTI20156100, TESTI20204450, TESTI20230850, TESTI20237520, TESTI20266740, TESTI20318090, TESTI20320670, TESTI20334410, TESTI20355020, TESTI20378190, TESTI20385960, TESTI20432820, TESTI20443090, TESTI20456110, THYMU20193640, THYMU20241210, THYMU20247480, TRACH20079690, TRACH20105870, TRACH20139820, TRACH20154860, TRACH20163170, TRACH20164980, TRACH20184490, TUTER20002830, UTERU20099720, UTERU20116570, UTERU20145480, UTERU20176130, UTERU20185230 [0079] The following 68 clones presumably belong to the category of ATP- and/or GTP-binding proteins. 3NB6910001910, BRACE20108130, BRACE20148240, BRAMY20134140, BRAMY20157820, BRAMY20174550, BRAWH20164460, BRCAN20003460, BRCAN20054490, BRCAN20283190, BRCOC20059510, BRCOC20144000, BRHIP20103090, BRHIP20115080, BRHIP20167880, BRSTN20005360, CD34C30004240, CTONG20095340, CTONG20121580, CTONG20200310, DFNES20037420, FCBBF20067810, FCBBF30012350, FCBBF30015940, FEBRA20007620, FEBRA20024100, FEBRA20144170, KIDNE20020150, KIDNE20028720, LIVER20002160, LIVER20087060, NT2RI20005750, NT2RI20041880, NT2RI20048840, NT2RI20273230, OCBBF20028650, OCBBF20046690, OCBBF20054760, OCBBF20108430, OCBBF20108630, SMINT20121220, SMINT20183530, SMINT20191530. SPLEN20026950, SPLEN20039240, SPLEN20099700, SPLEN20145720, SPLEN20179180, STOMA20006860, TESTI20035960, TESTI20355020, TESTI20397760, TESTI20400940, TESTI20417300, TESTI20443090, TESTI20455620, THYMU20105190, THYMU20202890, THYMU20209590, TKIDN20004640, TKIDN20047480, TRACH20005400, TRACH20019960, TRACH20057690, TRACH20084720, UTERU20168220, UTERU20176320, UTERU20185230

[0080] Among the clones other than the ones shown above, BRAMY20248490, FCBBF10002800, NTONG20092290, OCBBF20127040, SMINT20163960, THYMU20279750, TRACH20167220, are clones which were predicted to highly possibly belong to the category of secretory protein and/or membrane protein based on the result of domain search by Pfam.

FCBBF10002800, NTONG20092290, OCBBF20127040, SMINT20163960, TESTI20478850, THYMU20279750

[0081] The 6 clones shown above are clones which were predicted to highly possibly belong to the category of glycoprotein-related protein based on the result of domain search by Pfam.

BRACE20060720, BRACE20223330, BRALZ20058880, BRAMY20148130, BRAWH20101360, BRCAN20124080,

BRACE20060720, BRACE20223330, BRALZ20058880, BRAMY20148130, BRAWH20101360, BRCAN20124080, BRHIP20253660, CTONG10000620, CTONG20014280, CTONG20124010, KIDNE20109890, MESAN20171520, OCBBF20109310, OCBBF20140640, PROST20079500, PUAEN20078980, SPLEN20077500, SPLEN20143180, TESTI20017950, TESTI20184620, TESTI20208710, TESTI20211160, TESTI20226230, TESTI20234140, TESTI20258460, TESTI20275030

[0082] The 26 clones shown above are clones which were predicted to highly possibly belong to the category of

signal transduction-related protein based on the result of domain search by Pfam.

ADRGL20048330, ASTRO20064750, ASTRO20084250, BRACE20151320, BRALZ20058880, BRHIP20207990, CTONG20093950, FCBBF30195640, FEBRA10001900, FEBRA20090290, FEBRA20214970, FEBRA20222040, KIDNE20109890, LIVER20087510, MESAN20029400, MESAN20031900. MESAN20035290, MESAN20136110, NT2NE20130190, PEBLM20060310, PERIC20004780, PROST20171280, PUAEN20078980, SMINT20115880, SPLEN20095550, TESTI20023510, TESTI20083940, TESTI20152460, TESTI20185650, TESTI20189410, TESTI20200710. TESTI20308600, TESTI20343070, TESTI20369690, TESTI20381040, UTERU20050690

[0083] The 36 clones shown above are clones which were predicted to highly possibly belong to the category of transcription-related protein based on the result of domain search by Pfam.

BGGI120006160, BRACE20053480, BRACE20190040, BRACE20223330, BRAWH20101360, BRAWH20185060, BRCOC20023230, BRHIP20252450, BRSSN20105870, BRSSN20117990, BRTHA20000570, CTONG20098440, CTONG20129960, CTONG20146300, CTONG20155180, FEBRA20025270, HEART20083640, KIDNE20009470, LIVER20035680, MESAN20029400, MESAN20031900, MESAN20186700, NOVAR10000150, NTONG20029480, OCBBF20079310, OCBBF20082830, PEBLM20042900, PLACE60136500, PLACE60136720. PROST20114390, SKNSH20020540, SMINT20013480, SMINT20174360, SPLEN20077500, SPLEN20119810, SPLEN20126190, SPLEN20174260, SPLEN20211220, TESTI20046750, TESTI20057750, TESTI20061110, TESTI20197940, TESTI20211160, TESTI20226230, TESTI20255820, TESTI20317600, TESTI20377230, THYMU20111180, THYMU20115850. THYMU20143270, THYMU20240710, UTERU20055330, UTERU20055930, UTERU20064000, UTERU20119060

[0084] The 55 clones shown above are clones which were predicted to highly possibly belong to the category of enzyme and/or metabolism-related protein based on the result of domain search by Pfam. TESTI20127760, TESTI20392270

[0085] The 2 clone shown above is a clone which was predicted to highly possibly belong to the category of cell division and/or cell proliferation-related protein based on the result of domain search by Pfam.

FCBBF30262510. MESAN20031900, NT2NE20125050, SMINT20068010, SPLEN20163560, STOMA20092890, TESTI20382750

[0086] The 7 clones shown above are clones which were predicted to highly possibly belong to the category of cytoskeleton-related protein based on the result of domain search by Pfam. THYMU20118520

[0087] The clone shown above is clone which was predicted to highly possibly belong to the category of Nuclear protein and/or RNA synthesis-related protein based on the result of domain search by Pfam. BRACE20053480. BRACE20240740, KIDNE20009470, OCBBF20140890. SMINT20035690, UTERU20064000

[0088] The 6 clones shown above are clones which were predicted to highly possibly belong to the category of Protein

synthesis- and/or transport-related protein based on the result of domain search by Pfam.

ADRGL20048330, ASTRO20064750, ASTRO20084250, BRACE20151320. BRACE20190040, BRACE20223330, BRALZ20058880, BRAMY20103570, BRCOC20023230, BRHIP20207990. BRTHA20000570, CTONG20093950, CTONG20129960, CTONG20146300, CTONG20155180, CTONG20160560, FCBBF10004120, FCBBF30195640, FEBRA10001900, FEBRA20090290, FEBRA20214970, FEBRA20222040, HCHON20008150, HEART20083640, KIDNE20109890. LIVER20035680, LIVER20087510, MESAN20029400. MESAN20031900, MESAN20035290, MESAN20136110, MESAN20186700, NT2NE20130190, NT2RI20025640. NTONG20029480, PEBLM20060310, PERIC20004780, PROST20114390, PROST20171280, PUAEN20078980. SMINT20115880, SPLEN20095550, SPLEN20119810, TESTI20023510, TESTI20057750. TESTI20083940. TESTI20152460, TESTI20185650, TESTI20189410, TESTI20200710, TESTI20308600, TESTI20343070. TESTI20369690, TESTI20381040,

[0089] The 57 clones shown above are clones which were predicted to highly possibly belong to the category of DNA- and/or RNA-binding protein based on the result of domain search by Pfam. PLACE60136720

[0090] The clone shown above is a clone which was predicted to highly possibly belong to the category of ATP- and/ or GTP-binding proteins based on the result of domain search by Pfam.

[0091] The 213 clones shown below are clones which were unassignable to any of the above-mentioned categories, but have been predicted to have some functions based on homology search using their full-length nucleotide sequences and motif search in their estimated ORFs. Clone Name, Definition in the result of homology search or Motif Name in the motif search, demarcated by a double slash mark (//), are shown below.

ADRGL20028570//Rattus norvegicus MG87 mRNA, complete cds. ADRGL20061930//transposon-derived Busterl transposase-like protein ASTRO20012490//Eukaryotic initiation factor 1A ASTRO20072210//PERIAXIN.

THYMU20115850, UTERU20050690, UTERU20055330

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ASTRO20114370//Mus musculus SMAR1 mRNA, complete cds. ASTRO20125520//dnaj protein [Schizosaccharomyces pombe] ASTRO20143630//KH domain// Bacterial regulatory proteins, crp family ASTRO20155290//TPR Domain// TPR Domain// TPR Domain ASTRO20181690//oocyte-specific protein P100 BGGI110001930//UBX domain BRACE20011070//Mus musculus F-box protein FBX15 mRNA, partial cds. BRACE20039440//Drosophila melanogaster CHARYBDE (charybde) mRNA, complete cds. BRACE20050900//TPR Domain// TPR Domain// TPR Domain// TPR Domain BRACE20053280//Mus musculus Pdz-containing protein (Pdzx) mRNA, complete cds. BRACE20057730//toxin sensitivity protein KTI12 homolog BRACE20058580//Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds. BRACE20063780//NOL1/NOP2/sun family BRACE20269200//Heat-labile enterotoxin alpha chain BRACE20276430//Homo sapiens retinoblastoma-associated protein RAP140 mRNA, complete cds. BRACE20286360//Alpha adaptin carboxyl-terminal domain BRAMY10001300//Homo sapiens MAGE-E1b mRNA, complete cds. BRAMY20045240//Flagellar L-ring protein BRAMY20054880//Rattus norvegicus KPL2 (Kpl2) mRNA, complete cds. BRAMY20167060//Collagen triple helix repeat (20 copies) BRAMY20184670//Homo sapiens mRNA for ALEX1, complete cds. BRAMY20217460//Homo sapiens cardiac voltage gated potassium channel modulatory subunit mRNA, complete cds, alternatively spliced. BRAMY20240040//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds. BRAMY20247110//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds. BRAWH20004600//Mus musculus mRNA for NAKAP95, complete cds. BRAWH20011710//cytoplasmic linker 2 BRAWH20012390//Trichomonas vaginalis mRNA for centrin (ce1 gene). BRAWH20017010//Homo sapiens testes development-related NYD-SP22 mRNA, complete cds. BRAWH20029630//Homo sapiens bet3 (BET3) mRNA, complete cds. BRAWH20138660//Homo sapiens stonin 2 mRNA, complete cds. BRCOC20008500//Human ras inhibitor mRNA, 3' end. BRCOC20026640//Gag P30 core shell protein BRCOC20035130//14-3-3 PROTEIN EPSILON (MITOCHONDRIAL IMPORT STIMULATION FACTOR L SUBU-NIT) (PROTEIN KINASE C INHIBITOR PROTEIN-1) (KCIP-1) (14-3-3E). BRCOC20074760//CDC4-LIKE PROTEIN (FRAGMENT). BRCOC20110100//Integrase core domain BRCOC20176520//Rattus norvegicus mRNA for type II brain 4.1, complete cds. BRHIP20001630//Protein of unknown function DUF16 BRHIP20132860//Homo sapiens rhophilin-like protein mRNA, complete cds. BRHIP20143730//MYND finger BRHIP20175420//Mus musculus partial mRNA for stretch responsive protein 278 (sr278 gene). BRHIP20236950//Outer Capsid protein VP4 (Hemagglutinin) BRSSN20014260//RIBONUCLEASE INHIBITOR. BRSSN20018690//Homo sapiens NY-REN-25 antigen mRNA, partial cds. BRSSN20021600//RING CANAL PROTEIN (KELCH PROTEIN). BRSSN20177570//Phosducin BRSTN10000830//Kelch motif// Kelch motif// Kelch motif// Kelch motif CTONG10000220//Mus musculus cerebellar postnatal development protein-1 (Cpd1) mRNA, partial cds. CTONG10000930//Armadillo/beta-catenin-like repeats CTONG20027090//Glypican// Leucine Rich Repeat// Leucine Rich Repeat CTONG20076130//ZINC FINGER PROTEIN 185 (LIM-DOMAIN PROTEIN ZNF185) (P1-A). CTONG20096750//Disintegrin CTONG20100240//Mus musculus radial spokehead-L protein (Rshl1) mRNA, complete cds. CTONG20139860//Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16 mRNA, complete cds. CTONG20143690//MYND finger

CTONG20149460//RING CANAL PROTEIN (KELCH PROTEIN).

CTONG20165050//Keratin, high sulfur B2 protein CTONG20186320//RING CANAL PROTEIN (KELCH PROTEIN). D3OST20013280//ARP2/3 COMPLEX 16 KDA SUBUNIT (P16-ARC). D3OST20024360//Homo sapiens neuroendocrine differentiation factor mRNA, complete cds. D9OST20031370//Homo sapiens mRNA for partial putative TCPTP-interacting protein (ptpip5 gene). DFNES20014040//TRICHOHYALIN. FCBBF10000630//Homo sapiens huntingtin interacting protein HYPB mRNA, partial cds. FCBBF10000770//Homo sapiens REC8 mRNA, partial cds. FCBBF10005060//CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP). FCBBF10005500//Keratin, high sulfur B2 protein FCBBF20014270//ACYL-COA-BINDING PROTEIN (ACBP) (DIAZEPAM BINDING INHIBITOR) (DBI) (EN-DOZEPINE) (EP). FCBBF20042170//Homo sapiens NIBAN mRNA, complete cds. FCBBF30016320//SecA protein, amino terminal region FCBBF30033050//Sm protein FCBBF30054440//PLAT/LH2 domain FCBBF30225660//Ank repeat// Ank repeat// Ank repeat// K+ channel tetramerisation domain// BTB/POZ domain FCBBF30233680//G10 protein FCBBF30246630//H.sapiens mRNA for ZYG homologue. FCBBF30250730//TRICHOHYALIN. FCBBF30252520//Homo sapiens bicaudal-D (BICD) mRNA, alternatively spliced, partial cds. FCBBF30252800//NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43). FCBBF30252850//Mus musculus peripherial benzodiazepine receptor associated protein (Pap7) mRNA, complete cds. FCBBF30285280//Keratin, high sulfur B2 protein// Bacterial regulatory proteins, gntR family FEBRA20088360//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KDA COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN AL-PHA C SUBUNIT). FEBRA20184330//Rattus norvegicus glutamate receptor interacting protein 2 (GRIP2) mRNA, complete cds. FEBRA20192420//Cyclin-dependent kinase inhibitor// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif FEBRA20196370//Cyclin-dependent kinase inhibitor// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif FEBRA20225040//high-glucose-regulated protein 8 HCHON20001560//TRANSCRIPTION FACTOR-LIKE PROTEIN MORF4. HCHON20003440//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds. HCHON20010990//TPR Domain HCHON20059870//Hypothetical protein. HHDPC20034390//Cereal trypsin/alpha-amylase inhibito HHDPC20057420//Mus musculus proline-rich protein (Bprp) mRNA, complete cds. HHDPC20064600//SUPPRESSOR PROTEIN SRP40. HLUNG20023340//Mus musculus SLM-1 (S1m1) mRNA, complete cds. KIDNE20007210//Xenopus laevis mRNA for RPA interacting protein alpha (ripalpha gene). KIDNE20028830//K-box region KIDNE20115080//Homo sapiens mRNA for hNBL4, complete cds. KIDNE20124400//Homo sapiens mRNA for ALEX1, complete cds. KIDNE20127100//Drosophila melanogaster Diablo (dbo) mRNA, complete cds. KIDNE20127750//Homo sapiens partial mRNA for transport-secretion protein 2.1 (TTS-2.1 gene). KIDNE20190740//Rattus norvegicus SNIP-b mRNA, complete cds. LIVER10004790//EF hand LIVER20011130//Homo sapiens F-box protein FBL9 mRNA, partial cds. LIVER20064100//Ciona intestinalis mRNA for myoplasmin-C1, complete cds. LIVER20080530//Drosophila melanogaster forked mRNA for large Forked protein, complete cds.

MAMGL10000830//Drosophila melanogaster L82B (L82) mRNA, complete cds.

MESAN20036460//Corticotropin-releasing factor family

MESAN20127350//myelin expression factor-3

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MESAN20141920//Human ovarian cancer downregulated myosin heavy chain homolog (Docl) mRNA, complete NT2NE20010400//Homo sapiens GL013 mRNA, complete cds. NT2NE20122430//GLYOXYLATE-INDUCED PROTEIN. NT2NE20158600//erythroid ankyrin - Synechocystis sp. (strain PCC 6803). NT2RI20001330//Homo sapiens KE03 protein mRNA, partial cds. NT2RI20009870//lunatic fringe precursor [Mus musculus] NT2RI20046080//recA bacterial DNA recombination proteins NT2RI20091730//Molluscan rhodopsin C-terminal tail NT2RP60000850//Bos taurus RPGR-interacting protein-1 (RPGRIP1) mRNA, complete cds. NT2RP70080850//SPRY domain// Adenovirus EB1 55K protein / large t-an NT2RP70105210//Myc amino-terminal region NT2RP70188710//Yeast PIR proteins NT2RP70194450//Bacterial regulatory proteins, crp family NTONG20052650//Gallus gallus Xin mRNA, complete cds. NTONG20064400//REPETIN. NTONG20064840//Mus musculus s1p1 mRNA for synaptotagmin-like protein 1, complete cds. NTONG20066460//Mus musculus Gd mRNA for gasdermin, complete cds. NTONG20067090//Mus musculus mRNA for Sh3yl1, complete cds. NTONG20070340//collagen alpha 1(IX) chain NTONG20083650//TPR Domain// TPR Domain// TPR Domain// PPR repeat// TPR Domain// PPR repeat// TPR NTONG20088620//Homo sapiens genethonin 3 mRNA, partial cds. OCBBF10000540//Mus musculus rjs (rjs) mRNA, complete cds. OCBBF20019380//seizure related gene 6 OCBBF20022900//Homo sapiens SCHIP-1 mRNA, complete cds. OCBBF20030280//Rattus norvegicus hfb2 mRNA, complete cds. OCBBF20046470//ARFAPTIN 1. OCBBF20049840//Homo sapiens mRNA for neurabin II protein. OCBBF20068490//Mus musculus RW1 protein mRNA, complete cds. OCBBF20071960//Coturnix coturnix japonica qMEF2D gene. OCBBF20073540//Homo sapiens p30 DBC mRNA, complete cds. OCBBF20121390//RING CANAL PROTEIN (KELCH PROTEIN). OCBBF20127550//Outer Capsid protein VP4 (Hemagglutinin) OCBBF20148730//RING CANAL PROTEIN (KELCH PROTEIN). OCBBF20178150//Plasmodium falciparum ADA2-like protein gene, partial cds. PEBLM10000240//Domain found in Dishevelled, Eg1-10 and Ple PROST20047270//CRAL/TRIO domain. PROST20112970//Sterile alpha motif (SAM)/Pointed domain// SAM domain (Sterile alpha motif) PUAEN10000850//Uncharacterized protein family UPF0025// Secl family PUAEN20011880//Mus musculus mRNA for MIWI (piwi), complete cds. PUAEN20051100//Mus musculus otogelin mRNA, complete cds. PUAEN20108240//Drosophila melanogaster ankyrin 2 (Ank2) mRNA, complete cds. SKMUS20084740//Syndecan domain SMINT20053300//Homo sapiens hepatocellular carcinoma-associated antigen 59 mRNA, complete cds. SMINT20071400//NOL1/NOP2/sun family SMINT20101440//Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds. SMINT20110330//pKID domain SMINT20122910//Mus musculus StAR-related protein 1-4E mRNA, partial cds. SMINT20131810//ENV polyprotein (coat polyprotein) SMINT20168570//Homo sapiens mRNA for stabilin-1 (stab1 gene). SPLEN20008390//Human placenta (Diff48) mRNA, complete cds. SPLEN20084600//RING CANAL PROTEIN (KELCH PROTEIN). SPLEN20128000//Xenopus laevis XMAB21 (Xmab-21) mRNA, complete cds. SPLEN20149110//Dishevelled specific domain SPLEN20171470//Keratin, high sulfur B2 protein SPLEN20194050//Homo sapiens HOTTL protein mRNA, complete cds

SPLEN20214580//Mus musculus mdg1-1 mRNA, complete cds.

STOMA20057820//Uncharacterized protein family UPF0024 STOMA20063980//Collagen triple helix repeat (20 copies)

STOMA20069040//Keratin. high sulfur B2 protein

SYNOV20017080//UBX domain

TBAES20000590//Cytochrome P450// Cytochrome P450

TESTI20001°70//HORMA domain

TESTI20031810//Bacterial luciferase// Domain of unknown function DUF28

TESTI20044230//Mus musculus testis-specific Y-encoded-like protein (Tspyll) mRNA, complete cds.

TESTI20098350//VAT-Nn domain

TESTI20157520//K+ channel tetramerisation domain// K+ channel tetramerisation domain

TESTI20170350//Cystine-knot domain

TESTI20192800//Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16 mRNA, complete cds.

TESTI20199750//TRICHOHYALIN.

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TESTI20202650//Repeat in HS1/Cortactin

TESTI20229600//Drosophila melanogaster SP2353 mRNA, complete cds.

TESTI20231920//Gag P30 core shell protein

TESTI20242830//E2 (early) protein, C terminal// Syndecan domain

TESTI20254540//Homo sapiens hepatocellular carcinoma-associated antigen 59 mRNA, complete cds.

TESTI20320440//THIOREDOXIN.

TESTI2032768C//EF hand// EF hand

TESTI2032828C//KE2 family protein// Troponin

TESTI20351830//K-box region

TESTI2037002C//Bleomycin resistance protein

TESTI2039121C//IQ calmodulin-binding motif

TESTI2040815C//Keratin, high sulfur B2 protein

TESTI2045199C//SAP domain

TESTI2046797C://Neurohypophysial hormones N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hormones N-terminal Domain// Ne

THYMU201083\*0//Mouse NCBP-29 mRNA for PW29, complete cds.

THYMU20142040/WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).

THYMU20194360//Kelch motif

35 THYMU20239000//collagen alpha 1(XI) chain

TOVAR20004760//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat

TRACH20005020//Ank repeat// MutT-like domain

TRACH2C007020//TRICHOHYALIN.

TRACH20048450//PROTEIN K4 (PROTEIN K3).

TRACH2C063700//Homo sapiens adaptor protein CIKS mRNA, complete cds.

TRACH20076760//Keratin, high sulfur B2 protein

TRACH2C135520//TBC domain// Rhodanese-like domain

TRACH2C141240//Mus musculus G21 protein mRNA, complete cds.

THACH2C183170//Rattus norvegicus Sprague-Dawley SM-20 mRNA, complete cds.

UTERU2000740//Human fusion protein mRNA, complete cds.

UTERU20004240//CGI-96 protein

UTERU20005%0/rendoplasmic reticulum resident protein 58

UTERU20022940//Human (p23) mRNA, complete cds.

UTERU20046640//Mus musculus 1dlBp (LDLB) mRNA, complete cds.

UTERU20065930//GTP-RHO BINDING PROTEIN 1 (RHOPHILIN).

UTERU20115740//Human PMS2 related (hPMSR3) gene, complete cds.

UTERU20179880//TPR Domain// TPR Domain// TPR Domain// TPR Domain

[0092] Further the reason is that a polypeptide does not always belong solely to a single category of the above-described functional categories, and therefore, a polypeptide may belong to any of the predicted functional categories. Besides additional functions can be found for the clones classified into these functional categories by further analyses.

[0093] Since the polypeptide encoded by clones of the invention contains full-length amino acid sequence, it is possible to analyze its biological activity, and its effect on cellular conditions such as cell proliferation and differentiation

by expressing the polypeptide as a recombinant polypeptide using an appropriate expression system, injecting the recombinant into the cell, or raising a specific antibody against the polypeptide.

[0094] The biological activities of respective polypeptides can be analyzed by the methods as shown below.

Secretory protein, transmembrane protein:

## [0095]

"Ion Channels" (Ed., R. H. Ashley, 1995) of "The Practical Approach Series" (IRL PRESS),

"Growth Factors" (Eds., I. McKay, I. Leigh, 1993),

"Extracellular Matrix" (Eds., M. A. Haralson, J. R. Hassell, 1995);

Glycoprotein-related protein:

#### 15 [0096]

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"Glycobiology" (Eds., M. Fukuda, A. Kobata, 1993) of "The Practical Approach Series" (IRL PRESS),

"Glycoprotein Analysis in Biomedicine" (Ed., Elizabeth F.Hounsell, 1993) of "Method in Molecular Biology" (Humana Press) series;

Signal transduction-related protein:

## [0097]

"Signal Transduction" (Ed., G. Milligan, 1992) of "The Practical Approach Series" (IRL PRESS),

"Protein Phosphorylation" (Ed., D. G. Hardie, 1993), or

"Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J.Hill, 1995) of "Method in Molecular Biology" (Humana Press) series;

30 Transcription-related protein:

## [8000]

"Gene Transcription" (Eds., B. D. Hames, S. J. Higgins, 1993) of "The Practical Approach Series" (IRL PRESS), "Transcription Factors" (Ed., D.S.Latchman, 1993);

Enzyme and/or metabolism-related protein:

# [0099]

"Enzyme Assays" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "The Practical Approach Series" (IRL PRESS); Cell division and/or cell proliferation-related protein:

"Cell Growth, Differentiation and Senescence" (Ed., GEORGE STUDZINSKI, 2000) of "The Practical Approach Series" (IRL PRESS);

Cytoskeleton-related protein:

## [0100]

"Cytoskeleton: Signalling and Cell Regulation" (Eds., KERMIT L. CARRAWAY and CAROLIE A. CAROTHERS CARRAWAY, 2000) of "The Practical Approach Series" (IRL PRESS),

"Cytoskeleton Methods and Protocols" (Ed., Gavin, Ray H., 2000) of "Method in Molecular Biology" (Humana Press) series; Nuclear protein and/or RNA synthesis-related protein:

"Nuclear Receptors" (Ed., DIDIER PICARD, 1999) of "The Practical Approach Series" (IRL PRESS),

"RNA Processing" (Eds., STEPHEN J. HIGGINS and B. DAVID HAMES, 1994);

Protein synthesis and/or transport-related protein:

## [0101]

"Membrane Transport" (Ed., STEPHEN A. BALDWIN, 2000) of "The Practical Approach Series" (IRL PRESS), "Protein Synthesis Methods and Protocols" (Eds., Martin, Robin, 1998) of "Method in Molecular Biology" (Humana Press) series;

Cellular defense-related protein:

#### [0102]

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"DNA Repair Protocols" (Henderson, Daryl S., 1999) of "Method in Molecular Biology" (Humana Press) series, "Chaperonin Protocols" (Eds., Schneider, Christine, 2000); Development and/or differentiation-related protein: "Developmental Biology Protocols" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "Method in Molecular Biology" (Humana Press) series;

DNA- and/or RNA-binding protein:

#### 20 [0103]

"DNA-Protein Interactions Principles and Protocols" (Eds., Kneale, G. Geoff, 1994) of "Method in Molecular Biology" (Humana Press) series,

"RNA-Protein Interaction Protocols" (Eds., Haynes, Susan R., 1999);

ATP- and/or GTP-binding protein:

#### [0104]

"Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J. Hill, 1995) of "Method in Molecular Biology" (Humana Press) series.

[0105] In the categorization, the clone predicted to belong to the category of secretory and/or membrane protein means a clone having hit data with some annotation, such as growth factor, cytokine, hormone, signal, transmembrane, membrane, extracellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, connective tissue, etc., suggesting that it was a secretory or membrane protein, or a clone in which the presence of nucleotide sequence encoding a signal sequence or transmembrane region was suggested by the results of PSORT and SOSUI analyses for deduced ORF.

[0106] The clone predicted to belong to the category of glycoprotein-related protein means a clone having hit data with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein.

[0107] The clone predicted to belong to the category of signal transduction-related protein means a clone having hit data with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, SH2 domain, etc., suggesting that the clone encodes a signal transduction-related protein.

[0108] The clone predicted to belong to the category of transcription-related protein means a clone having hit data with some annotation, such as transcription regulation, zinc finger, homeobox, etc., suggesting that the clone encodes a transcription-related protein.

[0109] The clone predicted to belong to the category of disease-related protein means a clone having hit data with some annotation, such as disease mutation, syndrome, etc., suggesting that the clone encodes a disease-related protein, or a clone whose full-length nucleotide sequence has hit data for Swiss-Prot, GenBank, UniGene, or nr, where the hit data corresponds to genes or polypeptides which have been deposited in the Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is the human gene and disease database described later.

[0110] The clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having hit data with some annotation, such as metabolism, oxidoreductase, E. C. No. (Enzyme commission number), etc., suggesting that the clone encodes an enzyme and/or metabolism-related protein.

[0111] The clone predicted to belong to the category of cell division and/or cell proliferation-related protein means a clone having hit data with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth, apoptosis, etc., suggesting that the clone encodes a cell division and/or cell proliferation-related protein.

[0112] The clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data

with some annotation, such as structural protein, cytoskeleton, actin-binding, microtubles, etc., suggesting that the clone encodes a cytoskeleton-related protein.

[0113] The clone predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, polyadenylation, etc. suggesting that the clone encodes a nuclear protein and/or RNA synthesis-related protein.

[0114] The clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having hit data with some annotation, such as translation regulation, protein biosynthesis, amino-acid biosynthesis, ribosomal protein, protein transport, signal recognition particle, etc., suggesting that the clone encodes a protein synthesis and/or transport-related protein.

[0115] The clone predicted to belong to the category of cellular defense-related protein means a clone having hit data with some annotation, such as heat shock, DNA repair, DNA damage, etc., suggesting that the clone encodes a cellular defense-related protein.

[0116] The clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data with some annotation, such as developmental protein, etc., suggesting that the clone encodes a development and/or differentiation-related protein.

[0117] The clone predicted to belong to the category of DNA- and/or RNA-binding protein means a clone having hit data with some annotation, such as DNA-binding. RNA-binding, etc.

[0118] The clone predicted to belong to the category of ATP- and/or GTP-binding protein means a clone having hit data with some annotation, such as ATP-binding. GTP-binding. etc.

[0119] As to a protein involved in a disease, it is possible to perform a functional analysis as described above, but also possible to analyze correlation between the expression or the activity of the protein and a certain disease by using a specific antibody that is obtained by using expressed protein. Alternatively, it is possible to utilize the database OMIM, which is a catabase of human genes and diseases, to analyze the protein. Further, new information is constantly being deposited in the OMIM database. Therefore, it is possible for one skilled in the art to find a new relationship between a particular disease and a gene of the present invention in the most up-to-date database. The proteins involved in diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0120] Also as for a secretory protein, membrane protein signal transduction-related protein, glycoprotein-related protein or 'transcription-related protein, etc., search of the OMIM with the following keywords resulted in the finding that the proteins are involved in many diseases (the result of the OMIM search for secrete and membrane proteins is shown below). Also association between proteins related to signal transduction or transcription and diseases is reported in "Transcription Factor Research-1999" (Fujii, Tamura, Morohashi, Kageyama, and Satake edit, (1999) Jikkenlgaku Zoukan. Vol. 17. No.3), and "Gene Medicine" (1999) Vol.3, No.2). When cancer is used as an example, as described in "Biology of Cancer" (S. Matsubara, 1992) of Life Science series (Shokabo), many proteins are involved in cancers which include enzyme and/or metabolism-related proteins, cytoskeleton-related proteins, cell division and/or cell proliferation-related proteins as well as secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins but also secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, etc. are often involved in diseases, and thus they can be useful targets in the field of medical industry.

[0121] The result of the OMIM search for secretory and membrane proteins is shown below, in which the keywords,

- (1) secretion protein.
- (2) membrane protein.
- (3) channel and

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(4) extracellular matrix were used.

[0122] Shown in the search result are only the accession numbers in the OMIM. Using the number, data showing the relationship between a disease and a gene or protein can be seen. The OMIM data has been renewed everyday.

1) Secretion protein

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[0123] 354 entries found, searching for "secretion protein"

*604667. *104760 *176860, *151675, *139320, *107400, *604029, *118910, #200100, *176880, *603850, *147572, *604028 *179513 *125950. *139250, *246700, *600946, *600560, *602926, 185860, *605083, *603215, *602421, *157147 **79512 *600174 *109270, *604710. *138120, *179510, *600998, *179509, *170280, *179511, *600626, *603831 *601489 *154545. *179490, *603826. *122559 *603216. *102720, *147290. *164160, *603062, *112262, *602672, *605435, *605322, *131230,
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*600753, *600768, *118825, *600564,
*604252, *173120, *134370, *192340, *308230, *600322, *605359, *600046, *300090, 106160, *600041, #262500,
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*122560, *107300, *137241, *120140, *101000, *193400, *217000, *272800, *600937, #201710, *600377, #174800,
*106100, #274600, *173350, #177170, *147620, *214500, *131244, *202110, *120120, *601007, *191160, *147470,
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#### 2) Membrane protein

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[0124] 1489 entries found, searching for "membrane protein"
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*130500. *605704, *305360, *153330, *173610, *109270, *170995, *170993, *104776, *602333. *309060, *605703,
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      *300041, *121011, *125950, *114180, *602974, *600637, *113730, *118504, *605145, *604669, *118800, *121013,
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      *121015, *138491, *600421, *104610,
      *604045, *604594, *131230, *605487, *138247, *600467, #602485, *602481, *138251, *137192, *602403, 600851,
      *277900, *603785, *603152, *603199, *603475, #168600, #272120, *170280, *603852, #241200, *603053, *600465,
      #603034. *142461, *164920, *137164, *600884, *600442, *123885, *604001, *600232, *232200, *171050, *602103,
      *602014, *300211, *600983, *602887,
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      *604415, *604418, *300242, #300071, *604471, *600837, 168350, *118511, 193007, *600300, *604654, #601820,
      *180297, *600046, *603853, *604678, *604693, #604772, *118508, *603855, *605204, #254210, *182099, *182307,
      #130600, *601109, *114080, *300103, *182860, *605438, *601129, *603964, *600019, *516060, #185000, *138079,
      *104210, *605818, *603418, *305990, *305450
50 '
      4) Extracellular matrix
      [0126] 218 entries found, searching for "extracellular matrix"
       *605912, *603479, *602201, *604633, *601418, *601548, *115437, *154870, *600754, *602261, *602285, *602262,
       *134797, *120361, *604629, *604871, *603321, *603320, *601807, #154700, *116935, *185261, *120360, *185250,
       *605470, *603767, *253700, *190180, *128239, *308700, *276901, *193300, *120324, *188826, *602109, *155760,
       *600514, *600261, #177170, *600536,
       *147557, #116920, *150240, *601313, *120140, 601614, *605158, *120150, *120180, #200610, *605127, *193400,
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*192240 #173900 *152200 #136900 *135821 #130070 *120320 *120220 *112260 *310200 *600900 *600262
*605670, *600985, *179590, #245150, *602574, *601463, 183850, *601211, *604241, *600758, *186745, *604710,
*602369, *602090, *190182, *192975.
*602178, *230740, *600065, *601652, *158106, *190181, *156790, #158810, *193210, *155120, *192977, *193065,
#226700, *187380, *231050, *182120, *188060, *186355, 163200, *164010, #156550, *151510, *150370, *253800,
*156225, *150325, #194050, *150290, *216550, *147620, *600215, *222600, *147559, *165380, *182888, *600491,
*146650, *146640, *600564, *600596,
*600616, *600700, *600742, *138297, *182889, *154705, *600930, *301870, *153619, *601050, *601090, *601105,
*165070, *305370, *135820, *130660, *310300, *601492, *128240, *601587, #126600, *601636, *600119, *601692,
*601728, *125485, 601858, *601915, *602048, *175100, *602108, *121010, *600245, *120470, *120328, *120325,
*602264, *120280, *602366, *600309,
*602402, *602415, *602428, *602453, *602505, #166210, *602600, *602941, *603005, *603196, 603209, *603221,
*603234, *603319, *120250, *120210, *120120, *603489, *603551, *118938, *603799, *603842, *603924, *603963,
*604042, *604063, *604149, *604160, *601028, *604467, *604510, *604592, *116930, *116806, *601284, *604724,
*604806, *604807, *604808, *107269,
*605007, *605008, *605009, *600214, *600076, *605174, *605175, *605292, *605343, *605351, #600204, *605497,
*605546, *605587, *605623, *600211, *605702, *103320
[0127] In addition to these, the various keywords shown in the above-mentioned categorization or others can be
used for the OMIM search and the result may suggest the involvement thereof in diseases.
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[0128] Further, the use of nucleotide sequences of cDNAs of the present invention enables analyzing the expression frequency of genes corresponding to the cDNAs. In addition, functions of the genes can be predicted based on the information obtained by the expression frequency analysis.

[0129] There are several methods for analyzing the expression levels of genes involved in diseases. Differences in gene expression levels between diseased and normal tissues are studied by the analytical methods using, for example, Northern hybridization, RT-PCR, DNA microarray, etc. (Experimental Medicine, Vol.17, No. 8, 980-1056 (1999); Cell Engineering (additional volume) DNA Microarray and Advanced PCR Methods, Muramatsu & Nawa (eds.), Shujunsya (2000)). By computer analysis, in addition to these analysis methods, the nucleotide sequences of expressed genes can be compared to analyze the expression frequency. For example, there is a database called "BODYMAP"; gene clones are extracted at random from cDNA libraries of various tissues and/or cells, and the clones homologous to one another are assigned to a single cluster based on the information of nucleotide sequence homology at the 3'-end; genes are classified into any clusters, and the numbers of clones in the respective clusters are compared to gain the information on expression frequency (http://bodymap.ims.u-tokyo.ac.jp/).

[0130] When explicit difference in the expression levels between diseased tissues and normal tissues is observed for a gene by these analytical methods, it can be conclude that the gene is closely involved in a disease or disorder. Instead of diseased tissues, when gene expression is explicitly different between normal cells and cells reproducing disease-associated specific features, it can be concluded that the gene is closely involved in a disease or disorder.

[0131] From the 2443 clones whose full-length nucleotide sequences had been revealed, genes involved in particular pathology or functions were selected by the use of databases shown below (see Example 7; "Expression frequency analysis in silico"). The database used in the analyses of the present invention contains nucleotide sequences of 1,402,070 clones, and the population of the database is large enough for the analysis. The sequence information in the database was obtained by selecting cDNA clones at random from cDNA libraries derived from the various tissues and cells shown in Example 1 and determining the 5'-end sequences thereof.

[0132] Then, the nucleotide sequences of respective clones in this database were categorized (clustered) based on the nucleotide sequence homology determined with a search program: the number of clones belonging to every cluster of each library was determined and normalized; thus, the ratio of a certain gene in a cDNA library was determined. This analysis provided the information of the expression frequency of a gene in a tissue or cell that is the source of the cDNA library.

[0133] Then, in order to analyze the expression of genes corresponding to the nucleotide sequences of cDNAs of the present invention in tissues and cells, the libraries from the tissues or cells. which had been used in the large-scale cDNA analyses, were taken as subjects to compare the expression levels between different tissues or cells. Namely, the expression frequency was analyzed by comparing the previously normalized values between tissues or cells from which 600 or more cDNA clones whose nucleotide sequences had been analyzed were derived. The result of this analysis showed that the cDNA clones corresponded to the genes involved in the pathology and functions, which are indicated below. Each value in Tables 3 to 51 indicated below represents a relative expression frequency; the higher the value, the higher the expression level.

## Osteoporosis-related genes

[0134] Osteoporosis is a pathology in which bones are easily broken owing to overall decrease in components of bone. The onset correlates to the balance between the functions of osteoblast producing bone and osteoclast absorbing bone, namely bone metabolism. Thus, the genes involved in the increase of osteoclasts differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38. 642-648. (2001)) are genes involved in osteoporosis relevant to bone metabolism.

[0135] A nucleotide sequence information-based analysis was carried out to identify the genes whose expression frequencies are higher or lower in CD34+ cell (cell expressing a glycoprotein CD34) treated with the osteoclast differentiation factor (Molecular Medicine 38. 642-648. (2001)) than in the untreated CD34+ cell, which is the precursor cell of monocyte/macrophage line. The result of comparative analysis for the frequency between the cDNA libraries prepared from the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D3OST, D6OST or D9OST) showed that the genes whose expression levels were different between the two were 56 clones indicated in Table 3. These clones are involved in osteoporosis.

Genes involved in neural cell differentiation

[0136] Genes involved in neural cell differentiation are useful for treating neurological diseases. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in neurological diseases.

[0137] A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed that the genes whose expression levels were different between the two were 288 clones indicated in Table 4. These genes are neurological disease-related genes.

#### Cancer-related genes

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[0138] It has been assumed that, distinct from normal tissues, cancer tissues express a distinct set of genes, and thus the expression thereof can contribute to the carcinogenesis in tissues and cells. Thus, genes whose expression patterns in cancer tissues are different from those in normal tissues are cancer-related genes. Search was carried out for the genes whose expression levels in cancer tissues were different from those in normal tissues.

[0139] The result of comparative analysis of cDNA libraries derived from breast tumor (TBAES) and normal breast (BEAST) showed that the genes whose expression levels were different between the two were 35 clones indicated in Table 5

[0140] The result of comparative analysis of cDNA libraries derived cervical tumor (TCERX) and normal cervical duct (CERVX) showed that the genes whose expression levels were different between the two were 11 clones indicated in Table 6

[0141] The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN) and normal colon (COLON) showed that the genes whose expression levels were different between the two were 25 clones indicated in Table 7.

[0142] The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP) and normal esophagus (NESOP) showed that the genes whose- expression levels were different between the two were 41 clones indicated in Table 8.

[0143] The result of comparative analysis of cDNA libraries derived from kidney tumor (TKIDN) and normal kidney (KIDNE) showed that the genes whose expression levels were different between the two were 175 clones indicated in Table 9.

[0144] The result of comparative analysis of cDNA libraries derived from liver tumor showed that the genes whose expression levels were different between the two were clones indicated in Table 10.

[0145] The result of comparative analysis of cDNA libraries derived from lung turner (TLUNG) and normal lung (HLUNG) showed that the genes whose expression levels were different between the two were 62 clones indicated in Table 11

[0146] The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) showed the genes whose expression levels were different between the two were 23 clones indicated in Table 12.

[0147] The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) showed that the genes whose expression levels were different between the two were 70 clones indicated

in Table 13.

[0148] The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) showed that the genes whose expression levels were different between the two were 236 clones indicated in Table 14.

[0149] The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) showed that the genes whose expression levels were different between the two were 232 clones indicated in Table 15.

[0150] These genes are involved in cancers.

[0151] Further, there is a method to search for genes involved in development and differentiation, which is the expression frequency analysis in which the expression levels of genes are compared between developing and/or differentiating tissues and/or cells and adult tissues and/or cells. The genes involved in tissue development and/or differentiation are genes participating in tissue construction and expression of function, and thus are useful genes, which are available for regenerative medicine aiming at convenient regeneration of injured tissues.

[0152] By using the information of gene expression frequency gained from the database of 5'-end nucleotide sequences described above, genes involved in development or differentiation of particular tissues were selected from the 2443 clones whose full-length nucleotide sequence had been revealed (see Example 7).

[0153] The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN or BRTHA) showed that the genes whose expression levels were different between the two were 1195 clones indicated in Tables 16 to 48.

[0154] The result of comparative analysis of cDNA libraries derived from fetal heart (FEHRT) and adult heart (HEART) showed that the genes whose expression levels were different between the two were 45 clones indicated in Table 49. [0155] The result of comparative analysis of cDNA libraries derived from fetal kidney (FEKID) and adult kidney (KIDNE) showed that the genes whose expression levels were different between the two were 118 clones indicated in Table 50.

[0156] The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) showed that the genes whose expression levels were different between the two were 63 clones indicated in Table 51. These genes are involved in regeneration of tissues and/or cells.

[0157] The expression frequency or the like can be analyzed by PCR based on the nucleotide sequences of cDNAs of the present invention. There are some known methods for comparing the quantities of amplification products obtained by PCR. For example, the band intensities can be determined by ethidium bromide staining. With RI-labeled or fluorescently labeled primers, the RI signal or fluorescence intensity can be assayed for the quantity of labeled amplification products. Alternatively, the quantity of amplification products can also be determined by measuring the RI signal or the fluorescence intensity from the RI-labeled or fluorescently labeled probe hybridizing to the products. The assay results thus obtained are compared and then the clones exhibiting differences in the expression levels can be selected.

[0158] There are some quantitative PCR methods: a PCR method using internal standards: a competitive PCR, in which the quantification is achieved by adding, to a sample, a dilution series of a known quantity of a template RNA and by comparing the quantity of an amplification product derived from the RNA of interest with the quantity of an amplification product derived from the template RNA. These methods overcome the problems of errors in the amount of amplification products among tubes and of the plateau effect. ATAC-PCR (Adaptor-tagged competitive PCR) is a method of competitive PCR which is practiced by using multiple adapters of different sizes attached to a gene whose 3'-end nucleotide sequence has previously been determined. The ratio of expression frequency of a single mRNA species from a number of tissues (cells) can be assayed in a single step (Nucleic Acids Research 1997, 25(22): 4694-4696; "DNA Microarray and Advanced PCR Techniques", Cell Technology, supplement, Eds., Muramatsu and Nawa (Shujunsha, 2000): 104-112).

[0159] If it is observed, by using these analytical methods, that the expression levels of genes are evidently varied during major cellular events (such as differentiation and apoptosis), the genes are involved in the cellular events and accordingly are candidates for disease- and/or disorder-related genes. Further, genes exhibiting tissue-specific expression are genes playing important parts in the tissue functions and, therefore, can be candidates for genes involved in diseases and/or disorders affecting the tissues.

[0160] For example, inflammation is an important biological response that is known to be invoived in various diseases. The representative inflammation-inducing factors include TNF-α (Tumor Necrosis Factor-alpha). There exists a signaling cascade activated by TNF-α stimulations, wherein NF-κB is a transducing molecule (Cell 1995, 80:529-532). It has also been revealed that many inflammation-related genes, including IL-2, IL-6 and G-CSF, are varied in the expression levels thereof in response to the signal through the pathway (Trends Genet. 1999, 15(6): 229-235). It is assumed that genes whose expression levels are varied in response to the stimulation of TNF-α also participate in inflammation.

[0161] Further, the infection of *Helicobacter pylori* to the gastric epithelia is known to cause gastritis and gastroduodenal ulcer (Mebio 2000, July, 17(7): 16-33). Thus, the genes whose expression levels are altered depending on co-

culturing cells with *Helicobacter pylori* may be involved in gastritis and gastroduodenal ulcer. A recent study has suggested that *Helicobacter pylori* strongly activates the NF-κB pathway(Gastroenterology 2000, 119: 97-108).

[0162] THP-1 cell, which is a human monocyte cell line, was cultured in the presence of TNF-α (Tumor Necrosis Factor-alpha). The genes whose expression levels were altered owing to the presence of TNF-α were searched for, and the result showed that the clones whose expression levels were increased owing to the presence of TNF-α were ASTRO20152140, BRACE20057620, BRACE20060720, BRACE20090440, BRACE20152870, BRACE20229280, BRAMY20002770, BRAMY20266850, BRAMY20280720, BRAWH20106180, BRAWH20122770, BRHIP20096170, BRHIP20111200, BRHIP20186120, BRHIP20194940, BRHIP20207430, BRSSN20152380, CTONG20095270, CTONG20100240, CTONG20158150,

- CTONG20265130, D3OST20006540, D9OST20031370, FCBBF20071860, FCBBF30251420, FCBBF30252520, FCBBF40001420, FEBRA20017050, FEBRA20082100, HCHON20011160, KIDNE20141190, KIDNE20163880, KIDNE20182690, LIVER10004790, LIVER20038540, LIVER20085800, MESAN20130220, MESAN20174170, NT2NE20158600, NT2RI20005750, NT2RP70110860, NT2RP70169110, NT2RP70175670, NT2RP70188710, PERIC20002140, PLACE60155130, PROST20120160, PROST20149250, PROST20161950, PUAEN20015260, SKNSH20080430, SMINT20051610, SMINT20060780, SMINT20161220, SMINT20163960, SPLEN20101190, SPLEN20157300, SPLEN20163560, SPLEN20214580, SPLEN20279950, STOMA20048520, TESTI20076850, TESTI20370020, TESTI20108720, TESTI2020100, TESTI20239510, TESTI20266740, TESTI20342430, TESTI20370020, TESTI20391210, TESTI20401020, TESTI20415640, THYMU20130890, THYMU20286290, TRACH20060150, TRACH20099340, UTERU20004240, UTERU20068990, UTERU20119060.
- [0163] On the other hand, the clones whose expression levels were decreased owing to the presence of TNF-α were ASTRO20032120, ASTRO20084250, ASTRO20181690, BRACE20062640, BRACE20067430, BRACE20235400, BRALZ20018340, BRALZ20069760, BRALZ20075450, BRAMY20163270, BRAMY20204450, BRAMY20218670, BRAMY20229800, BRAWH10000930, BRAWH20107540, BRAWH20132190, BRAWH20158530, BRCAN20273340, BRHIP20105710, BRHIP20186120,
- BRSSN20176820, CTONG20095290, DFNES20031920, FCBBF30033050, FCBBF30071520, FCBBF30083820, HCHON20008980, HCHON20022470, HHDPC20034390, KIDNE20028720, KIDNE20079440, KIDNE20127750, KIDNE20148900, LIVER20011130, MAMGL10000830, MESAN20127350, NT2NE20181650, NT2RI20023160, NT2RP70102350, NT2RP70157890, NTONG20029480, OCBBF20020830, OCBBF20041680, OCBBF20061720, OCBBF20127040, OCBBF20139260, OCBBF20178990, PEBLM20013120, PLACE60003480, PLACE60181070, PROST20151240, PUAEN20003740, PUAEN20011880, PUAEN20078980, PUAEN20085150, SKNSH20080430, SMINT20001760. SMINT20047810, SMINT20108530, SPLEN20158990. SPLEN20283650. STOMA20010250, STOMA20057820, TESTI20060400, TESTI20161970, TESTI20275620, TESTI20369690, TESTI20386230, THYMU20253250, THYMU20272490, TRACH20153810, UTERU20176130, UTERU20186740.
  - [0164] These clones are inflammation-related genes.

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- [0165] MKN45, which is a gastric cancer cell line, was co-cultured with *Helicobacter pylori*. The genes whose expression levels were altered owing to the presence of *Helicobacter pylori* were searched for, and the result showed that the clones whose expression levels were increased owing to the presence of *Helicobacter pylori* were ADRGL20067670, BLADE20004630, BRACE20039040, BRACE20151320, BRACE20229280, BRACE20235400, BRALZ20058880, BRAMY20060920, BRAMY20184670, BRAMY20218670, BRAMY20229800, BRCAN20147880, BRHIP20196410, BRHIP30004880, BRSSN20187310, CD34C30004940, CTONG20265130, DFNES20031920, FCBBF30278630, FCBBF40001420,
- HHDPC20095280, KIDNE20130450, LIVER20011130, LIVER20038540. NT2NE20172590, NT2RP70169110, OCBBF20085200, OCBBF20180840, PEBLM10000240, PLACE60003480. PROST20120160, PROST20151240, PUAEN20011880, SKMUS20031680, SKNSH20080430, SMINT20056210. SMINT20105000. SPLEN20019450, SPLEN20211570, STOMA20048520, TESTI20004890, TESTI20083940. TESTI20168480, TESTI20239510, TESTI20308600, TESTI20478010, UTERU20126880.
- [0166] On the other hand, the clones whose expression levels were decreased owing to the presence of *Helicobacter* pylori were
- ASTRO20032120, BRACE20090440, BRACE20114780, BRALZ20064740. BRAMY20002770, BRAMY20210400, BRAMY20215230, BRAMY20247280, BRAMY20267130, BRAWH20029630, BRAWH20100690, BRAWH20118230, BRCOC20105100, BRHIP20218580, BRSSN20046570, CTONG20138030. CTONG20146970, CTONG20158150, D3OST20037970, FCBBF30001840, FCBBF30033050, FEBRA20082100. HCHON20035130, HCHON20043590, HCHON20067220, NT2NE20174920, NT2RI20009870, NT2RI20023160. NT2RP70062230, NT2RP70130020, NTONG20070340, OCBBF20020150, OCBBF20094240, OCBBF20107920. PROST20144220. PROST20149160, PROST20153320, PUAEN20003740, PUAEN20025680, PUAEN20040670. SMINT20014580, SPLEN20101190, STOMA20076800, TESTI20087620, TESTI20098530, TESTI20123080. TESTI20161970. TESTI20234140, TESTI20288110, TESTI20357960, TESTI20391210, TESTI20424730. THYMU20158250, THYMU20226600,

TRACH2005020, TRACH20134950, TRACH20184490, TSTOM20001390, UTERU20119060, UTERU20134910, UTERU20176130.

[0167] Those clones are involved in gastritis or gastroduodenal ulcer.

[0168] For example, if the polypeptide encoded by the cDNA of the present invention is a regulatory factor of cellular conditions such as growth and differentiation, it can be used for developing medicines as follows. The polypeptide or antibody provided by the invention is injected into a certain kind of cells by microinjection. Then, using the cells, it is possible to screen low molecular weight compounds, etc. by measuring the change in the cellular conditions, or the activation or inhibition of a particular gene. The screening can be performed as follows.

[0169] First the polypeptide is expressed and purified as recombinant. The purified polypeptide is microinjected into cells such as various cell lines, or primary culture cells, and the cellular change such as growth and differentiation can be examined. Alternatively, the induction of genes whose expression is known to be involved in a particular change of cellular conditions may be detected by the amount of mRNA or polypeptide. Alternatively, the amount of intracellular molecules flow molecular weight compounds, etc.) that is changed by the function of the gene product (polypeptide) which is known to be involved in a particular change of cellular conditions may be detected. The compounds to be screened (both low and high molecular compounds are acceptable) can be added to the culture media and assessed for their activity by measuring the change of the cellular conditions.

[0170] Instead of microinjection, cell lines introduced with the gene obtained in the invention can be used for the screening of the gene product is turn out to be involved in a particular change in the cellular conditions, the change of the product can be used as a measurement for screening. Once a compound is screened out which can activate or inhibit the function of the polypeptide of the invention, it can be applied for developing medicines.

[0171] If the polypeptide encoded by the cDNA of the present invention is a secretory protein, membrane protein, or protein involved in signal transduction, glycoprotein, transcription, or diseases, it can be used in functional assays for developing medicines.

[0172] In case of a membrane protein, it is most likely to be a polypeptide that functions as a receptor or ligand on the cell surface. Therefore, it is possible to reveal a new relationship between a ligand and receptor by screening the membrane protein of the invention based on the binding activity with the known ligand or receptor. Screening can be performed according to the known methods.

[0173] For example a ligand against the polypeptide of the invention can be screened in the following manner. Namely a ligand that binds to a specific polypeptide can be screened by a method comprising the steps of: (a) contacting a test sample with the polypeptide of the invention or a partial peptide thereof, or cells expressing these, and (b) selecting a test sample that binds to said polypeptide, said partial peptide, or said cells.

[0174] On the other hand, for example, screening using cells expressing the polypeptide of the present invention that is a receptor protein can also be performed as follows. It is possible to screen receptors that is capable of binding to a specific polypeptide by using procedures (a) attaching the sample cells to the polypeptide of the invention or its partial peptide, and (b) selecting cells that can bind to the said polypeptide or its partial peptide.

[0175] In a following screening as an example, first the polypeptide of the invention is expressed, and the recombinant polypeptide is purified. Next, the purified polypeptide is labeled, binding assay is performed using a various cell lines or primary cultured cells, and cells that are expressing a receptor are selected (Growth and differentiation factors and their receptors. Shin-Seikagaku Jikken Kouza Vol.7 (1991) Honjyo, Arai, Taniguchi, and Muramatsu edit, p203-236, Tokyo-Kagaku-Doujin). A polypeptide of the invention can be labeled with RI such as <sup>125</sup>I, and enzyme (alkaline phosphatase etc.)

[0176] Alternatively, a polypeptide of the invention may be used without labeling and then detected by using a labeled antibody against the polypeptide. The cells that are selected by the above screening methods, which express a receptor of the polypeptide of the invention, can be used for the further screening of an agonists or antagonists of the said receptor

[0177] Once the ligand binding to the polypeptide of the invention, the receptor of the polypeptide of the invention or the cells expressing the receptor are obtained by screening, it is possible to screen a compound that binds to the ligand and receptor. Also it is possible to screen a compound that can inhibit both bindings (agonists or antagonists of the receptor for example) by utilizing the binding activities.

[0178] When the polypeptide of the invention is a receptor, the screening method comprises the steps of (a) contacting the polypeptide of the invention or cells expressing the polypeptide of the invention with the ligand, in the presence of a test sample (b) detecting the binding activity between said polypeptide or cells expressing said polypeptide and the ligand and (c) selecting a compound that reduces said binding activity when compared to the activity in the absence of the test sample. Furthermore, when the polypeptide of the invention is a ligand, the screening method comprises the steps of (a) contacting the polypeptide of the invention with its receptor or cells expressing the receptor in the presence of samples (b) detecting the binding activity between the polypeptide and its receptor or the cells expressing the receptor and (c) selecting a compound that can potentially reduce the binding activity compared to the activity in the absence of the sample.

[0179] Samples to screen include cell extracts, expressed products from a gene library, synthesized low molecular compound, synthesized peptide, and natural compounds, for example, but are not construed to be listed here. A compound that is isolated by the above screening using a binding activity of the polypeptide of the invention can also be used as a sample.

[0180] A compound isolated by the screening may be a candidate to be an agonist or an antagonist of the receptor of the polypeptide. By utilizing an assay that monitors a change in the intracellular signaling such as phosphorylation which results from reduction of the binding between the polypeptide and its receptor, it is possible to identify whether the obtained compound is an agonist or antagonist of the receptor. Also, the compound may be a candidate of a molecule that can inhibit the interaction between the polypeptide and its associated proteins (including a receptor) in vivo. Such compounds can be used for developing drugs for precaution or cures of a disease in which the polypeptide is involved.

[0181] Secretory proteins may regulate cellular conditions such as growth and differentiation. It is possible to find out a novel factor that regulates cellular conditions by adding the secretory protein of the invention to a certain kind of cell, and performing a screening by utilizing the cellular changes in growth or differentiation, or activation of a particular gene.

[0182] The screening can be performed, for example, as follows. First, the polypeptide of the invention is expressed and purified in a recombinant form. Then, the purified polypeptide is added to a various kind of cell lines or primary cultured cells, and the change in the cell growth and differentiation is monitored. The induction of a particular gene that is known to be involved in a certain cellular change is detected by the amounts of mRNA and polypeptide. Alternatively, the amount of an intracellular molecule (low-molecular-weight compounds, etc.) that is changed by the function of a gene product (polypeptide) that is known to function in a certain cellular change is used for the detection.

[0183] Once the screening reveals that the polypeptide of the invention can regulate cellular conditions or the functions, it is possible to apply the polypeptide as a pharmaceutical and diagnostic medicine for related diseases by itself or by altering a part of it into an appropriate composition.

[0184] As is above described for membrane proteins, the secretory protein provided by the invention may be used to explore a novel ligand-receptor interaction using a screening based on the binding activity to a known ligand or receptor. A similar method can be used to identify an agonist or antagonist. The resulting compounds obtained by the methods can be a candidate of a compound that can inhibit the interaction between the polypeptide of the invention and an interacting molecule (including a receptor). The compounds may be able to use as a preventive, therapeutic, and diagnostic medicine for the diseases, in which the polypeptide may play a certain role.

[0185] Proteins involved in signal transduction or transcription may be a factor that affects a certain polypeptide or gene in response to intracellular/extracellular stimuli. It is possible to find out a novel factor that can affect a polypeptide or gene by expressing the polypeptide provided by the invention in a certain types of cells, and performing a screening utilizing the activation of a certain intracellular polypeptide or gene.

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[0186] The screening may be performed as follows. First, a transformed cell line expressing the polypeptide is obtained. Then, the transformed cell line and the untransformed original cell line are compared for the changes in the expression of a certain gene by detecting the amount of its mRNA or polypeptide. Alternatively, the amount of an intracellular molecule (low molecular weight compounds, etc.) that is changed by the function of a certain gene product (polypeptide) may be used for the detection. Furthermore, the change of the expression of a certain gene can be detected by introducing a fusion gene that comprises a regulatory region of the gene and a marker gene (luciferase, β-galactosidase, etc.) into a cell, expressing the polypeptide provided by the invention into the cell, and estimating the activity of a marker gene product (polypeptide).

[0187] If the polypeptide or gene of the invention is involved in diseases, it is possible to screen a gene or compound that can regulate its expression and/or activity either directly or indirectly by utilizing the polypeptide of the present invention.

[0188] For example, the polypeptide of the invention is expressed and purified as a recombinant polypeptide. Then, the polypeptide or gene that interacts with the polypeptide of the invention is purified, and screened based on the binding. Alternatively, the screening can be performed by adding with a compound of a candidate of the inhibitor added in advance and monitoring the change of binding activity. In another method, a transcription regulatory region locating in the 5'-upstream of the gene encoding the polypeptide of the invention that is capable of regulating the expression of other genes is obtained, and fused with a marker gene. The fusion is introduced into a cell, and the cell is added with compounds to explore a regulatory factor of the expression of the said gene.

[0189] The compound obtained by the screening can be used for developing pharmaceutical and diagnostic medicines for the diseases in which the polypeptide of the present invention is involved. Similarly, if the regulatory factor obtained in the screening is turn out to be a polypeptide, compounds that can newly affect the expression or activity of the polypeptide may be used as a medicine for the diseases in which the polypeptide of the invention is involved.

[0190] If the polypeptide of the invention has an enzymatic activity, regardless as to whether it is a secretory protein, membrane protein, or proteins involved in signal transduction, glycoprotein, transcription, or diseases, a screening

may be performed by adding a compound to the polypeptide of the invention and monitoring the change of the compound. The enzymatic activity may also be utilized to screen a compound that can inhibit the activity of the polypeptide. [0191] In a screening given as an example, the polypeptide of the invention is expressed and the recombinant polypeptide is purified. Then, compounds are contacted with the purified polypeptide, and the amount of the compound and the reaction products is examined. Alternatively, compounds that are candidates of an inhibitor are pretreated, then a compound (substrate) that can react with the purified polypeptide is added, and the amount of the substrate and the reaction products is examined.

[0192] The compounds obtained in the screening may be used as a medicine for diseases in which the polypeptide of the invention is involved. Also they can be applied for tests that examine whether the polypeptide of the invention functions normally *in vivo*.

[0193] Whether the secretory protein, membrane protein, signal transduction-related protein, glycoprotein-related protein, or transcription-related protein of the present invention is a novel protein involved in diseases or not is determined in another method than described above, by obtaining a specific antibody against the polypeptide of the invention, and examining the relationship between the expression or activity of the polypeptide and a certain disease. In an alternative way, it may be analyzed referred to the methods in "Molecular Diagnosis of Genetic Diseases" (Elles R. edit, (1996) in the series of "Method in Molecular Biology" (Humana Press).

[0194] Proteins involved in diseases are targets of screening as mentioned, and thus are very useful in developing drugs which regulate their expression and activity. Also, the proteins are useful in the medicinal industry as a diagnostic marker of the related disease or a target of gene therapy.

[0195] Compounds isolated as mentioned above can be administered patients as it is, or after formulated into a pharmaceutical composition according to the known methods. For example, a pharmaceutically acceptable carrier or vehicle, specifically sterilized water, saline, plant oil, emulsifier, or suspending agent can be mixed with the compounds appropriately. The pharmaceutical compositions can be administered to patients by a method known to those skilled in the art, such as intraarterial, intravenous, or subcutaneous injections. The dosage may vary depending on the weight or age of a patient, or the method of administration, but those skilled in the art can choose an appropriate dosage properly. If the compound is encoded by polynucleotide, the polynucleotide can be cloned into a vector for gene therapy, and used for gene therapy. The dosage of the polynucleotide and the method of its administration may vary depending on the weight or age of a patient, or the symptoms, but those skilled in the art can choose properly.

[0196] The present invention further relates to databases comprising at least a sequence of polynucleotide and/or polypeptide, or a medium recorded in such databases, selected from the sequence data of the nucleotide and/or the amino acids indicated in Table 1. The term "database" means a set of accumulated information as machine-searchable and readable information of nucleotide sequence. The databases of the present invention comprise at least one of the novel nucleotide sequences of polynucleotides provided by the present invention. The databases of the present invention can consist of only the sequence data of the novel polynucleotides provided by the present invention or can comprise other information on nucleotide sequences of known full-length cDNAs or ESTs. The databases of the present invention can be comprised of not only the information on the nucleotide sequences but also the information on the gene functions revealed by the present invention. Additional information such as names of DNA clones carrying the full-length cDNAs can be recorded or linked together with the sequence data in the databases.

[0197] The database of the present invention is useful for gaining complete gene sequence information from partial sequence information of a gene of interest. The database of the present invention comprises nucleotide sequence information of full-length cDNAs. Consequently, by comparing the information in this database with the nucleotide sequence of a partial gene fragment yielded by differential display method or subtraction method, the information on the full-length nucleotide sequence of interest can be gained from the sequence of the partial fragment as a starting clue. [0198] The sequence information of the full-length cDNAs constituting the database of the present invention contains not only the information on the complete sequences but also extra information on expression frequency of the genes as well as homology of the genes to known genes and known polypeptides. Thus the extra information facilitates rapid functional analyses of partial gene fragments. Further, the information on human genes is accumulated in the database of the present invention, and therefore, the database is useful for isolating a human homologue of a gene originating from other species. The human homologue can be isolated based on the nucleotide sequence of the gene from the original species.

[0199] At present, information on a wide variety of gene fragments can be obtained by differential display method and subtraction method. In general, these gene fragments are utilized as tools for isolating the full-length sequences thereof. When the gene fragment corresponds to an already-known gene, the full-length sequence is easily obtained by comparing the partial sequence with the information in known databases. However, when there exists no information corresponding to the partial sequence of interest in the known databases, cDNA cloning should be carried out for the full-length cDNA. It is often difficult to obtain the full-length nucleotide sequence using the partial sequence information as an initial clue. If the full-length of the gene is not available, the amino acid sequence of the polypeptide encoded by the gene remains unidentified. Thus the database of the present invention can contribute to the identification of full-

length cDNAs corresponding to gene fragments, which cannot be revealed by using databases of known genes.

[0200] The present invention has provided 2443 polynucleotides. As has not yet proceeded the isolation of full-length cDNA within the human, the invention has great significance. It is known that secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, and so on are involved in many diseases. The genes and proteins involved in diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0201] In particular, cDNA assumed to encode secretory proteins, which were provided by this invention, are very important for the industry since the encoded proteins themselves are expected to be useful as pharmaceutical agents and many disease-related genes may be included in them. In addition, membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins, and genes encoding them can be used as indicators for diseases, etc. These cDNA are also very important for the industry, which are expected to regulate the activity or expression of the encoded protein to treat diseases, etc.

[0202] Any patents, patent applications, and publications cited herein are incorporated by reference.

[0203] The invention is illustrated more specifically with reference to the following examples, but is not to be construed as being limited thereto.

## EXAMPLE 1

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#### Preparation of cDNA library by oligo-capping

(1) Extraction and purchase of mRNA -

[0204] Total RNAs as mRNA sources were extracted from human tissues (shown below) by the method as described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis. Molecular Cloning Second edition, Cold Spring harbor Laboratory Press. 1989). Further, by the method as described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989), total RNAs as mRNA sources were extracted from human culture cells and human primary culture cells (shown below) which had been cultivated by the methods described in the catalogs.

[0205] The I brary names and the origins are indicated below in the order of "Library name: Origin". When a library was prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library.

<Extraction of mRNA from human tissues>

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[0206]
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NTONG Normal tongue; CTONG Tongue cancer; FCBBF Fetal brain: OCBBF Fetal brain:

PLACE Placenta:

SYNOV Synovial membrane tissue (from rheumatioid arthritis);

CORDB Cord blood.

<Extraction of mHNA from culture cells>

## [0207]

BNGH4 H4 cells (ATCC #HTB-148);
IMR32 IMR32 cells (ATCC #CCL-127);
SKNMC SK-N-MC cells (ATCC #HTB-10);
3NB69 NB69 cells (RCB #RCB0480);
BGGI1 GI1 cells (RCB #RCB0763);
NB9N4 NB9 cells (RCB #RCB0477);
SKNSH SK-N-SH cells (RCB #RCB0426);
AHMSC Human mesenchymal (HMSC) cells;
CHONS Chondrocytes:
ERLTF TF-1 cells rerythroleukemia);
HELAC HeLa cells:

JCMLC: Leukemia, myelogenous; MESTC: Mesenchyme stem cells; N1ESE: Mesenchymal stem cells; NCRRM: Embryonal carcinoma;

NCRRP: Embryonal carcinoma treated with retinoic acid (RA) to induce the differentiation;

T1ESE: Mesenchymal stem cells treated with trichostatin and 5-azacytidine to induce the differentiation;

NT2RM: NT2 cells (STARATAGENE #204101):

NT2RP: NT2 cells treated with retinoic acid (RA) for 5 weeks to induce the differentiation;

NT2RI: NT2 cells treated with RA for 5 weeks to induce the differentiation, followed by the treatment with the growth inhibitor for 2 weeks:

NT2NE: NT2 cells were treated with RA and the growth inhibitor for the neuronal differentiation, and the resultant neurons were concentrated and harvested (NT2 Neuron);

NTISM: NT2 cells (STARATAGENE #204101) were treated with RA for 5 weeks to induce the differentiation, and then treated with the growth inhibitor for 2 weeks; mRNA was prepared from the cells and a cDNA library was constructed from the mRNA; the cDNAs of the library whose nucleotide sequences were shared by those of mRNAs from undifferentiated NT2 cells were subtracted by using a Subtract Kit (Invitrogen #K4320-01); the subtracted library (NT2RI-NT2RM) was provided by this procedure.

[0208] RCB indicates that the cell was provided by the Cell Bank, RIKEN GENE BANK, The Institute of Physical and Chemical Research; ATCC indicates that the cell was provided by American Type Culture Collection.

Extraction of mRNA from primary culture cells>

## [0209]

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ASTRO Normal human astrocyte NHA5732, Takara Shuzo #CC2565;

DFNES Normal human dermal fibroblast (neonatal skin); NHDF-Neo NHDF2564, Takara Shuzo #CC2509;

MFSAN Normal human mesangial cell NHMC56046-2, Takara Shuzo #CC2559;

NHNPC Normal human neural progenitor cell NHNP5958, Takara Shuzo #CC2599;

PEBLM Normal human peripheral blood mononuclear cell HPBMC5939, Takara Shuzo #CC2702;

HSYRA Human synoviocyte HS-RA (from rheumatioid arthritis), Toyobo #T404K-05;

PUAEN Normal human pulmonary artery endothelial cells, Toyobo #T302K-05;

UMYEN Normal human umbilical vein endothelial cell HUVEC, Toyobo #T200K-05;

HCASM Normal human coronary artery smooth muscle cell HCASMC, Toyobo #T305K-05;

HCHON Normal human chondrocyte HC, Toyobo #T402K-05:

HHDPC Normal human dermal papilla cell HDPC, Toyobo #THPCK-001;

CD34C CD34+ cells (AllCells, LLC #CB14435M);

D3OST CD34+ cells treated with the osteoclast differentiation factor (ODF) for 3 days to induce the differentiation;

D6OST CD34+ cells treated with ODF for 6 days to induce the differentiation;

D9OST CD34+ cells treated with ODF for 9 days to induce the differentiation;

**ACTVT Activated T-cells:** 

LYMPB Lymphoblasts, EB virus transferred B cells;

NETRP Neutrophils.

[0210] Then total RNAs extracted from the following human tissues were purchased and used as mRNA sources. The library names and the origins are indicated below in the order of "Library name: Origin". When a library was prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library.

<Purchase of total RNA containing mRNA extracted from human tissues>

## [0211]

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ADRGL: Adrenal gland, CLONTECH #64016-1; BRACE: Brain (cerebellum), CLONTECH #64035-1; BRAWH: Whole brain, CLONTECH #64020-1; FEBRA: Fetal brain, CLONTECH #64019-1; FELIV: Fetal liver, CLONTECH #64018-1; HEART: Heart, CLONTECH #64025-1;

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HLUNG: Lung, CLONTECH #64023-1;
        KIDNE: Kidney, CLONTECH #64030-1:
        LIVER: Liver, CLONTECH #64022-1;
        MAMGL: Mammary Gland, CLONTECH #64037-1;
        PANCR: Pancreas, CLONTECH #64031-1;
        PROST: Prostate, CLONTECH #64038-1;
        SALGL: Salivary Gland, CLONTECH #64026-1;
         SKMUS: Skeletal Muscle, CLONTECH #64033-1;
         SMINT: Small Intestine, CLONTECH #64039-1;
         SPLEN: Spleen, CLONTECH #64034-1;
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         STOMA: Stomach, CLONTECH #64090-1;
         TBAES: Breast (Tumor), CLONTECH #64015-1;
         TCERX: Cervix (Tumor), CLONTECH #64010-1;
         TCOLN: Colon (Tumor), CLONTECH #64014-1;
         TESTI: Testis, CLONTECH #64027-1;
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         THYMU: Thymus, CLONTECH #64028-1;
         TLUNG: Lung (Tumor), CLONTECH #64013-1;
         TOVAR: Ovary (Tumor), CLONTECH #64011-1;
         T-RACH: Trachea, CLONTECH #64091-1;
         TUTER: Uterus (Tumor), CLONTECH #64008-1;
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         UTERU: Uterus, CLONTECH #64029-1;
         ADIPS: Adipose, Invitrogen #D6005-01;
         BLADE: Bladder, Invitrogen #D6020-01;
         BRALZ: Corobral cortex from an Alzheimer patient (Brain, cortex, Alzheimer), Invitrogen #D6830-01;
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         CERVX: Cervix. Invitrogen #D6047-01;
         COLON: Colon. Invitrogen #D6050-0;
         NESOP: Esophagus, Invitrogen #D6060-01;
         PERIC: Pericardium, Invitrogen #D6105-01;
         RECTM: Rectum. Invitrogen #D6110-01;
         TESOP: Esophageal (Tumor), Invitrogen #D6860-01;
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         TKIDN: Kidney (Tumor), Invitrogen #D6870-01;
         TLIVE: Liver (Tumor), Invitrogen #D6880-01;
         TSTOM: Stomach (Tumor), Invitrogen #D6920-01;
         BEAST: Adult breast, STARATAGENE #735044;
          FEHRT: Fetal heart, STARATAGENE #738012;
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          FEKID: Fetal kidney, STARATAGENE #738014;
          FELNG: Fetal lung, STARATAGENE #738020;
          NOVAR: Adult ovary, STARATAGENE #735260;
          BRASW: subtracted library (BRALZ-BRAWH). A cDNA library was constructed from mRNA prepared from tissues
          of cerebral cortex obtained from an Alzheimer patient [BRALZ: Cerebral cortex from an Alzheimer patient (Brain,
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          cortex. Alzheimer) . Invitrogen #D6830-01]; the cDNAs of this library whose nucleotide sequences were shared
          by those of mRNAs from whole brain tissue [BRAWH: Whole brain, CLONTECH #64020-1] were subtracted by
          using a Subtract Kit (Invitrogen #K4320-01).
      [0212] Further, mRNAs extracted and purified as poly A(+) RNAs from the human tissues shown below were pur-
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      chased. A cDNA library was prepared from an RNA mixture in which the poly A(+) RNA from each tissue had been
      combined with poly A(-) RNA. The poly A(-) RNA was prepared by removing poly A(+) RNA from the total RNA of whole
      brain tissue (CLONTECH #64020-1) by using oligo dT cellulose. The library names and the origins are indicated below
      in the order of "Library name: Origin".
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      <Purchase of mRNAs of human tissues as poly A(+) RNAs>
      [0213]
          BRAMY: Brain (amygdala), CLONTECH #6574-1;
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          BRCAN: Brain (caudate nucleus), CLONTECH #6575-1;
          BRCOC: Brain (corpus callosum), CLONTECH #6577-1;
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BRHIP: Brain (hippocampus), CLONTECH #6578-1;

BRSSN: Brain (substantia nigra), CLONTECH #6580-1; BRSTN: Brain (subthalamic nucleus), CLONTECH #6581-1;

BRTHA: Brain (thalamus), CLONTECH #6582-1.

## (2) Preparation of cDNA library

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[0214] cDNA library was prepared from each RNA by the improved method (WO 01/04286) of oligo capping [M. Maruyama and S. Sugano, Gene, 138: 171-174 (1994)]. A series of procedures, BAP (Bacterial Alkaline Phosphatase) treatment, TAP (Tobacco Acid Pyrophosphatase) treatment. RNA ligation, first strand cDNA synthesis and RNA removal, were carried out using the oligo-cap linker (SEQ ID NO: 5455) and oligo dT primer (SEQ ID NO: 5456), as described in WO 01/04286. Then, the single-stranded cDNA was converted to a double-stranded cDNA by PCR (polymerase chain reaction) using 5' (SEQ ID NO: 5457) and 3' (SEQ ID NO: 5458) PCR primers, and then digested with *Sfi*l. Then, a fraction of cDNA fragments, typically 2-kb or longer (3-kb or longer in some cases), was unidirectionally cloned into a *Dralli*-digested pME18SFL3 vector (Figure 1) (GenBank AB009864, Expression vector); the cDNA library was thus prepared.

[0215] The names of cDNA libraries, which were used in the analysis of full-length cDNA sequences, and their origins are shown in Table 2.

#### Table 2

		Table 2
Library	Туре	Origin, etc.
3NB69	Culture cell	NB69 cells (RCB #RCB0480)
ADIPS	Tissue	Adipose (Invitrogen #D6005-01)
ADRGL	Tissue	Adrenal gland (CLONTECH #64016-1)
ASTRO	Primary culture cell	Normal Human Astrocyte NHA5732 (Takara Shuzo #CC2565)
BEAST	Tissue	Adult Breast (STARATAGENE #735044)
BGGI1	Culture cell	Gi1 cells (RCB #RCB0763)
BLADE	Tissue	Bladder (Invitrogen #D6020-01)
BNGH4	Culture cell	H4 cells (ATCC #HTB-148)
BRACE	Tissue	Brain, cerebellum (CLONTECH #64035-1)
BRALZ	Tissue	Brain, cortex, Alzheimer (Invitrogen #D6830-01)
BRAMY	Tissue	Brain, amygdala (CLONTECH #6574-1)
BRAWH	Tissuc	Brain, whole (CLONTECH #64020-1)
BRCAN	Tissue	Brain, caudate nucleus (CLONTECH #6575-1)
BRCOC	Tissue	Brain, corpus callosum (CLONTECH #6577-1)
BRHIP	Tissue	Brain, hippocampus (CLONTECH #6578-1)
BRSSN	Tissue	Brain, substantia nigra (CLONTECH #6580-1)
BRSTN	Tissue	Brain, subthalamic nucleus (CLONTECH #6581-1)
BRTHA	Tissue	Brain, thalamus (CLONTECH #6582-1)
CD34C	Primary culture cell	CD34+ cells (AllCells, LLC #CB14435M)
COLON	Tissue	Colon (Invitrogen #D6050-0)
CTONG	Tissue	Tongue, Cancer
D3OST	Primary culture cell	CD34+ cells (ODF induction for 3 days)
D6OST	Primary culture cell	CD34+ cells (ODF induction for 6 days)
D9OS	Primary culture cell	CD34+ cells (ODF induction for 9 days)
DFNES	Primary culture cell	Normal Human Dermal Fibroblasts (Neonatal Skin); NHDF-Neo NHDF2564 (Takara Shuzo #CC2509)

Table 2 (continued)

	Library	Туре	Origin, etc.
<u> </u>	FCBBF	Tissue	Brain, Fetal
	FEBRA	Tissue	Brain, Fetal (CLONTECH #64019-1)
	FEHRT	Tissue	Heart, Fetal (STARATAGENE #738012)
	FELNG	Tissue	Lung, Fetal (STARATAGENE #738020)
· L	HCASM	Primary culture cell	Human coronary artery smooth muscle cells HCASMC (Toyobo #T305K-05)
	HCHON	Primary culture cell	Human Chondrocytes HC (Toyobo #T402K-05)
	HEART	Tissue	Heart (CLONTECH #64025-1)
15 -	HHDPC	Primary culture cell	Human dermal papilla cells HDPC (Toyobo #THPCK-001)
	HLUNG	Tissue	Lung (CLONTECH #64023-1)
ľ	IMR32	Culture cell	IMR32 cells (ATCC #CCL-127)
	KIDNE	Tissue	Kidney (CLONTECH #64030-1)
20	LIVER	Tissue	Liver (CLONTECH #64022-1)
	MAMGL	Tissue	Mammary Gland (CLONTECH #64037-1)
	MESAN	Primary culture cell	Normal human mesarigial cells NHMC56046-2 (Takara Shuzo #CC2559)
	NESOP	Tissue	Esophagus (Invitrogen #D6060-01)
.*	NOVAR	Tissue	Adult Ovary (STARATAGENE #735260)
	NT2NE	Culture cell	NT2 cells concentrated after differenciation (NT2 Neuron)
	NT2HI	Culture cell	NT2 cells treated by growth inhibitor for 2 weeks after RA induction for 5 weeks
مد	NT2RP	Culture cell	NT2 cells treated by RA for 5 weeks
	NTONG	Tissue	Tongue
	осзв <sup>=</sup>	Tissue	Brain, Fetal
	PANCR	Tissue	Pancreas (CLONTECH #64031-1)
J5	PEBLM	Primary culture cell	Human peripheral blood mononuclear cells HPBMC5939 (Takara Shuzo #CC2702)
	PERIC	Tissue	Pericardium (Invitrogen #D6105-01)
40	PLACE	Tissue	Placenta
40	PROST	Tissue	Prostate (CLONTECH #64038-1)
	PUAEN	Primary culture cell	Human pulmonary artery endothelial cells (Toyobo #T302K-05)
ŀ	RECTM	Tissue	Rectum (Invitrogen #D6110-01)
45	SALGL	Tissue	Salivary Gland (CLONTECH #64026-1)
	SKMUS	Tissue	Skeletal Muscle (CLONTECH #64033-1)
	SKNMC	Culture cell	SK-N-MC cells (ATCC #HTB-10)
50 .	SKNSH	Culture cell	SK-N-SH cells (RCB #RCB0426)
30	SMINT	Tissue	Small Intestine (CLONTECH #64039-1)
	SPLEN	Tissue	Spleen (CLONTECH #64034-1)
55	STOMA	Tissue	Stomach (CLONTECH #64090-1)
	SYNOV	Tissue	Synovial membrane tissue from rheumatioid arthritis
	TBAES	Tissue	Breast, Tumor (CLONTECH #64015-1)

Table 2 (continued)

Library	Туре	Origin, etc.
TCOLN	Tissue	Colon, Tumor (CLONTECH #64014-1)
TESOP	Tissue	Esophageal, Tumor (Invitrogen #D6860-01)
TESTI	Tissue	Testis (CLONTECH #64027-1)
THYMU	Tissue	Thymus (CLONTECH #64028-1)
TKIDN	Tissue	Kidney, Tumor (Invitrogen #D6870-01)
TOVAR	Tissue	Ovary, Tumor (CLONTECH #64011-1)
TRACH	Tissuc	Trachea (CLONTECH #64091-1)
TSTOM	Tissue	Stomach, Tumor (Invitrogen #D6920-01)
TUTER	Tissue	Uterus, Turnor (CLONTECH #64008-1)
UMVEN	Primary culture cell	Human umbilical vein endothelial cells HUVEC (Toyobo #T2OOK-05)
UTERU	Tissue	Uterus (CLONTECH #64029-1)

[0216] The cDNA library with the high fullness ratio (the fullness ratio of 5'-end, which was calculated for each cDNA library by using the protein coding region found in known mRNA species as an index, was 90% in average) prepared by the improved oligo-capping method was constructed by using a eukaryotic expression vector pME18SFL3. The vector contains SR  $\alpha$  promoter and SV40 small t intron in the upstream of the cloning site, and SV40 polyA added signal sequence site in the downstream. As the cloning site of pME18SFL3 has asymmetrical DrallI sites, and the ends of cDNA fragments contain Sfil sites complementary to the DrallI sites, the cloned cDNA fragments can be inserted into the downstream of the SR  $\alpha$  promoter unidirectionally. Therefore, clones containing full-length cDNA can be expressed transiently by introducing the obtained plasmid directly into COS cells, etc. Thus, the clones can be analyzed very easily in terms of the proteins that are the gene products of the clones, or in terms of the biological activities of the proteins.

(3) Assessment of the 5'-end completeness of clones derived from the cDNA library prepared by oligo-capping

[0217] With respect to the plasmid DNAs of clones derived from the libraries, the nucleotide sequences of cDNA 5'-ends (3'-ends as well in some cases) were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction was conducted by using a DNA sequencing reagent (BigDye Terminator Cycle Sequencing FS Ready Reaction Kit. PE Biosystems) according to the manual. A database was constructed based on the obtained data. [0218] The 5'-end completeness of about 1110,000 clones derived from the human cDNA libraries prepared by the improved oligo-capping method was determined by the following method. The clones whose 5'-end sequences were consistent with those of known human mRNA in the public database were judged to be "full-length" if they had a longer 5'-end sequence than that of the known human mRNA; or even though the 5'-end sequence was shorter, if it contained the translation initiation codon it was judged to have the "full-length" sequence. Clones which did not contain the translation initiation codon were judged to be "not-full-length". The fullness ratio ((the number of full-length clones)/(the number of full-length and not-full-length clones)) at the 5'-end of the cDNA clones was determined by comparing with known human mRNA. As a result, the fullness ratio of the 5'-ends was 90%. The result indicates that the fullness ratio at the 5'-end sequence was extremely high in the human cDNA clones obtained by the oligo-capping method.

## **EXAMPLE 2**

# Sequencing analysis of cDNA ends and selection of full-length clones

[0219] With respect to the plasmid DNAs of clones obtained from each cDNA library, the 5'-end nucleotide sequences of the cDNAs were determined in a DNA sequencer (ABI PRISM 3700. PE Biosystems), after sequencing reaction was conducted by using a DNA sequencing reagent (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction Kit or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed using the data obtained.

[0220] For the analyzed 5'-end sequences of cDNA clones, the data with the annotation of "complete cds" in the GenBank and UniGene were searched by BLAST homology search. When identical to certain human mRNA sequences

es, such cDNA clones were excluded. Then, clustering was carried out. When the identity was 90% or higher, and the length of consensus sequence was 50 base pairs or longer, the cDNA clones were assumed to belong to an identical cluster, and thus clustered. cDNA clones longer in the 5' direction were selected from the members belonging to a cluster; if required, the 3'-end sequences of the selected clones were determined by the same analysis method as used to determine the 5'-end sequences. The data of the end sequences obtained were analyzed, and then the clones forming a sequence contig at 5'- and 3'-ends were excluded. Further, as mentioned above, the data was analyzed again by BLAST homology search; when identical to certain human mRNA sequences (including sequences patented and applied for), the cDNA clones were excluded. Thus, the cDNAs clones to be analyzed for their nucleotide sequence were obtained.

## EXAMPLE 3

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## Analysis of the full-length nucleotide sequences

[0221] The full-length nucleotide sequences of the selected clones were determined. The nucleotide sequence determination was mainly performed by primer walking method comprising the dideoxy terminator method using custom-made synthetic DNA primers. Namely, the nucleotide sequences of the DNAs were determined in a sequencer from PE Biosystems, after sequencing reaction was carried out with a DNA sequencing reagent from the same supplier using the custom-made synthetic DNA primers according to the manual. A part of the clones were analyzed with a DNA sequencer from Licor.

[0222] Further, the nucleotide sequences of a part of the clones were determined by the shotgun method where the plasmids containing the cDNAs were digested at random were used, instead of the use of custom-made primers, by the same method in the DNA sequencer. The full-length nucleotide sequences were finally determined by completely assembling the partial nucleotide sequences obtained by the above method.

[0223] Then, the regions translatable to proteins were deduced from the determined full-length nucleotide sequences, and thereby the amino acid sequences were determined. SEQ ID NOs corresponding to the respective sequences are shown in Table 1.

# **EXAMPLE 4**

## Functional prediction by homology search

[0224] For the determined nucleotide sequences, GenBank, SwissProt, UniGene, and nr were searched by BLAST. The clones exhibiting higher homology, which were convenient to predict their functions based on the nucleotide sequences and deduced amino acid sequences, were selected based on the BLAST search hit data whose P value or E value was 10<sup>-4</sup> or lower and for which the length of consensus sequence x homology = 30 or higher in the amino acid database search. Further, from them, representative clones were selected, which are shown as Homology Search Result Data in the last part herein. Accordingly, the data shown herein are merely the representative data, and the molecule exhibiting homology to each clone is not limited thereto. Further, with respect to a part of clones, the BLAST search hit data that did not meet the criteria as described above are not shown herein.

## EXAMPLE 5

# Search for signal sequence, transmembrane domain and other functional domains in the deduced amino acid sequences

[0225] With respect to the amino acid sequences deduced from the full-length nucleotide sequences, the prediction was made for the presence of signal sequence at the amino terminus, the presence of transmembrane domain, and the presence of functional protein domains (motifs). The signal sequence at the amino terminus was searched for by PSORT [K. Nakai & M. Kanehisa, Genomics, 14: 897-911 (1992)]; the transmembrane domain, by SOSUI [T. Hirokawa et al., Bioinformatics, 14: 378-379 (1998)] (Mitsui Knowledge Industry); the function domain, by Pfam (http://www.sanger.ac.uk/Software/Pfam/index.shtml). The amino acid sequence in which the signal sequence at the amino terminus or transmembrane domain had been predicted to be present by PSORT or SOSUI were assumed to be a secretory or membrane protein. Further, when the amino acid sequence hit a certain functional domain by the Pfam functional domain search, the protein function can be predicted based on the hit data, for example, by referring to the function categories on the PROSITE (http://www.expasy.ch/cgi-bin/prosite-list.pl). In addition, the functional domain search can also be carried out on the PROSITE.

[0226] The search results obtained with the respective programs are shown below.

[0227] The clones whose deduced amino acid sequences were detected to have the signal sequences by PSORT are as follows. ADRGL20013520, ASTRO20005330, ASTRO20055750, BNGH420088500, BRACE20038000, BRACE20081720, BRACE20101710, BRACE20224480, BRACE20257100, BRACE20273890, BRALZ20013500, BRALZ20054710, BRALZ20077930, BRAMY20063970, BRAMY20284910, BRAWH20016860, BRAWH20064050, BRCOC10000870, BRCOC20078640, BRCOC20090520, BRCOC20101230, BRCOC20114180, BRCOC20121720, BRCOC20134480, BRCOC20136750, BRHIP20179200, BRHIP20198190, BRHIP20217620, BRSSN20003120, BRSSN20137020, COLON10001350, COLON20093370, CTONG20158660, CTONG20267700, D3OST20036070, D3OST20038560, D6OST20005070, FCBBF10001210, FCBBF10002430, FCBBF10003760, FCBBF10005740, FCBBF20042560, FCBBF30086440, FCBBF30095260, FCBBF30172550. FCBBF30238870, FEBRA20009090, FEBRA20029860, FEBRA20086620, FEBRA20092890, FEBRA20111460, FEBRA20130190, FEBRA20145780, FEBRA20235500. HCHON20064590, HCHON20067700, HCHON20086720, HEART20049410, HHDPC20001040, HHDPC20014320, KIDNE20011400, KIDNE20022620, KIDNE20126130, KIDNE20127450, LIVER20064690, MESAN10001260, MESAN20038510, MESAN20115970, MESAN20152770, MESAN20153910, NT2NE20118960, NT2NE20124480, NT2NE20183760, NT2RI20003480, NT2RI20023910, NT2RI20028470, NT2RI20040930, NT2RP70134990, NTONG20029700, NTONG20063010, OCBBF20019830, OCBBF20078920, OCBBF20086400, OCBBF20087010, OCBBF20116850, OCBBF20122620, OCBBF20130910, OCBBF20188730, PEBLM20075980, PLACE60086400, PROST20175290, SKNSH20028660, SMINT20009840, SMINT20022020, SMINT20073650, SMINT20095050, SMINT20105330. SMINT20127930, SMINT20153260, SMINT20157450, SMINT20173240, SMINT20178550, SMINT20191420, SMINT20192000, SPLEN20079510, SPLEN20095810, SPLEN20118300, SPLEN20141360, SPLEN20157880, SPLEN20171890, SPLEN20213830, STOMA20005390, STOMA20056640, STOMA20080500, STOMA20088380, SYNOV20001520, SYNOV20001730, SYNOV20002790, SYNOV20002970. SYNOV20004260, SYNOV20007000, SYNOV20008240, SYNOV20009230, SYNOV20010880, SYNOV20011110, SYNOV20013000, TESOP20005690, TESTI20123560, TESTI20208400, TESTI20211220, TESTI20272960, TESTI20309170, TESTI20316870, TESTI20385960, TESTI20390260, TESTI20391770, TESTI20396130, TESTI20415170, TESTI20421490, TESTI20441940, TESTI20444180, TESTI20463580, THYMU10005360, THYMU20027560, THYMU20032870, THYMU20039810, THYMU20066100, THYMU20106710, THYMU20111830, THYMU20161640, THYMU20162190, THYMU20194420, THYMU20222890, THYMU20241850, TKIDN20005210, TRACH20029540, TRACH20034840, TRACH20050040, TRACH20069180, TRACH20085400, TRACH20136710, TRACH20145440, TRACH20180840, UTERU20158300, UTERU20158800, UTERU20161570 [0228] The clones whose deduced amino acid sequences were detected to have the transmembrane domains by SOSUI are as follows. Numerals indicate the numbers of transmembrane domains detected in the deduced amino acid sequences. Of the search result, the clone name and the number of transmembrane domains are demarcated by a double slash mark (//). ADIPS10000640//3, ADRGL20018540//1, ADRGL20035850//2, ASTRO20001410//1, ASTRO20005330//3, ASTRO20190390//1, BEAST20004540//1, BGGI110000240//2. BRACE20006400//1. ASTRO20058630//4, BRACE20038470//1, BRACE20039040//1, BRACE20039540//1, BRACE20051380//1, BRACE20059370//1, BRACE20061050//1, BRACE20063630//2, BRACE20067430//1, BRACE20069090//2, BRACE20101700//2, BRACE20116110//2, BRACE20147800//1, BRACE20153680//5, BRACE20163350//1, BRACE20179340//6, BRACE20188470//4, BRACE20195100//1, BRACE20201570//1, BRACE20210140//1, BRACE20224480//1, BRACE20228480//1, BRACE20232840//1, BRACE20238000//2, BRACE20274080//1. 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       UTERU20158800//2. UTERU20161570//6, UTERU20178100//1. UTERU20186740//1
       [0229] I he Names of clones whose deduced amino acid sequences were detected to have functional domains with
       Pfam, and the name of hit functional domains are as follows. The search result is indicated as "clone name//functional-
       domain name." When the clone has multiple hit functional domains, they are listed and demarcated by a double slash
       mark (n). When the clone has multiple hits of an identical functional domain, each is listed without abridgment.
20
             3NB6910001910//tRNA synthetases class II (A)// tRNA synthetases class II (A)// DHHA1 domain
             3NB6920014590//Homeobox domain
             ADIPS 20004250 // Zinc finger, C2H2 type// DNA binding domain with preference for // Zinc finger, C2H2 type// Zinc
             finger C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2
             type// UvrD/REP helicase// Zinc finger, C2H2 type// Zinc finger, C2H2 t
25
             ADRGL10001470//Cytochrome P450// Cytochrome P450
             ADRGL2C011190//Calponin homology (CH) domain// Calponin homology (CH) domain// Pou domain - N-terminal
             to homeobox domain
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             ADRGL20035850//Cytochrome P450
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             ADRGL20043330//PHD-finger// Rabphilin-3A effector domain// C2 domain// C2 domain/
             ASTRO2C003010//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
             type// Zinc finger C2H2 type ASTRO20012490//Eukaryotic initiation factor 1A
             ASTRO20027430//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
             Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
             ASTRO20033160//Mitochond carrier proteins// Mitochondrial carrier proteins// Mitochondrial carrier proteins
             ASTRO20055750//Collagen triple helix repeat (20 copies)// Heavy-metal-associated domain
             ASTRO20058630//Vacuolar sorting protein 9 (VPS9) domain
             ASTRO20064750//Zinc finger, C2H2 type// Nuclear transition protein 2 ASTRO20072210//PDZ domain (Also
             known as DHR or GLGF).
             ASTRO20084250//KH domain// Zinc finger, C3HC4 type (RING finger) ASTRO20105820//FAD binding domain
             ASTRO20106150//Calpain family cysteine protease// Calpain large subunit, domain III
             ASTRO2C108190//Rap/ran-GAP
             ASTRO20125520//DnaJ domain
             ASTRO2013500;/ThiF family// Repeat in ubiquitin-activating (UBA) pro ASTRO20143630//KH domain// Bacterial
             regulatory proteins icrp family ASTRO20155290//TPR Domain// TPR Domain// TPR Domain
             ASTRO2C168470//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
             type// Zinc finger C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger,
             C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type
             BGGI110001930//UBX domain
             BGGI120006160//Fumarylacetoacetate (FAA) hydrolase fam
             BLADE20003400//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc
             finger C2H2 type// Zinc finger, C2H2 type
             BLADE20003890//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Src homology domain 2// Zinc
             finger C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
             type// Zinc tinger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Src ho-
             mology domain 2// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
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type// Zinc finger C2H2 type

BNGH420088500//SAM domain (Sterile alpha motif) BRACE20003070//SAM domain (Sterile alpha motif) BRACE20011070//F-box domain. BRACE20027620//Dienelactone hydrolase family// Dienelactone hydrolase family BRACE20038000//ATP synthase, Delta/Epsilon chain// Dual specificity phosphatase, catalytic d BRACE20039540//Immunoglobulin domain// Adenovirus E3 region protein CR2 BRACE20050900//TPR Domain// TPR Domain// TPR Domain// TPR Domain BRACE20052160//SAM domain (Sterile alpha motif) BRACE20053280//PDZ domain (Also known as DHR or GLGF). BRACE20053480//Ribosomal protein L22p/L17e// Glycosyl hydrolases family 38 BRACE20053630//Plant thionins// Mitochondrial carrier proteins// Mitochondrial carrier proteins BRACE20057620//Eukaryotic initiation factor 4E BRACE20058580//L1 (late) protein BRACE20059370//FERM domain (Band 4.1 family) BRACE20060550//Ank repeat// Ank repeat// Ank repeat// PEP-utilizing enzymes BRACE20060720//WD domain, G-beta repeat// WD domain, G-beta repeat BRACE20060890//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type BRACE20062640//Alanine racemase// RNB-like proteins BRACE20063780//NOL1/NOP2/sun family BRACE20064880//KH domain// KH domain// KH domain BRACE20068590//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type BRACE20096200//Sir2 family// Sir2 family BRACE20107530//short chain dehydrogenase BRACE20115920//Spectrin repeat// Fes/CIP4 homology domain// Interleukin 10 BRACE20148240//Ras family BRACE20151320//Zinc finger, C3HC4 type (RING finger) BRACE20153680//Sir2 family// Ion transport protein BRACE20163350//Immunoglobulin domain// Immunoglobulin domain BRACE20177200//RanBP1 domain. BRACE20188470//ABC transporter// Thymidylate kinase BRACE20190040//Integrase DNA binding domain BRACE20192440//Translation initiation factor IF-3 BRACE20223330//3'-5' exonuclease// Adenylylsulfate kinase// Protein of unknown function DUF82 BRACE20232840//4Fe-4S binding domain// ABC transporter// ABC transporter// ATPases associated with various BRACE20240740//Ribosomal protein L36 BRACE20253330//PDZ domain (Also known as DHR or GLGF). BRACE20269200//Heat-labile enterotoxin alpha chain BRACE20273890//UBA domain BRACE20284100//Polysaccharide lyase family 8 BRACE20286360//Alpha adaptin carboxyl-terminal domain BRALZ20013500//Keratin, high sulfur B2 protein// u-PAR/Ly-6 domain BRALZ20054710//Zinc finger, C3HC4 type (RING finger)// TRAF-type zinc finger BRALZ20058880//STAT protein BRALZ20077930//Ribosomal protein S27a BRAMY20000520//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) BRAMY20002770//DB module BRAMY20025840//Sec7 domain BRAMY20045240//Flagellar L-ring protein BRAMY20054880//Pou domain - N-terminal to homeobox domain BRAMY20103570//DNA binding domain with preference for A/T r BRAMY20104640//Eukaryotic protein kinase domain// Protein kinase C terminal domain BRAMY20111960//Ribosomal protein L36 BRAMY20121620//TPR Domain// TPR Domain// TPR Domain// TPR Domain// PPR repeat

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BRAMY20124260//ZU5 domain// Death domain

BRAMY20148130/WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// TBC domain BRAMY20153110//ACT domain// Biopterin-dependent aromatic amino acid hydroxylase BRAMY20157820//Kinesin motor domain BRAMY20162510//MAGE family BRAMY20167060//Collagen triple helix repeat (20 copies) BRAMY20174550//ABC transporter transmembrane region.// Phosphoribulokinase// Adenylylsulfate kinase// FtsK/SpollIE family// ABC transporter BRAMY20211390//Zinc finger, C3HC4 type (RING finger) BRAMY20211420//Transient receptor// GGL domain BRAMY20213100//LIM domain containing proteins// GATA zinc finger// 'Paired box' domain BRAMY20215230//ribonuclease. BRAMY20217460//EF hand// EF hand// EF hand BRAMY20218250//Ion transport protein// Sir2 family// Ion transport protein BRAMY20240040//Nuclear transition protein 2

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BRAMY20245300//Fanconi anaemia group C protein// Metallo-beta-lactamase superfamily

BRAMY20248490//Sodium:sulfate symporter transmembrane

BRAMY20260910//Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

BRAMY20270730//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C3HC4 type (RING finger)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

BRAMY20271400//Phorb esters/diacylglycerol binding dom// PHD-finger

BRAMY20277170//Ki channel tetramerisation domain// NADH-ubiquinone/plastoquinone oxidoreduc// Ion transport protein// Transmembrane region cyclic Nucleotide G

BRAMY20285160//NTR/C345C module

BRAWH20002320//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat BRAWH20011710//Ank repeat// Ank repeat// Ank repeat// CAP-Gly domain// CAP-Gly domain

BRAWH20012390//EF hand// EF hand// EF hand

BRAWH20016620//Eukaryotic protein kinase domain// EIAV coat protein. gp90 BRAWH20018730//Sugar (and other) transporter

BRAWH20028110//4Fe-4S binding domain// LIM domain containing proteins// LIM domain containing proteins// LIM domain containing proteins// LIM domain containing proteins// Villin headpiece domain

BRAWH20030250//jmjN domain 35

> BRAWH20064050//Sushi domain (SCR repeat)// EGF-like domain// Trypsin Inhibitor like cysteine rich domain// EGF-like domain// Granulins// Granulins// EGF-like domain

> BRAWH20075700//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

> BRAWH20096780//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type

BRAWH20101360//Hexokinase

BRAWH20103290//CRAL/TRIO domain.// Spectrin repeat// Extracellular link domain// RhoGEF domain// PH do-

BRAWH20110960/iPCI domain

BRAWH20112940//Similarity to lectin domain of ricin beta-chain, 3 copies.

BRAWH20114000//Glutamate/Leucine/Phenylalanine/Valine dehydrogenase

BRAWH20117950//Carboxylesterases

BRAWH20118230//Transforming growth factor beta like domain

BRAWH20121640//eubacterial secY protein// Transmembrane amino acid transporter protein

BRAWH20132190//Acetyltransferase (GNAT) family

BRAWH20137480//Villin headpiece domain 55

BRAWH20138660//Adaptor complexes medium subunit family

BRAWH20149340//IQ calmodulin-binding motif// RhoGEF domain

BRAWH20164460//Sigma-54 interaction domain// ATPases associated with various cellular activities (AAA)

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BRAWH20171030//Adenylate kinase// NB-ARC domain// ATPases associated with various cellu BRAWH20185060//Integrase core domain BRCAN10001490// chromo' (CHRromatin Organization MOdifier) BRCAN20003460//Thioredoxin BRCAN20071190//Ubiquitin family// UBX domain BRCAN20091560//Rieske [2Fe-2S] domain// Phosphoglucose isomerase// FAD binding domain// Pyridine nuclectide-disurph de oxidoreductase// Phytoene dehydrogenase related enzyme BRCAN2C124080/WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD comain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat BRCAN20273550//FATC domain BRCAN20273640//Formin Homology 2 Domain BRCAN20280210//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type BRCAN20280360//PAP2 superfamily BRCOC20001860//FliP family// Glycosyl hydrolase family 47 BRCOC20004040/i7 transmembrane receptor (rhodopsin family)// Neurohypophysial hormones, C-terminal Domain BRCOC20006370/iPlexin repeat BRCOC20008160//Spectrin repeat// Spectrin repeat// Tropomyosinsi/ Spectrin repeat// Adenylate cyclase// Spectrin repeat// FF domain// Spectrin repeat// Spectrin repeat/ BRCOC20008500//Vacuolar sorting protein 9 (VPS9) domain// Ras association (RalGDS/AF-6) domain BRCOC20023230//Reverse transcriptase (RNA-dependent DNA polymerase) BRCOC20026640//Gag P30 core shell protein BRCOC20027510//Leucine Rich Repeat// Leucine Rich Repeat BRCOC20031250/, Triosephosphate isomerase BRCOC20035130//14-3-3 proteins BRCOC20037320/iApolipoprotein A1/A4/E family BRCOC20055420/iHelix-loop-helix DNA-binding domain// Myristoyl-CoA BRCOC20074760/iHerpesvirus UL25 family// Beige/BEACH domain BRCOC20110100//Integrase core domain BRCOC20121720/iPHD-finger BRCOC20144000//Helicases conserved C-terminal domain BRCOC20178270//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 35 type// Zinc finger C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger C2H2 type BRCOC20178560//LIM domain containing proteins// LIM domain containing proteins// LIM domain containing proteins// Ribosomal protein L24e// LIM domain containing proteins BRHIP10001290//Ribosomal protein S3, C-terminal domai// Similarity to lectin domain of ricin b 40 BRHIP20001630//Protein of unknown function DUF16 BRHIP20003120//Dehydrins// Reticulon BRHIP20005530//ThiF family BRHIP20046850//ICE-like protease (caspase) p20 domain// Aminotransferases class-l BRHIP20\*15080//PH domain 45 BRHIP20118910//Fibronectin type I domain BRHIP20\*19330./KRAB box// Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS): Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// 50 Zinc finger C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger. C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type BRHIP20 32860//PDZ domain (Also known as DHR or GLGF). BRHIP20:43730//MYND finger BRHIP20\*53600//RNA recognition motif. (a.k.a. RRM, RBD, or 55 BRHIP20\* 74040//GAF domain// GAF domain// Transposase, Mutator family// 3'5'-cyclic nucleotide phosphodi-

BRHIP20\*76420//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

BRHIP20183690//DEAD/DEAH box helicase// Integral membrane protein DUF6// Integral membrane protein DUF7 BRHIP20189980//bZIP transcription factor

BRHIP20191860//Helix-loop-helix DNA-binding domain

BRHIP20207990//Phorbol esters/diacylglycerol binding dom// Zinc finger, C3HC4 type (RING finger)// PHD-finger BRHIP20222280//Zinc finger, C2H2 type// Zinc finger, C2H2 typ

BRHIP20236950//Outer Capsid protein VP4 (Hemagglutinin)

BRHIP20238600//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain. G-beta repeat

BRHIP20238880//wnt family of developmental signaling protei

BRHIP20249110//Hexokinase// Hexokinase

BRHIP20252450//Spectrin repeat// Spectrin repeat// Spectrin repeat// Phosphoenolpyruvate carboxykinase// Spectrin repeat// Spectrin repeat

BRHIP20253660//SH3 domain

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BRHIP20283030//Cadherin domain// Cadherin domain

BRHIP20285830//Intermediate filament proteins

BRHIP30004570//Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi comair (SCR repeat)

BRHP30004880//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Fibronectin type III d

BRSSN20003120//7 transmembrane receptor (metabotropic gluta

BRSSN:2C013420//Histone deacetylase family// Zn-finger in ubiquitin-hydrolases and o

BRSSN2C014260//Leucine Rich Repeat// Leucine 
BRSSN20015790//Pyridoxal-dependent decarboxylase

BRSSN20021600//BTB/POZ domain// Kelch motif// BRSSN20038200//Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif// Initiator RepB crotein RasGEF domain

BRSSN2C039370//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type

BRSSN:2C046790//Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type BRSSN:2C1011C0//'Cold-shock' DNA-binding domain

BRSSN2C105870//ATPases associated with various cellular activities (AAA)

BRSSN2C117990//short chain dehydrogenase

BRSSN2C120810//Trypsin

BRSSN2C146100//Adenylate and Guanylate cyclase catalytic domain// Adenylate and Guanylate cyclase catalytic comain:// Zinc finger, C4 type (two domains)// Adenylate and Guanylate cyclase catalytic domain

BRSSN2C176820//Wiskott Aldrich syndrome homology region 2

BHSSN2C177570//Phosducin

BHSSN2C18/310//Ank repeat// Ank repeat// Ank repeat// Ank repeat/

BRSTN10000830//Kelch motif// Kelch motif// Kelch motif// Kelch motif/

BRSTN20005360//TPR Domain// TPR Domain

BRTHA20000570//Reverse transcriptase (RNA-dependent DNA pol

BRTHA20004740//Phosphoglycerate kinases// lactate/malate dehydrogenase// Flavoprotein// short chain dehydrogenase// Zinc-binding dehydrogenases

BRTHA20046290//Transmembrane 4 family

CD34C30004240//RhoGAP domain

COLON10001350//Immunoglobulin domain// Immunoglobulin 
CTONG10000220//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat

CTONG10000620//Sec7 domain// PH domain// Josephin

CTONG10000930//Armadillo/beta-catenin-like repeats

CTONG10000940//Ank repeat// Ank repeat// Ank repeat

CTONG10002770//Calponin homology (CH) domain// Calponin homology (CH) domain

CTONG20009770//Proteasome/cyclosome repeat// Proteasome/cyclosome cyclosome/cyclosom ome/cyclosome repeat

CTONG20014280//WD domain, G-beta repeat// WD domain, G-beta repeat CTONG20027090//Glypican// Leucine Rich Repeat// Leucine Rich Repeat

CTONG20050280//KRAB box// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type// Zinc finger, C

CTONG20075860//Ribulose bisphosphate carboxylase, smal 10

CTONG20076130//Hepatitis C virus non-structural protein NS2

CTONG20085950//SCAN domain// Zinc finger, C2H2 type// Zinc finger, C2H2 type

CTONG20092570//Integral membrane protein DUF6// Uncharacterized protein family UPF0005

CTONG20092700//BTB/POZ domain 15

CTONG20093950//Zinc finger, C2H2 type// Zinc finger, C2H2 type

CTONG20095340//E1-E2 ATPase

CTONG20096750//Disintegrin

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CTONG20098440//Acyltransferase

CTONG20099550//GGL domain

CTONG20105080//Integral membrane protein DUF6

CTONG20106520//Pyridoxal-phosphate dependent enzyme CTONG20114290//Apolipoprotein A1/A4/E family CTONG20118150//WD domain, G-beta repeat// WD domain, G-beta repeat/ CTONG20118250//Eukaryotic-type carbonic anhydrase

CTONG20121010/iZinc finger, C2H2 type// CONSTANS family zinc finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C C2H2 type// Zinc finger. C2H2 type

CTONG20121580//Kinesin motor domain// FHA domain// Histidine carboxylase PI chain

CTONG20124010//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat CTONG20125640//Ribosomal protein L10// 60s Acidic ribosomal protein CTONG20128430//Beta/Gamma crystallin// Beta/Gamma crystallin// Beta/Gamma crystallin// Beta/ Gamma crystallin// Beta/Gamma crystallin// Similarity to lectin domain of ricin b

CTONG20129960//F-box domain.// UvrD/REP helicase// UvrD/REP helicase// Viral (Superfamily 1) RNA helicase CTONG20131560//PDZ domain (Also known as DHR or GLGF).

CTONG20133390//Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc fing finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C3HC4 type (RING finger)// Zinc finger, C2H2 type// Zinc finger, C2H2 type

CTONG20133520//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2

type CTONG20139860//Ank repeat// Ank repeat// Ank repeat CTONG20140580//Domain of unknown function DUF25// SNF2 and others N-terminal domain// SNF2 and others N-terminal domain// Small cytokines (intecrine/chemokine), inter

CTONG20143690//MYND finger

CTONG20146300//Reverse transcriptase (RNA-dependent DNA pol

CTONG20149460//BTB/POZ domain// Kelch motif// Kelch motif// Kelch motif// Domain of unknown function// Kelch 50 motif// Kelch motif// Kelch motif

CTONG20153300//C. clegans Srg family integral membrane prote// TBC domain

CTONG20153580//F-box domain.// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat

CTONG20155180//RNA helicase 55

CTONG20156780//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

CTONG20158040//UTP-glucose-1-phosphate uridylyltransferase

CTONG20158660//Latrophilin/CL-1-like GPS domain// 7 transmembrane receptor (Secretin family)

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CTONG20159530//Glypican CTONG20160560//DNA binding domain with preference for A/T rich regions CTONG20161850//Immunoglobulin domain CTONG20165050//Keratin, high sulfur B2 protein CTONG20186320//Kelch motif// Kelch motif// Kelch motif// Kelch motif/ CTONG20200310//RNB-like proteins D3OST20006180//Dual specificity phosphatase, catalytic domain D3OST20036070//Leucine Rich Repeat D9OST20023970//Glycosyl hydrolases family 18// Glycosyl hydrolases family 18 D9OST20026730//Leucine Rich Repeat// Leucine Rich Repeat/ D9OST20033970//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C C2H2 type// Zinc finger, C2H2 type// Putative zinc finger in N-recognin// Zinc finger, C2H2 type// Zinc finger, C2H2 type D9OST20035940//Mitochondri carrier proteins// Mitochondrial carrier proteins D9OST20040180//7 transmembrane receptor (rhodopsin family) DFNES20037420//Elongation factor Tu family DFNES20071130//Phosphotriesterase family// Phosphotriesterase family// Phosphotriesterase family/ FCBBF10000240//Phosphoenolpyruvate carboxylase// Bacterial Cytochrome Ubiquinol Oxidas// Glycosyl trans-FCBBF10000630//Molluscan rhodopsin C-terminal tail// WW domain FCBBF10001150//Cadherin domain// Cadherin domain// Cadherin domain// Cadherin domain// Cadherin domain FCBBF10001210//lmmunoglobulin domain// lmmunoglobulin domain FCBBF10001550//Glutamate/Leucine/Phenylalanine/Valine dehydrogenase FCBBF10001710//DM DNA binding domain// Zinc finger, C2H2 type// Zinc finger, C2H2 type FCBBF10002800//lmmunoglobulin domain// lmmunoglobulin domain// lmmunoglobulin domain// lmmunoglobulin Immunoglobulin domain FCBBF10003670//Ubiquitin carboxyl-terminal FCBBF10003770//PDZ domain (Also known as DHR or GLGF).// PDZ domain (Also known as DHR or GLGF).// pfkB family carbohydrate kinase// PDZ domain (Also known as DHR or GLGF).// ThiC family// PDZ domain (Also known as DHR or GLGF).// PDZ domain (Also known as DHR or GLGF).// PDZ domain (Also known as DHR or GLGF).// TIR domain FCBBF10004120//RNA recognition motif. (a.k.a. RRM, RBD, or FCBBF10004370//KRAB box// Zinc finger, C2H2 type// Ribosomal protein L37e// Zinc finger. C2H2 type// Zinc finger, C2H2 type FCBBF10005060//CRAL/TRIO domain. FCBBF10005460//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Fibronectin type III domain// Fibronectin type III domain FCBBF10005500//Keratin, high sulfur B2 protein FCBBF10005740//Mitocho carrier proteins// Mitochondrial carrier proteins PCBBF20014270//Acyl CoA binding protein FCBBF20042170//Fibrillar collagen C-terminal domain FCBBF20049300//Olfactomedin-like domain FCBBF20059090//Zinc finger, C2H2 type FCBBF20064520//RNA recognition motif. (a.k.a. RRM, RBD, or FCBBF20067810//Nerve growth factor family// GTP1/OBG family// GTP1/OBG family// GTPase of unknown function// ADP-ribosylation factor family// Ras family FCBBF20068820//Zinc finger, C2H2 type// Zinc finger, C2H2 type FCBBF30010810//KRAB box// Rieske [2Fe-2S] domain// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHDfinger// Zinc finger, C2H2 type// Zinc finger, finger, C2H2 type// Zinc finger, C2H2 type FCBBF30012350//Eukaryotic protein kinase domain FCBBF30012810//Ubiquitin carboxyl-terminal hydrolases famil

FCBBF30025560//Prolyt oligopeptidase family// Pou domain - N-terminal to homeobox doma// Homeobox domain

FCBBF30015940//Methyl-accepting chemotaxis protein (MCP) signaling domain

FCBBF30016320//SecA protein, amino terminal region

FCBBF30018550//Oxysterol-binding protein

#### FCBBF30033050//Sm protein

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FCBBF30039020//Herpesvirus UL6 like// Growth-Arrest-Specific Protein 2 Domain

FCBBF30049550//Ank repeat// Ank dotransferases class-II// Ank repeat// Ank r ZU5 domain

FCBBF30054440//PLAT/LH2 domain

FCBBF30057290//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type

FCBBF30078290//DNA binding domain with preference for A/T r FCBBF30086440//Pilin (bacterial filament) FCBBF30090690//Leucine rich repeat N-terminal domain// Leucine Rich Repeat// Leucine rich repeat C-terminal domain

FCBBF30095260//DHHC zinc finger domain

FCBBF30129630//Zinc finger, C2H2 type// Zinc finger, C FCBBF30175310//Clq domain// CDP-alcohol phosphatidyltransferase FCBBF30190850//Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Keratin, high sulfur B2 protein// Sushi domain (SCR repeat)// Phosphate transporter family

FCBBF30195640//PHD-finger// CONSTANS family zinc finger// PHD-finger// PHD-finger// Hsp20/alpha crystallin

FCBBF30225660//Ank repeat// Ank repeat// K+ channel tetramerisation domain// BTB/POZ domain FCBBF30233680//G10 protein

FCBBF30238870//Laminin G domain// Thrombospondin N-terminal -like domains// Laminin G domain// von Willebrand factor type C domain// von Willebrand factor type C domain// EGF-like domain// EB module// EGF-like domain// EGF-like domain// Trypsin Inhibitor like cysteine rich domain// Metallothionein// EGF-like domain// EGFlike domain// EGF-like domain

FCBBF30240960//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger. C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger, C2H2 type

FCBBF30246630//Leucine Rich Repeat// Leucine Rich Repeat FCBBF30247930//Uncharacterized protein family **UPF0004** 

FCBBF30262510//Ank repeat// Fibronectin type III domain FCBBF30281880//Regulator of G protein signaling domain// PX domain FCBBF30285280//Keratin, high sulfur B2 protein// Bacterial regulatory proteins, gntR family FCBBF40001730//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain. G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat

FEBRA10001880//Eukaryotic protein kinase domain// Eukaryotic protein kinase domain

FEBRA10001900//Zinc finger, C2H2 type 40

FEBRA20004620//Rap/ran-GAP

FEBRA20007620//Bacterial type II secretion system protein// DEAD/DEAH box helicase// Helicases conserved C-terminal domain

FEBRA20018690//Zinc finger, C2H2 type

FEBRA20024100//Ank repeat// Ank repeat// Myosin head (motor domain)// Myosin head (motor domain) 45 FEBRA20025270//Sulfotransferase proteins

FEBRA20026110//Dictyostelium (slime mold) repeats// Zinc finger, C2H2 type// Dictyostelium (slime mold) repeats// Zinc finger, C2H2 type// Dictyostelium (slime mold) repeats// Zinc finger, C2H2 type// Zinc finger, C C2H2 type// Zinc finger, C2H2 type// Zinc fing finger, C2H2 type// Dictyostelium (slime mold) repeats// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Dictyostelium (slime mold) repeats// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Dictyostelium (slime mold) repeats// Zinc finger, C2H2 type

FEBRA20034680//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// DnaJ central domain (4 repeats)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc 55 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type FEBRA20040530//KRAB box// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Bacterial dnaA protein// Zinc finger, C2H2 type// Zinc finger, C2H2

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HCHON20040020//Syntaxin

HCHON20059870//Bromodomain// Bromodomain

type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type FEBRA20080810//POT family FEBRA20082010//KRAB box// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type FEBRA20086620//Olfactomedin-like domain FEBRA20088360//Alpha adaptin carboxyl-terminal domai FEBRA20090290//Zinc finger, C3HC4 type (RING finger) FEBRA20092890//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Fibronectin type III domain FEBRA20097310//SAP domain// RNA recognition motif. (a.k.a. RRM, RBD, or FEBRA20111460//Hemagglutinin FEBRA20130190//Galactosyltransferase// Fringe-like FEBRA20132740//PH domain FEBRA20144170//Eukaryotic protein kinase domain// Protein kinase C terminal domain// Eukaryotic protein kinase domain FEBRA20167390//Sialyltransferase family FEBRA20171380//KRAB box// wnt family of developmental signaling protei// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Putative zinc finger in N-recognin// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type/ FEBRA20184330//PDZ domain (Also known as DHR or GLGF). FEBRA20192420//Cyclin-dependent kinase inhibitor// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif FEBRA20195820//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type FEBRA20196370//Cyclin-dependent kinase inhibitor// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif FEBRA20196630//DEAD/DEAH box helicase// Helicases conserved C-terminal domain FEBRA20214970//Reverse transcriptase (RNA-dependent DNA pol FEBRA20222040//bZIP transcription factor// K-box region FEBRA20223220//EGF-like domain// EGF-like domain// Cadherin domain FEBRA20229630//NADH-Ubiquinone/plastoquinone (complex I) FEBRA20235500//Sodium Bile acid symporter family// ABC 3 transport family FEBRA20237640//SAM domain (Sterile alpha motif) FEHRT20003250//Phosphatidylinositol 3- and 4-kinases HCASM10000500//Ribonucleotide reductases// Nucleotidyltransferase domain HCHON10001760//Histone deacetylase family HCHON20000380//Glucose-6-phosphate dehydrogenase HCHON20003220//Formyl transferase// Phosphopantetheine attachment sitei/ Protein of unknown function DUF132// Aldehyde dehydrogenase family HCHON20007510//Phosphotyrosine interaction domain (PTB/PID)// TBC domain HCHON20008150//RNA recognition motif. (a.k.a. RRM, RBD. or HCHON20008320//Glutamine synthetase// Zinc finger, C2H2 type/i Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger. C2H2 type// Zinc finger. C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type HCHON20009560//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger, C2H2 type HCHON20010990//TPR Domain HCHON20015350//FtsJ cell division protein HCHON20015980//FG-GAP repeat// von Willebrand factor type A domain HCHON20016040//Insulin-like growth factor binding proteins HCHON20016650//Leucine rich repeat C-terminal domain// Immunoglobulin domain// Latrophilin/CL-1-like GPS domain// 7 transmembrane receptor (Secretin family) HCHON20035130//Zinc finger, C2H2 type// Zinc finger, C2H2 type HCHON20036420//Death effector domain

HCHON20064590//Alpha-2-macroglobulin family N-terminal regi// Alpha-2-macroglobulin family N-terminal regi HCHON20068410//IQ calmodulin-binding motif// IQ calmodulin-binding motif/ binding motif// IQ calmodulin-binding motif// IQ calmodulin-bindin ulin-binding motif// IQ calmodulin-binding motif HCHON20086720//Insulin-like growth factor binding pr// Thyroglobulin type-1 repeat

HCHON20100740//EGF-like domain// F5/8 type C domain// F5/8 type C domain

HEART20003060//Immunoglobulin domain// Immunoglobulin domain

HEART20005410//u-PAR/Ly-6 domain

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HEART20017730//Ank repeat// Ank 15

HEART20025980//Calponin homology (CH) domain

HEART20034320//Glycosyl hydrolase family 9// Glycosyl hydrolase family 9

HEART20061950//PDZ domain (Also known as DHR or GLGF).

HEART20077670//Protein phosphatase 2A regulatory B subunit

HEART20083640//NAD-dependent DNA ligase 20

HEART20090000//Inositol polyphosphate phosphatase family, c

HHDPC10000830//Zinc finger, C3HC4 type (RING finger)

HHDPC20014320//Reprolysin family propeptide

HHDPC20031130//Zinc finger, C2H2 type// Zinc finger, C C2H2 type// Zinc finger, C2H2 type// Z type// Zinc finger, C2H2 type

HHDPC20034390//Cereal trypsin/alpha-amylase inhibito

HHDPC20034720//Glutathione S-transferases 30

HHDPC20068620//Immunoglobulin domain// Immunoglobulin domain

HHDPC20091780//CUB domain// F5/8 type C domain

HHDPC20092080//Thyroglobulin type-1 repeat

HLUNG20016330//Methyl-accepting chemotaxis protein (MCP) s// PH domain// PH domain// Methanol dehydrogenase beta subunit

HLUNG20017120//Peptidyl-tRNA hydrolase domain

HLUNG20023340//KH domain

HLUNG20033780//Birnavirus VP3 protein// RhoGEF domain// PH domain// SH3 domain

IMR3220002430//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat KIDNE20002520//tRNA synthetases class I (E and Q)// tRNA synthetases class I (K)// tRNA synthetases class I (E and Q)

KIDNE20003940//Phosphotransferase system. EIIC// FecCD transport family// ABC 3 transport family

KIDNE20007770//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain/

KIDNE20008010//Dihydropyridine sensitive L-type calcium

KIDNE20009470//G-patch domain// Peptidase family M1

KIDNE20017130//MYND finger// DM DNA binding domain// Ribosomal protein L36 KIDNE20020150//Ribosomal protein S13/S18// Hsp70 protein

KIDNE20021680//3-hydroxyacyl-CoA dehydrogenase

KIDNE20022620//Glycosyl transferase family 8

KIDNE20024830//C2 domain// C2 domain 50

KIDNE20027250//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type KIDNE20027950//KRAB box

KIDNE20028390//Galactose-1-phosphate uridyl transfer// Galactose-1-phosphate uridyl transfer

KIDNE20028720//ATP synthase (C/AC39) subunit

KIDNE20028830//K-box region 55

KIDNE20100070//AMP-binding enzyme

KIDNE20101510//EGF-like domain// Trypsin Inhibitor like cysteine rich d// EGF-like domain// Keratin, high sulfur B2 protein// Zona pellucida-like domain

KIDNE20102710//Ank repeat// Ank transcription factor (CBF/// GHMP kinases putative ATP-binding prote KIDNE20107620//Eukaryotic protein kinase domain// Dihydropyridine sensitive L-type calcium KIDNE20109730//Sodium KIDNE20109890//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// Zinc finger, C4 type (two domains)// WD domain, G-beta repeat// WD domain, G-beta repeat KIDNE20121880//PMP-22/EMP/MP20/Claudin family KIDNE20125630//ATP1G1/PLM/MAT8 family 10 KIDNE20127100//Kelch motif// Kelch motif// Kelch motif KIDNE20127750//Bacterial regulatory proteins, tetR family KIDNE20137340//Uncharacterized membrane protein family UPFO KIDNE20182690//BAH domain// ELM2 domain LIVER10004790//EF hand 15 LIVER20002160//Hsp70 protein LIVER20035680//UvrD/REP helicase LIVER20055440//RhoGAP domain LIVER20064690//Serpins (serine protease inhibitors) LIVER20080530//Ank repeat// Ank repeat// Ank repeat// SAM domain (Sterile alpha motif) 20 LIVER20087060//Guanylate-binding protein LIVER20087510//PHD-finger MAMGL10000830//LysM domain MESAN10001260//von Willebrand factor type C domain// von Willebrand factor type C domain// von Willebrand factor type C domain// von Willebrand factor type C domain// TILa domain// von Willebrand factor type C domain// Keratin, high sulfur B2 protein// PEP-utilizing enzymes// von Willebrand factor type D domain// Plant PEC family 25 metallothionein// Trypsin Inhibitor like cysteine rich: MESAN20029400//Zinc finger, C3HC4 type (RING finger)// RNA polymerases M/15 Kd subunits MESAN20031900//Zinc finger, C3HC4 type (RING finger)// Peroxidase// Zinc finger, C3HC4 type (RING finger)// B-box zinc finger.// Fibronectin type III domain MESAN20035290//FYVE zinc finger 30 MESAN20036460//Corticotropin-releasing factor family MESAN20038510//Oxidoreductase molybdopterin binding d MESAN20101140//LIM domain containing proteins MESAN20103120//Sodium/calcium exchanger protein MESAN20125860//Transferrin MESAN20127350//Zinc knuckle MESAN20130220// chromo' (CHRromatin Organization Modifier)// Enoyl-CoA hydratase/isomerase family MESAN20136110//KH domain// KH domain// Zinc finger, C3HC4 type (RING finger) MESAN20141920//Troponin// Tropomyosins// Borrelia ORF-A MESAN20154010//Tryptophan synthase alpha chain// Ribulose-phosphate 3 epimerase family// Indole-3-qlycerol phosphate synthases MESAN20171520//PH domain MESAN20174170//Regulator of G protein signaling domain MESAN20186700//Hepatitis C virus RNA dependent RNA polymerase NOVAR10000150//Cytosolic long-chain acyl-CoA thioester hydrolase NT2NE20010490//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// DM DNA binding domain// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type 50 NT2NE20021620//Vacuolar sorting protein 9 (VPS9) domain NT2NE20080170//CRAL/TRIO domain. NT2NE20089970//KRAB box NT2NE20118960//Gram-negative pili assembly chaperone NT2NE20125050//Ezrin/radixin/moesin family

NT2NE20157470//von Willebrand factor type A domain// Trypsin

NT2NE20132170//GNS1/SUR4 family// Transmembrane amino acid transporter protein

NT2NE20130190//Zinc finger, C2H2 type

NT2NE20142210//PAS domain// PAS domain

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NT2NE20158600//Ank repeat// Ank repeat NT2NE20177520//Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR repeat) NT2NE20181650//Src homology domain 2 NT2NE20183760//Calcitonin / CGRP / IAPP family NT2NE20184900//FF domain NT2RI20001330//Ank repeat// Ank repeat NT2RI20003480//Glypican NT2RI20005750//Cell division protein// Sigma-54 interaction domain// ADP-ribosylation factor family// ABC transporter// Ras family NT2RI20009870//Fringe-like NT2RI20025640//Reverse transcriptase (RNA-dependent DNA pol NT2RI20040930//Mitochondrial carrier proteins// Mitochondrial carrier proteins NT2RI20040990//Ank repeat// Ank NT2RI20046080//recA bacterial DNA recombination proteins NT2RI20048840//ADP-ribosylation factor family// G-protein alpha subunit NT2RI20054050//HSF-type DNA-binding domain NT2RI20056700//Spectrin repeat// Apolipoprotein A1/A4/E family// Olfactomedin-like domain NT2RI20091730//Molluscan rhodopsin C-terminal tail NT2RI20240080//TPR Domain// TPR Domain// TPR Domain NT2RI20244600//PAP2 superfamily. NT2RI20273230//DEAD/DEAH box helicase NT2RP60000770//Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type NT2RP60000850//C2 domain NT2RP70027380//PX domain// SH3 domain// RhoGAP domain NT2RP70032610//Peptidase family M20/M25/M40// Enol-ase NT2RP70036880//TBC. domain NT2RP70043480//KRABbox// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger, C2H2 type// Zinc finger. finger, C2H2 type NT2RP70044280//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) NT2RP70062230//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Pancreatic hormone peptides// Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger, C2H2 type NT2RP70063950//RhoGEF domain// Extracellular link domain// PH domain NT2RP70078420//PH domain// Putative GTP-ase activating protein for Arf// Ank repeat// Ank repeat NT2RP70080850//SPRY domain// Adenovirus EB1 55K protein / large t-an NT2RP70102350//Viral methyltransferase// Helix-loop-helix DNA-binding domain NT2RP70105210//Myc amino-terminal region NT2RP70157890//KRAB box NT2RP70159960//PH domain NT2RP70179710//Zinc finger, C3HC4 type (RING finger)// PHD-finger NT2RP70188710//Yeast PIR proteins NT2RP70192730//alpha/beta hydrolase fold NT2RP70194450//Bacterial regulatory proteins, crp family NT2RP70195430//Zinc-binding dehydrogenases NT2RP70198350//PWWP domain NTONG20009770//Coronavirus S2 glycoprotein// Peptidase family M3 NTONG20013620//Sulfotransferase proteins NTONG20015870//Transposase// Outer membrane efflux protein// Intermediate filament proteins NTONG20028070//von Willebrand factor type C domain NTONG20029480//NAD-dependent DNA ligase NTONG20029700//Laminin N-terminal (Domain VI)// Laminin EGF-like (Domains III and V)// Laminin EGF-like

NTONG20051530//Mov34/MPN/PAD-1 family// Extracellular link domain// Adhesin lipoprotein// Lectin C-type do-

NTONG20046140//Eukaryotic protein kinase domain// Aminoglycoside phosphotransferase

(Domains III and V)// Laminin EGF-like (Domains III and V)

main

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NTONG20056570//WD domain, G-beta repeat// WD domain, G-beta repeat

NTONG20063010//EGF-like domain// Trypsin Inhibitor like cysteine rich domain// EGF-like domain// EGF-like domain// Keratin. high sulfur B2 protein// Chitin binding Peritrophin-A domain// Zona pellucida-like domain

NTONG20064840//C2 domain// C2 domain

NTONG20067830//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat/

NTONG20070200//Zinc finger, C2H2 type// Zinc f

NTONG20070340//Collagen triple helix repeat (20 copies)// Collagen triple helix repeat (20 copies)// Collagen triple helix repeat (20 copies)

NTONG20075220//RyR domain

NTONG20076930//Alpha-2-macroglobulin family

N1ONG20083650//TPR Domain// TPR Domain// TPR Domain// PPR repeat// TPR Domain// PPR repeat// TPR Domain

NTONG20092290//Immunoglobulin domain// Immunoglobulin domain

NTONG20092330//Putative membrane protein

OCBBF 10001850//KRAB box// Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger, C2H2 type// DM DNA binding comain// Zinc finger. C2H2 type// Zinc finger. C2H2 type// MYND finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger. 
OCBBF20019380//Sushi domain (SCR repeat)// CUB domain

OCBBF20019830//Fibronectin type III domain// Fibronectin type III domain// EGF-like domain// Metallothionein fam ty 5

OCBBF2C020830//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA binding domains)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA binding domains)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA binding domains)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA binding domains)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA binding domains)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA binding domains)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA binding domains)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA binding domains)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA binding domains)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA binding domains)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA binding domains)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA binding domains)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio-family RNA bindi

OCBBF20022900//IQ calmodulin-binding motif// Dishevelled specific domain// Kunitz/Bovine pancreatic trypsin inhibitor domain

OCBBF20023050//Phorbol esters/diacylglycerol binding domain (C1 domain)// Zinc finger, C3HC4 type (RING finger)// PHD-finger

OCBBF20023650//Ank repeat// Ank repeat// Helicases conserved C-terminal domain

OCBBF20030280//Lipoprotein amino terminal region

OCBBF20035930//NSF attachment protein

OCBBF20037440//Zinc finger, C3HC4 type (RING finger)

OCBBF2C046120//Zinc finger, C2H2 type// Zinc f

OCBBF2004 4300//KRAB box// Zinc finger, C2H2 type// Putative zinc finger in N-recognin// Zinc finger, C2H2 type// DM DNA binding domain// Zinc finger, C2H2 type

OCBBF20049840//PDZ domain (Also known as DHR or GLGF).

OCBBF2C050770//Dehydrins// Carnitate acyltransferase

OCBBF20053430//Extracellular link domain// Eukaryotic protein kinase domain// Protein kinase C terminal domain OCBBF20053730//Ank repeat// Ank repeat// Patatin OCBBF20054760//Death domain

OCBBF20059560//UvrB/uvrC motif

OCBBF20066390//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger C2H2 type

OCBBF20071210//Spectrin repeat

OCBBF2C0718-0//Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger,

C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C3HC4 type (RING finger)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

OCBBF20079310//Acetyltransferase (GNAT) family

- OCBBF20080410//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 ty
  - OCBBF20082830//alpha/beta hydrolase fold
- OCBBF20086400//ADP-ribosylation factor family// ABC transporter// FtsK/SpoIIIE family// Ras family
  - OCBBF20086910//HMG (high mobility group) box
  - OCBBF20107090//Cadherin domain
  - OCBBF20108190//Zinc finger, C2H2 type// Zinc finger, C2H2 type// IBR domain// Zinc finger, C2H2 type// Zinc finger, C2H2
  - type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
    - OCBBF20108430//ADP-ribosylation factor family// G-protein alpha subunit
    - OCBBF20108580//Caspase recruitment domain
    - OCBBF20108630//ABC transporter
    - OCBBF20109310//PH domain// Arrestin (or S-antigen)
- 20 OCBBF20116850//Leucine rich repeat N-terminal domain// Leucine Rich Repeat// Leuci
  - OCBBF20120390//Caveolin// Hepatitis C virus core protein// Sodium:neurotransmitter symporter family
  - OCBBF20121390//BTB/POZ domain// Kelch motif// Kelch motif// Kelch motif// Kelch motif// Kelch motif//
- 25 OCBBF20124360//CNH domain

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- OCBBF20125530//Vpu protein// Zinc finger, C3HC4 type (RING finger)
- OCBBF20127040//Interleukin-6/G-CSF/MGF family
- OCBBF20127140//WD domain, G-beta repeat// WD domain, G-beta repeat
- OCBBF20127550//Outer Capsid protein VP4 (Hemagglutinin)
- 30 OCBBF20128120//DnaJ domain// DnaJ central domain (4 repeats)// DnaJ C terminal region
  - OCBBF20129360//PH domain// EF hand// Ribosomal RNA adenine dimethylases// EF hand// Sulfotransferase proteins// Somatotropin hormone family// Phosphatidylinositol-specific phospholi// Phosphatidylinositol-specific phospholi// C2 domain
  - OCBBF20132850//Leucine rich repeat N-terminal domain// Leucine Rich Repeat// Leucine Ric
  - OCBBF20140640//Phosphotyrosine interaction domain (PTB/PID)
  - OCBBF20140890//Ribosomal protein L11
  - OCBBF20145760//Glypican
- OCBBF20148280//Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type OCBBF20148730//BTB/POZ domain// Kelch motif// Kelc
  - OCBBF20155060//EGF-like domain// Laminin EGF-like (Domains III and V)// Laminin G domain// EGF-like domain// Laminin G domain// EGF-like domain OCBBF20173980//Regulator of chromosome condensation// Regulator of chromosome condensation// Regulator of chromosome condensation// Regulator of chromosome condensation// BTB/POZ domain// Thymidylate synthase
  - OCBBF20178880//Granulins
  - OCBBF20180120//Sodium:sulfate symporter transmembrane// Sodium:sulfate symporter transmembrane// Sodium:sulfate symporter transmembrane
- 50 PEBLM10000240//Domain found in Dishevelled, Egl-10, and Ple
  - PEBLM20013120//PH domain
  - PEBLM20024320//Cation efflux family
  - PEBLM20042900//Chitin synthase
  - PEBLM20044520//Ubiquitin carboxyl-terminal hydrolase fam// Exonuclease
- 55 PEBLM20052820//Protein phosphatase 2C
  - PEBLM20060310//IBR domain// Zinc finger, C3HC4 type (RING finger)
  - PEBLM20060360//KRAB box
  - PEBLM20075980//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain/

PEBLM20078320//Zinc finger, C2H2 type// Zinc finger, C C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// DnaJ central domain (4 repeats)// Zinc finger, C2H2 type// Zinc finger, C2H2 type

PERIC10000250//Prokaryotic DNA topoisomerase

PERIC20003870//Ribosomal L32p protein family// NAC domain// TS-N domain

PERIC20004220//Domain of unknown function

PERIC20004780//bZIP transcription factor

PLACE60003480//Chorismate synthase

PLACE60060420//Ribosomal protein L44

PLACE60079250//Bacterial flagellin N-terminus// Spectrin repeat// Spectrin repeat// Spectrin repeat// Caulimovirus movement protein// Spectrin repeat// Spectrin re trin repeat// Flagellar hook-associated protein 2// Spectrin repeat// KE2 family protein

PLACE60136500//dUTPase

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PLACE60136720//Porphobilinogen deaminase// GHMP kinases putative ATP-binding prot

PLACE60177140//7 transmembrane receptor (rhodopsin family)

PROST20047270//CRAL/TRIO domain.

PROST20047390//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C PROST20050670//Endothelin family

PROST20066880//Zinc finger, C2H2 type// Zinc f type// Zinc finger, C2H2 type

PROST20079500//Hepatitis C virus non-structural protein NS4b// Ras association (RalGDS/AF-6) domain

PROST20100460//Cystine-knot domain

PROST20112970//Sterile alpha motif (SAM)/Pointed domain// SAM domain (Sterile alpha motif)

PROST20114390//Integrase DNA binding domain

PROST20161950//RasGEF domain

PROST20169800//Cytochrome P450

PROST20170980//Immunoglobulin domain// Adenovirus E3 region protein CR1

PROST20171280//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

PROST20176170//LIM domain containing proteins// LIM domain containing proteins// LIM domain containing proteins

PROST20185830//GATA zinc finger

PROST20189770//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 ty C2H2 type// Zinc finger, C2H2 type// Zinc fing finger. C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

PROST20191640//Zinc finger, C3HC4 type (RING finger)// IBR domain// Keratin, high sulfur B2 protein// Zinc finger. C3HC4 type (RING finger)

PUAEN10000850//Uncharacterized protein family UPF0025// Secl family

PUAEN20011880//ZAP domain// Piwi domain

PUAEN20015860//PDZ domain (Also known as DHR or GLGF).// Regulator of G protein signaling domain

PUAEN20018820//Sterile alpha motif (SAM)/Pointed domain// Ets-domain

PUAEN20030180//Eukaryotic-type carbonic anhydrase

PUAEN20040670//FERM domain (Band 4.1 family)// FERM domain (Band 4.1 family)

PUAEN20055020//PH domain// START domain

PUAEN20078980//PH domain// FYVE zinc finger// Domain of unknown function DUF123// PH domain

PUAEN20083140//EF hand// PH domain// Neuregulin family

PUAEN20108240//Ank repeat// Ank repeat// Ank repeat// Ank repeat/

SALGL10001710//ENV polyprotein (coat polyprotein)

SKMUS20001980//Nebulin repeat// Nebulin 
SKMUS20003610//Syndecan domain// Mitochondrial carrier proteins// Mitochondrial carrier proteins// Mitochondrial 55 drial carrier proteins

SKMUS20007800//Matrix protein (MA), p15// Prenyltransferase and squalene oxidase re

SKMUS20016220//Nebulin repeat// Nebulin 
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comain// Immunoglobulin domain

repeat// Nebulin repeat// Nebulin repeat// Nebulin repeat SKMUS20018230//Ank repeat SKMUS20018500//Coronavirus S2 glycoprotein SKMUS20024750//Leucine Rich Repeat// Leucine Rich Repeat SKMUS20029200//Ank repeat// Respiratory-chain NADH dehydrogenase, 4// Ank repeat// Ank repeat// Ank repeat SKMUS20048970//Actin// Actin SKMUS20049030//Nebulin repeat// Nebulin repeat// Nebulin repeat// Nebulin repeat// Nebulin repeat// Nebulin SKMUS20084740//Syndecan domain SKNSH20008190//KRAB box// Zinc finger, C2H2 type// AN1-like Zinc finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger C2H2 type SKNSH2C020540//Arginase family SKNSH2C063040//Transmembrane 4 family// Transmembrane 4 family SMINT20001760//PHD-finger// Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type SMINT20009840//Immunoglobulin domain// Immunoglobulin domain SMINT20013480//Metallo-beta-lactamase superfamily SMINT20028820//Eukaryotic protein kinase domain SMINT20035690//Ribosomal L29 protein SMINT20049090//Eukaryotic protein kinase domain SMINT2005C750//Kazal-type serine protease inhibitor domain SMINT20068010//Kinesin motor domain SMINT20071400//NOL1/NOP2/sun family SMINT20073650//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin comain// Immunoglobulin domain SMINT20102780//Quinolinate phosphoribosyl transferase SMINT20106290//Formamidopyrimidine-DNA glycosylase SMINT20106720//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin comair SMINT20110330//pKID domain SMINT20112730//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin gomairii Immunoglobulin domain SMINT20115880//Zinc finger, C2H2 type// Zinc finger. C2H2 type// Zinc finger, C2H2 type SMINT20121220//Myosin tail SMINT20121950//2Fe-2S iron-sulfur cluster binding domains SMINT20122910//START domain SMINT20127930//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin comair// Immunoglobulin domain SMINT2013C320//NB-ARC domain// ATPases associated with various cellular act SMINT20131810//ENV polyprotein (coat polyprotein) SMINT2013c130//Immunoglobulin domain SMINT20138900//Hrl repeat motif// Apolipoprotein A1/A4/E family// Intermediate filament proteins SMINT20144430://mmunoglobulin domain SMINT20144800/KRAB box// Zinc finger, C2H2 type// Zinc fing finger C2H2 type SMINT20152940//Sigma-54 interaction domain// ATPases associated with various cellular activities (AAA) SMINT20154540//Glutathione S-transferases. SMINT20163960//Immunoglobulin domain SMINT20168570//Fasciclin domain SMINT20174360//haloacid dehalogenase-like hydrolase SMINT20177360//RNA recognition motif. (a.k.a. RRM, RBD, or SMINT20175740//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin

SMINT20183530//ABC transporter// ABC transporter

SMINT20190170//Immunoglobulin domain// Immunoglobulin 
SMINT20191530//DEAD/DEAH box helicase// Helicases conserved C-terminal domain

- SPLEN20006070//Ank repeat// Ank   - SPLEN20008740//Importin beta binding domain// Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-like repeats
  - SPLEN20011410//RhoGAP domain

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- SPLEN20026950//SNF2 and others N-terminal domain// Bromodomain// Helicases conserved C-terminal domain// Bromodomain
- SPLEN20027440//Zinc finger present in dystrophin, CBP/p300// Ank repeat// Ank repea

SPLEN20077500//PH domain// Transposase

- SPLEN20079260//Zinc finger, C2H2 type// Zinc finger, C2H2 type SPLEN20084600//BTB/POZ domain// Kelch motif// Kelch m
  - SPEEN20095410//Zinc finger, C2H2 type// Zinc finger, C2H2 type// SPEEN20095550//bZIP transcription factor// bZIP transcription factor// Hpt domain
  - SPEEN.20099700//Sigma-54 interaction domain// ATPases associated with various cellular ac// Thymidine kinase from horpesvirus
  - SP: FN20103950//Ribosomal S17
  - SPLEN20118300//Transmembrane amino acid transporter protein
    - SPLEN20119810//Reverse transcriptase (RNA-dependent DNA polymerase)
    - SPLEN20126190//Lipoate-protein ligase B
    - SPLEN20140800//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 ty
  - Inger C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type SPLEN20142100//von Willebrand factor type A domain
    - SPLEN20143180//Src homology domain 2
    - SPEEN20145720//PH domain
    - SPLEN20147110//HECT-domain (ubiquitin-transferase).
- SPLEN20147390//KRABbox// Zinc finger, C2H2 type// Zinc finger, C2H2 typ
  - SPLEN20149110//Dishevelled specific domain
  - SPLEN20150940//Histone deacetylase family
- 45 SPLEN20151210//FERM domain (Band 4.1 family)// FERM domain (Band 4.1 family)// Isocitrate lyase
  - SPLEN20157880//Immunoglobulin domain
  - SPLEN20163560//Kinesin motor domain
  - SPLEN20165310//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin comain
- 50 SPLEN20170310//PH domain
  - SPLEN20171470//Keratin, high sulfur B2 protein
  - SPLEN20173510//TPR Domain// TPR Domain// TPR Domain// TPR Domain// TPR Domain// TPR Domain// NADH-ubiquinone/ plastoquinone oxidoreduct
  - SPLEN20174260//Penicillin amidase// Bacterial regulatory proteins, lac! f// Vacuolar sorting protein 9 (VPS9) dom
- 55 SPLEN20179180//EF hand
  - SPLEN20179810//S-adenosylmethionine synthetase
  - SPLEN20181810//Phorbol esters/diacylglycerol binding domain (C1 domain)// FYVE zinc finger
  - SPLEN20186430//7 transmembrane receptor (rhodopsin family)// 7 transmembrane receptor (rhodopsin family)

- SPLEN20211220//Metalloenzyme superfamily SPLEN20212730//Calpain large subunit, domain III// EF hand// EF hand// EF hand/ SPLEN20222270//PTB domain (IRS-1 type) SPLEN20245300//Pancreatic hormone peptides SPLEN20250170//RhoGEF domain// PH domain// FYVE zinc fingeri/ Domain of unknown function DUF123// PH domain SPLEN20250390//EF hand// EF hand SPLEN20252190//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type SPLEN20267650//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type SPLEN20292950//Phosphoribulokinase// ABC transporter// Aldehyde oxidase and xanthine dehydrogenase, C terminus SPLEN20304950//Transmembrane 4 family SPLEN20305620//Dihydroorotate dehydrogenase STOMA20001830//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain STOMA20005390//Sodium and polassium ATPases// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain STOMA20005670//Immunoglobulin.domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin STOMA20006400//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin STOMA20006780//Hepatitis C virus RNA dependent RNA polymera// Somatotropin hormone family STOMA20008880//Olfactomedin-like domain STOMA20032890//Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type STOMA20034770//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin dpmain// Immunoglobulin domain// Immunoglobulin domain STOMA20046680//bZIP transcription factor STOMA20056640//Immunoglobulin domain STOMA20056670//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain STOMA20057820//Uncharacterized protein family UPF0024 STOMA20062130//Immunoglobulin domain STOMA20063980//Collagen triple helix repeat (20 copies) STOMA20064470//Leucine Rich Repeat// Leucine Rich Repeat STOMA20069040//Keratin, high sulfur B2 protein STOMA20077450//Repeat in ubiquitin-activating (UBA) pro// Repeat in ubiquitin-activating (UBA) pro STOMA20080500//ABC transporter STOMA20083610//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain STOMA20088380//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
- 45
  - STOMA20092530//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
  - STOMA20092890//Myosin head (motor domain)

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- 50 SYNOV20001520//Immunoglobulin domain// Immunoglobulin domain
  - SYNOV20001730//lmmunoglobulin domain// lmmunoglobulin domain// lmmunoglobulin domain// lmmunoglobulin
  - SYNOV20002510//mmunoglobulin domain// lmmunoglobulin domain// lmmunoglobulin domain// lmmunoglobulin
- SYNOV20002790//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin 55
  - SYNOV20002970//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain

- SYNOV20004260//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain//
- SYNOV20007000//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain//
- SYNOV20008240//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain/
  - SYNOV20009230//Immunoglobulin domain// Immunoglobulin   - SYNOV20010880//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain//
  - SYNOV20011110//Immunoglobulin domain// Immunoglobulin   - SYNOV20013000//Immunoglobulin domain// Immunoglobulin   - SYNOV20013560//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain//
  - SYNOV20013900//Immunoglobulin domain// Immunoglobulin   - SYNOV20017080//UBX domain

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- 20 SYNOV30001840//Asparagine synthase// AMP-binding enzyme
  - TBAES20000590//Cytochrome P450// Cytochrome P450
  - TBAES20002550//Peptidase family M1// Sigma-70 factor (ECF subfamily)
  - TBAES20003150//Cytochrome P450
  - TESOP20004000//Papain family cysteinc protease
  - TESOP20005270//Sulfotransferase proteins
  - TESTI20001000//Formamidopyrimidine-DNA glycosylase
  - TESTI20001170//HORMA domain
  - TESTI20002780//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// PEP-utilizing enzymes
  - TESTI20017950//Regulator of G protein signaling domain
  - TESTI20023510//Transcription termination factor nusG
    - TESTI20031810//Bacterial luciferase// Domain of unknown function DUF28
    - TESTI20035960//Coproporphyrinogen III oxidase// WD domain, G-beta repeat//   - TESTI20036380//Sulfate transporter family// Sodium Bile acid symporter family// STAS domain
    - TESTI20041690//Zinc finger, C3HC4 type (RING finger)// PHD-finger// IBR domain// Zinc finger, C3HC4 type (RING finger)// B-box zinc finger.// lactate/malate dehydrogenase// Fibronectin type III domain
    - TESTI20044230//Nucleosome assembly protein (NAP)// Nucleosome assembly protein (NAP)// Nucleosome assembly protein (NAP)
  - TESTI20044310//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Chorismate synthase// UvrB/uvrC motif TESTI20046750//Respiratory-chain NADH dehydrogenase, 4
    - TESTI20057750//RNase H// Integrase Zinc binding domain
    - TESTI20061110//Heavy-metal-associated domain// ATPases associated with various cellular act
    - TESTI20063830//Transposase
- 45 TESTI20066670//Acyl-CoA dehydrogenase
  - TESTI20067200//K-box region// Homeobox domain
  - TESTI20082330//Tudor domain
  - TESTI20083200//Dual specificity phosphatase, catalytic doma
  - TESTI20083940//Progesterone receptor
  - TESTI20088220//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc fi
- 55 TESTI20094470//Ets-domain
  - TESTI20098350//VAT-Nn domain
  - TESTI20108720//Protein phosphatase 2C
  - TESTI20121550//Putative GTP-ase activating protein for Arf

TESTI20127760//Cyclin// Calcitonin / CGRP / IAPP family

TESTI20130010//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

TESTI20136710//Glypican// PHD-finger

TESTI20143390//Integral membrane protein DUF6// Integral membrane protein DUF6

TESTI20148000//Thioredoxin// Calsequestrin// Thioredoxin

TESTI20152460//Putative zinc finger in N-recognin// PHD-finger

TESTI20156100//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

TESTI20157520//K+ channel tetramerisation domain// K+ channel tetramerisation domain

TESTI20168480//Immunoglobulin domain// Immunoglobulin 
TESTI20170350//Cystine-knot domain

TESTI20184620//PH domain// Oxysterol-binding protein

TESTI20185650//AN1-like Zinc finger

5 TESTI20189410//PHD-finger

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TESTI20192800//HCO3- transporter family// Ank repeat// Ank repeat// Ank repeat// Alpha-2-macroglobulin family

TESTI20197940//Domain of unknown function DUF27// Aconitase family (aconitate hydratase)

TESTI20200710//PHD-finger// LIM domain containing proteins

TESTI20202650//Repeat in HS1/Cortactin

TESTI20204450//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Homeobox domain

TESTI20208400//NOL1/NOP2/sun family

TESTI20208710//WD domain, G-beta repeat// WD domain, G-beta repeat

TESTI20211160//Hydroxyethylthiazole kinase family

TESTI20214250//Mitochondrial carrier proteins// Mitochondrial carrier proteins

TESTI20215990//F-box domain.// Leucine Rich Repeat// Leucine Rich

TESTI20216370//Carboxylesterases

TFSTI20226230//Adenylate kinase// Pou domain - N-terminal to homeobox d

TESTI20229600//EGF-like domain// Metallothionein family 5// Replication protein// Laminin G domain// EGF-like comain// Laminin G domain// Insulin-like growth factor binding prot// EGF-like domain// Laminin G domain

TESTI20230850//PAS domain

TESTI20231920//Gag P30 core shell protein

TESTI20232140//Phosphatidylinositol-specific phospholipase// Phosphatidylinositol-specific phospholipase

TESTI20234140//EF hand// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//

WD domain. G-beta repeat

TESTI20234360//WW domain// PPIC-type PPIASE domain.

TESTI20238610//MAGE family// Uncharacterized protein family UPF0057

TESTI2024283C//E2 (early) protein, C terminal// Syndecan domain

TESTI20244190//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin comain

TESTI20254860//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin comain// Recler domain// Fibronectin type III domain// Fibronectin type III domain

TESTI20255820//FERM domain (Band 4.1 family)// FERM domain (Band 4.1 family)// Isocitrate lyase

TEST120258460//PH domain

TESTI20265970//Guanylate-binding protein

TESTI2026674C//Nucleotidyltransferase domain

TESTI20272960//7 transmembrane receptor (rhodopsin family)

TESTI20275030/WD domain, G-beta repeat// WD domain. G-beta repeat

TESTI20288910//SH3 domain

50 TESTI20291960//Rhomboid family

TESTI20303220//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Fibronectin type III domain// Fibronectin typ

TESTI20303360//ENV polyprotein (coat polyprotein)

55 TESTI20305540//Hantavirus nucleocapsid protein// Troponin// Apolipoprotein A1/A4/E family

TESTI20308600//Homeobox domain

TESTI20309170//TPR Domain// Zinc finger, C3HC4 type (RING finger)// Aldo/keto reductase family// ATP-dependent protease La (LON) domain

TESTI20314180//Trypsin// Trypsin
TESTI20317600//Terpene synthase family
TESTI20318090//Zinc finger. C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
Zinc finger, C2H2 type
TESTI20320440//Thioredoxin
TESTI20320670//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)// RNA recognition motif. (a.k.a. RRM,
RBD, or RNP domain)
TESTI20326810//RanBP1 domain.
TESTI20327680//EF hand// EF hand
TESTI20328280//KE2 family protein// Troponin
TESTI20333000//Immunoglobulin domain// Immunoglobulin domain
TESTI20334410//DEAD/DEAH box helicase// Helicases conserved C-terminal domain
TESTI20335050//Zinc finger, C3HC4 type (RING finger)
TEST/20335200//Immunoglobulin domain TEST/2034377//Transprinting factor E3E/dimerication partner (TDR)
TEST/20343070//Transcription factor E2F/dimerisation partner (TDP)
TESTI20351830//K-box region
TESTI20352620//Saposin A-type domain
TESTI20355020//Tudor domain
TESTI20358980//Homeobox domain// Collagen triple helix repeat (20 copies)
TESTI20366910//Pyridine nucleotide-disulphide oxidoreductase
TESTI20368330//Rhodanese-like domain
TESTI20369690//PHD-finger
TESTI20370020//Bleomycin resistance protein
TESTI20370810//lon transport protein// Polysaccharide biosynthesis protein// Sugar (and other) transporter
TESTI20371030//Kelch motif// Kelch motif// Kelch motif// Kelch motif/
TESTI20375340//Phosphatidylinositol-specific phospholi// UvrD/REP helicase// Phosphatidylinositol-specific
phospholi// C2 domain TESTI20377230//Thymidylate synthase
TESTI20378190//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2
type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
TESTI20381040//Putative zinc finger in N-recognin
TESTI20382750//Kinesin motor domain
TESTI20383880//DnaJ domain
TESTI20385960//Zinc finger, C3HC4 type (RING finger)// SPRY domain
TESTI20390410//Arsenical pump membrane protein
TESTI20391210//IQ calmodulin-binding motif
TESTI20391770//Domain of unknown function DUF19// Thioredoxin
TESTI20392250//PH domain// Phorbol esters/diacylglycerol binding domain (C1 domain)
TESTI20392270//Cyclin TESTI20392760//Leucine Rich Repeat// Leucine
cine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat/
·
TESTI20393530//Mitochondrial carrier proteins
TEST/20397760//E1-E2 ATPase
TESTI20400940/K-box region
TESTI20401020//Mitochondrial carrier proteins// Mitochondrial carrier proteins
TESTI20408150//Keratin, high sulfur B2 protein
TESTI20416640//Choline/ethanolamine kinase
TESTI20432750//Cytochrome C and Quinol oxidase polypeptide
TESTI20432820//Zinc finger. C2H2 type// Zinc finger, C2H2 type// Zinc f
Zinc finger, C2H2 type// Zinc finger, C2H2 typ
type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type//
Zinc finger, C2H2 type// Zinc finger, C2H2 type
TESTI20436560//Spectrin repeat// Intermediate filament proteins// Intermediate filament tail domain
TESTI20442760//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain// Immunoglobulin domain
TESTI20443090//SAP domain// Zinc knuckle// Zinc finger, C3HC4 type (RING finger)
TESTI20444130//ENV polyprotein (coat polyprotein)

TESTI20449200//7 transmembrane receptor (metabotropic gluta

	TESTI20451990//SAP domain
	TESTI20455090//Intermediate filament proteins
	TESTI20455620//Hsp70 protein
	TESTI20456110//B-box zinc finger.// Spectrin repeat// SPRY domain
5	TESTI20463580//Ubiquitin carboxyl-terminal hydrolases famil// Immunoglobulin domain// Ubiquitin carboxyl-ter-
	minal hydrolase family
	TESTI20467320//Wiskott Aldrich syndrome homology region 2
	TESTI20467970//Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypop
	main// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial h
	rohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Neurohypophysial hormones, N-terminal Neurohypophypophysial hormones, N-terminal Neurohypophypophypophypophypophypophypophyp
	sial hormones, N-terminal Domain// Neuronypophysial hormones, N-terminal Bornain// Neuronypophysial hormones,
	mones, N-terminal Domain
	TESTI20471410//Protein phosphatase 2C
	TESTI20478850//Herpesvirus Glycoprotein B THYMU10005360//Immunoglobulin domain// Viral coat protein// Immunoglobulin domain
15	THYMU10005360//immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
	domain THYMU20023380//Copper/zinc superoxide dismutase (SODC)
	THYMU20023560//Copper/Title superoxide distributes (2000) THYMU20027560//Domain of unknown function
••	THYMU20039810//MAC/Perforin domain
20	THYMU20105190//Myosin head (motor domain)
	THYMU30106710//immunoglobulin domain
	THYMU20111180//Domain of unknown function DUF27// Aconitase family (aconitate hydratase)
	THYMU20115850//Reverse transcriptase (RNA-dependent DNA pol
25	THYMU20118520//Ubiquitin family
	THYAN I DO 1 20720/A/HS domain
	THYMU201267307/VH3 domain THYMU20126900//3-hydroxyacyl-CoA dehydrogenase// UDP-glucose/GDP-mannose dehydrogenase fa
	TUVMI I20130890//Ribosomal protein S9/S16
	THYMU20141670//Phorbol esters/diacylglycerol binding dom// PHD-finger// FYVE zinc linger
30	THYMU20142040//Wiskott Aldrich syndrome homology region 2
	TUVA U DO 1 42270//Cytochrome C ovidase subunit !!
	THYM020143270//Cytocinome C oxidase subtine in THYMU20147770//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
	domain THYMU20159430//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
35	domain// Immunoglobulin domain
	THYMU20161640//PMP-22/EMP/MP20/Claudin family// Integral membrane protein DUF6
	THYMU20169680//Ank repeat// Ank repeat
	THYMU20172150/WD domain, G-beta repeat
	THYMU20194360//Kelch motif
40	THYMU20194360//Reich Hotili THYMU20201980//PH domain// Phorbol esters/diacylglycerol binding domain (C1 domain)// FYVE zinc finger/
	PH domain
	THYMU20202890//Eukaryotic protein kinase domain THYMU20209590//PH domain// Dynamin GTPase effector domain
	THYMU20216840//PHD-finger THYMU20229220//Closterovirus coat protein
45	THYMU20239000//Collagen triple helix repeat (20 copies)
	THYMU20240710//tRNA synthetases class I (E and-Q)
	Ti way too o 44 050 //Close thickocompatibility antigen, befa// Immunoglobulin domain
	THYMU20241850//Class if histocompatibility altigoti, 2012 type// Zinc finger, C2H2 type// Zinc f
50	finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
50	THYMU20279750//Immunoglobulin domain
	TKIDN1000010//Mitochondrial import inner membrane transloc
	TKIDN20004640//GHMP kinases putative ATP-binding protei
	TKIDN20047480//Fukaryotic protein kinase domain
55	TOVAR20004760//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
	TRACH20002870//PMP-22/EMP/MP20/Claudin family

TRACH20003590//Cytochrome P450 TRACH20005020//Ank repeat// MutT-like domain

TRACH20005400//ADP-ribosylation factor family// Ras family

TRACH20016210//Fucosyl transferase

TRACH20019960//Na+/K+ ATPase C-terminus

TRACH20028030//DnaJ domain// DnaJ central domain (4 repeats)// DnaJ C terminal region

TRACH20033230//Nucleoside transporter// Sugar (and other) transporter// Influenza RNA-dependent RNA polymerase subunit PB2

TRACH20041830//Thioredoxin// Thioredoxin

TRACH20042920//Glutamine synthetase

TRACH20048450//Phospholipase D. Active site motif// Phospholipase D. Active site motif

TRACH20050040//Plexin repeat

TRACH20067620//Core-2/I-Branching enzyme

TRACH20069180//Immunoglobulin domain// Immunoglobulin 
TRACH20076740//Reduced folate carrier

TRACH20076760//Keratin, high sulfur B2 protein

TRACH20077540//Zinc finger, C2H2 type// G-patch domain

TRACH20079690//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type// Zinc finger, C2H2 typ

TRACH20084720//tRNA synthetases class I (C)// tRNA synthetases class I (I, L, M and V)

TRACH20085400//Immunoglobulin domain// Immunoglobulin 
TRACH20085830//Cytochrome P450

TRACH20096610//Intermediate filament proteins// Intermediate filament tail domain

TRACH20105870//Regulatory subunit of type II PKA R-subunit// eIF4-gamma/eIF5/eIF2-epsilon

TRACH20121380//Raf-like Ras-binding domain// Leptin// Raf-like Ras-binding domain// LGN motif, putative GEF specific for G-alpha GTPase

TRACH20128230//Immunoglobulin domain// Chitin synthase// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain/

TRACH20135520//TBC domain// Rhodanese-like domain

TRACH20136710//Immunoglobulin domain

TRACH20141240//Granulins

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TRACH20145440//von Willebrand factor type D domain

TRACH20154860//Squash family of serine protease inhibito// Zinc finger, C4 type (two domains)// T-box// Zinc finger, C4 type (two domains)// Ligand-binding domain of nuclear hormone

TRACH20163170//Homeobox domain

TRACH20164980//Zinc finger, C2H2 type// Zinc f

TRACH20167220//wnt family of developmental signaling protei// PLAT/LH2 domain// Fibroblast growth factor TRACH20184490//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2

TRACH20190240//EGF-like domain// EGF-like domain// Trypsin Inhibitor like cysteine rich domain// EGF-like domain

TSTOM20005690//BTB/POZ domain// Kelch motif// Kelch motif// Kelch motif

TUTER20002830//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

UMVEN10001860//PH domain// RhoGAP domain// bZIP transcription factor

UMVEN20000690//F5/8 type C domain

UTERU20030570//ABC 3 transport family// Voltage gated chloride channels// CBS domain// CBS domain UTERU20046640//Rotavirus NS26

UTERU20046980//EB module//TNFR/NGFR cysteine-rich region// Furin-like cysteine rich region// Thrombospondin type 1 domain

UTERU20050690//Androgen receptor

UTERU20055330//Reverse transcriptase (RNA-dependent DNA polymerase)

UTERU20055480//AMP-binding enzyme

UTERU20055930//Helper component proteinase

UTERU20064000//Peptidase family M1

UTERU20065930//Hr1 repeat motif// PDZ domain (Also known as DHR or GLGF).

UTERU20115740//KRAB box

UTERU20116570//Villin headpiece domain

UTERU20119060//ADP-ribosyl cyclase

UTERU20144640//Choloylglycine hydrolase

UTERU20145480//KRAB box// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// TRAF-type zinc finger/, C2H2 type// Zinc finger, C2H2 type/

UTERU20146310//Diacylglycerol kinase accessory domain (pres

UTERU20161570//7 transmembrane receptor (rhodopsin family)

UTERU20168220//Cell division protein// Integrase Zinc binding domain// GTPase of unknown function

UTERU20176130//Putative GTP-ase activating protein for Arf

UTERU20176320//SMC domain N terminal domain// Tropomyosins

UTERU20178100//Aminotransferases class-III pyridoxal-pho

UTERU20179880//TPR Domain// TPR Domain// TPR Domain// TPR Domain

UTERU20183640//Immunoglobulin domain

UTERU20185230//DUP family of yeast membrane proteins

## **EXAMPLE 6**

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# Functional categorization based on the full-length nucleotide sequences

[0230] The functional prediction and categorization of the proteins encoded by the clones were carried out based on the result of homology search of the databases of GenBank, Swiss-Prot, UniGene and nr (see the Homology Search Result Data) for the full-length nucleotide sequences and the result of domain search of the amino acid sequences deduced from the full-length nucleotide sequences (see Example 5).

[0231] The clone predicted to belong to the category of secretory protein/membrane protein means a clone having hit data with some annotation, such as growth factor, cytokine, hormone, signal, transmembrane, membrane, extracellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, connective tissue, etc., suggesting that it is a secretory or membrane protein, or means a clone in which the presence of nucleotide sequence encoding a signal sequence or transmembrane domain was suggested by the results of PSORT and SOSUI analyses for deduced ORF.

[0232] The clone predicted to belong to the category of glycoprotein-related protein means a clone having hit data with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein.

[0233] The clone predicted to belong to the category of signal transduction-related protein means a clone having hit data with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, SH2 domain, etc., suggesting that the clone encodes a signal transduction-related protein.

[0234] The clone predicted to belong to the category of transcription-related protein means a clone having hit data with some annotation, such as transcription regulation, zinc finger, homeobox, etc., suggesting that the clone encodes a transcription-related protein.

[0235] The clone predicted to belong to the category of disease-related protein means a clone having hit data with some annotation, such as disease mutation, syndrome, etc., suggesting that the clone encodes a disease-related protein, or means a clone whose full-length nucleotide sequence has hit data for Swiss-Prot, GenBank, or UniGene, where the hit data corresponds to genes or proteins which have been deposited in the Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is the human gene and disease database.

[0236] The clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having hit data with some annotation, such as metabolism, oxidoreductase. E. C. No (Enzyme commission number), etc., suggesting that the clone encodes an enzyme and/or metabolism-related protein.

[0237] The clone predicted to belong to the category of cell division and/or cell proliferation-related protein means a clone having hit data with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth, apoptosis, etc., suggesting that the clone encodes a cell division and/or cell proliferation-related protein.

[0238] The clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data with some annotation, such as structural protein, cytoskeleton, actin-binding, microtubles, etc., suggesting that the clone encodes a cytoskeleton-related protein.

[0239] The clone which is predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase polyadenylation, etc., suggesting that the clone encodes a nuclear protein and/or RNA synthesis-related protein

[0240] The clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having hit data with some annotation, such as translation regulation, protein biosynthesis, amino-acid biosynthesis ribosomal protein, protein transport, signal recognition particle, etc., suggesting that the clone encodes a protein synthesis and/or transport-related protein.

[0241] The clone predicted to belong to the category of cellular defense-related protein means a clone having hit data with some annotation, such as heat shock, DNA repair, DNA damage, etc., suggesting that the clone encodes a cellular defense-related protein.

[0242] The clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data with some annotation, such as developmental protein, etc., suggesting that the clone encodes a development and/or differentiation-related protein.

[0243] The clone predicted to belong to the category of DNA-binding and/or RNA-binding protein means a clone having hit data with some annotation, such as DNA-binding. RNA-binding, etc.

[0244] The clone predicted to belong to the category of ATP-binding and/or GTP-binding protein means a clone having hit data with some annotation, such as ATP-binding. GTP-binding, etc.

[0245] In this functional categorization, when a single clone corresponded to multiple categories of those shown above the clone was assigned to the multiple categories. However, the function of a protein is not restricted to the functional category in this classification, and there is the possibility that other functions are newly assigned to the protein.

[0246] The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 632 clones

ADIPS10000640 ADRGL10001470, ADRGL20013520. ADRGL20018540, ADRGL20035850, ASTRO20001410, ASTRO2005330 ASTRO20033160, ASTRO20055750, ASTRO20058630, ASTRO20190390, BEAST20004540, BGGI110000240 BNGH420088500, BRACE20006400, BRACE20038000, BRACE20038470, BRACE20039040, BRACE20639540 BRACE20051380, BRACE20053630. BRACE20059370, BRACE20060550, BRACE20061050, BRACE20163530 BRACE20067430, BRACE20069090. BRACE20081720, BRACE20101700, BRACE20101710, BRACF20116110 BRACE20147800, BRACE20153680. BRACE20163350, BRACE20179340, BRACE20188470, BRACE20195100 BRACE20201570, BRACE20210140. BRACE20224480, BRACE20224500, BRACE20228480, BRACE20232340 BRACE20238000, BRACE20273890. BRACE20274080. BRALZ20013500, BRALZ20054710, BRALZ20064740 BRALZ20069760, BRALZ20073760. BRALZ20077930. BRAMY20000860, BRAMY20002770, BRAMY20025840 BRAMY20039260, BRAMY20060920. BRAMY20063970, BRAMY20111960, BRAMY20112800, BRAMY20124260 BRAMY20134140, BRAMY20135900, BRAMY20136210, BRAMY20144620, BRAMY20152110, BRAMY20174550 BRAMY20181220, BRAMY20195090. BRAMY20211390, BRAMY20211420, BRAMY20215230, BRAMY20218250 BRAMY20218670, BRAMY20229800. BRAMY20231720, BRAMY20247280. BRAMY20252180, BRAMY20273960 BRAMY20277170, BRAMY20284910, BRAMY20285160, BRAWH20015350, BRAWH20015890, BRAWH2001€863 BRAWH20018730, BRAWH20030250, BRAWH20064050, BRAWH20110790, BRAWH20112940, BRAWH20117950 BRAWH20118230, BRAWH20121640. BRAWH20122580, BRAWH20132190, BRCAN20064010, BRCAN20071190 BRCAN20091560, BRCAN20103740, BRCAN20224720, BRCAN20273550, BRCAN20280360, BRCAN20285450 BRCOC10000870, BRCOC20004040, BRCOC20006370, BRCOC20041750, BRCOC20077690, BRCOC20078640 BRCOC20090520, BRCOC20101230, BRCOC20107300, BRCOC20114180, BRCOC20121720, BRCOC20\*34480 BRCOC20136750, BRHIP10001290, BRHIP20000870, BRHIP20003120, BRHIP20103090, BRHIP20111230 BRHIP20118380. BRHIP20118910. BRHIP20121410, BRHIP20135100, BRHIP20174040, BRHIP20179200 BRHIP20183690, BRHIP20191490, BRHIP20191770, BRHIP20198190, BRHIP20207430, BRHIP2020827C BRHIP20208590, BRHIP20217620, BRHIP20233090, BRHIP20234380, BRHIP20238880, BRSSN20137020 BRSSN20142940, BRSSN20146100, BRSSN20151990, BRSSN20169050. BRSTN20002200, BRTHA2000474C BRTHA20046290, BRTHA20046420, COLON10001350, COLON20093370, CTONG10000100, CTONG10000940 CTONG10001650, CTONG20004690, CTONG20009770, CTONG20092570. CTONG20092580, CTONG20095340 CTONG20099380, CTONG20103480, CTONG20105080, CTONG20114740, CTONG20119200, CTONG20\*20770 CTONG20124730, CTONG20131490, CTONG20132220, CTONG20133480. CTONG20139340, CTONG20149950 CTONG20155400, CTONG20158660, CTONG20159530, CTONG20161850, CTONG20267700, D3OST:000109C D3OST20036070, D3OST20038560, D3OST30002580, D6OST20005070, D9OST20002780, D9OST2001547C D9OST20023970, D9OST20026730, D9OST20035940, D9OST20040180, DFNES20025880, FCBBF10000240 FCBBF10000380, FCBBF10001150. FCBBF10001210, FCBBF10001550, FCBBF10002430, FCBBF10002700 FCBBF10003220, FCBBF10003760, FCBBF10005460, FCBBF10005740, FCBBF20032970, FCBBF20042560 FCBBF20049300, FCBBF20051220, FCBBF30008470, FCBBF30024750, FCBBF30078290,

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                                                                             TESTI20291310,
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                                              TESTI20272960,
                                              TESTI20303420,
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                                                                             TESTI20309170,
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 TESTI20352620, TESTI20357960, TESTI20370810, TESTI20373820,
                                                              TESTI20383880,
                                                                             TFSTI20390260.
                                              TESTI20396130,
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                                                              TEST120397760,
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TESTI20444130, TESTI20444180, TESTI20449200, TESTI20463520, TESTI20463580, TESTI20465350, THYMU10005360, THYMU10005540, THYMU20027560, THYMU20032870, THYMU20039810, THYMU20066100, THYMU20081490, THYMU20100410, THYMU20106710, THYMU20111830, THYMU20141670, THYMU20147770, THYMU20159430, THYMU20161640, THYMU20162190, THYMU20173980, THYMU20194420. THYMU20208300, THYMU20216840, THYMU20228890, THYMU20229220, THYMU20241850, THYMU20277390, TKIDN20005210, TRACH20002870, TRACH20003590, TRACH20016210, TRACH20019960, TRACH20029540, TRACH20033230, TRACH20034840, TRACH20042920, TRACH20050040, TRACH20067620, TRACH20068660, TRACH20069180, TRACH20076740, TRACH20188400, TRACH20134950, TRACH20109650, TRACH20111130, TRACH20121380, TRACH20128110, TRACH20128230, TRACH20134950, TRACH20136710, TRACH20139820, TRACH20140820, TRACH20145440, TRACH20168350, TRACH20180840, TRACH20190240, UMVEN20000690, UTERU20030570, UTERU20040610, UTERU20046980, UTERU20055480, UTERU20064860, UTERU20076390, UTERU20094350, UTERU20135860, UTERU2014640, UTERU20158300, UTERU20158800, UTERU20161570, UTERU20178100, UTERU20186740

[0247] The clones predicted to belong to the category of glycoprotein-related protein are the following 128 clones. ADIPS10000640, BRACE20059370, BRACE20163350, BRAMY20277170, BRAMY20285160, BRAWH20064050,

BRAWH20112940, BRAWH20117950, BRAWH20118230, BRCAN20103740, BRCOC20004040, BRCOC20006370, BRHIP10001290, BRHIP20103090, BRHIP20283030, BRHIP30004570, BRSSN20003120, BRSSN20146100, BRTHA20046290, COLON10001350, CTONG20159530, D9OST20023970 D9OST20040180 FCBBF10001150, FCBBF30049300, FCBBF30024750, FCBBF30083620, FCBBF30190850, FCBBF30238870, FEBRA20086620, FEBRA20092890, HCHON20015980, HCHON20016040, HCHON20064590, HCHON20086720, HCHON20100740, HEART20003060. HHDPC20014320, HHDPC20068620, HHDPC20092080, KIDNE20003940, KIDNE20007770, KIDNE20101510. LIVER20064690, MESAN20125860, NT2NE20118960, NT2NE20157470, NT2NE20177520, NT2RI20003480, NT2RI20056700, NT2RP70192730, NTONG20051530, NTONG20076930, OCBBF20107090, OCBBF20108630. OCBBF20120390, OCBBF20145760, OCBBF20155060, PLACE60177140, SMINT20050750, SMINT20073650. SMINT20105330, SMINT20106720, SMINT20112730, SMINT20127930, SMINT20153260, SMINT20179740. SMINT20190170, SPLEN20021660, SPLEN20142100, SPLEN20157880, SPLEN20165310, SPLEN20179810. SPLEN20186430, STOMA20001830, STOMA20005390, STOMA20005670, STOMA20006400, STOMA20008880, STOMA20034770, STOMA20056640, STOMA20056670, STOMA20083610, STOMA20088380, STOMA20092530, SYNOV20001520, SYNOV20001730, SYNOV20002510, SYNOV20002790, SYNOV20002970, SYNOV20004260, SYNOV20007000, SYNOV20008240, SYNOV20009230, SYNOV20010880, SYNOV20011110, SYNOV20013000, SYNOV20013560, SYNOV20013900, TESOP20004000, TESTI20136100, TESTI20216370, TESTI20244190. TESTI20254860. TESTI20303220, TESTI20335200, TESTI20352620, TESTI20358980, TESTI20442760. TESTI20449200. TESTI20455090, THYMU10005360, THYMU10005540, THYMU20147770, THYMU20159430. THYMU20241850, TRACH20016210, TRACH20050040, TRACH20067620. TRACH20069180, TRACH20076740, TRACH20128230, UTERU20046980, UTERU20064860, UTERU20144640, UTERU20158800, UTERU20161570. UTERU20183640

[0248] The clones predicted to belong to the category of signal transduction-related protein are the following 84 clones

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ASTRO20108190. BRACE20115920, BRACE20154120, BRACE20177200, BRACE20237270, BRAMY20104640, BRAMY20242470, BRAMY20271400, BRAWH20016620, BRAWH20103290, BRAWH20149340, BRCOC20021550, BRCOC20091960, BRHIP20189980, BRHIP20218580, BRHIP20238600, BRSSN20038200, CD34C30004240, CTONG20118150, CTONG20127450, CTONG20200310, FCBBF30012350, FCBBF40001730, FEBRA10001880, FEBRA2004620, FEBRA20132740, FEBRA20144170, FEHRT20003250, HCHON20007510, HLUNG20033780, IMR3220002430, KIDNE20008010, KIDNE20102710, KIDNE20107620, NT2NE20080170, NT2NE20181650, NT2RP70027380. NT2RP70036880, NT2RP70063950, NT2RP70078420, NT2RP70159960, NTONG20046140, NTONG20056570. OCBBF20028050, OCBBF20053430, OCBBF20054760, OCBBF20124360. OCBBF20127140, OCBBF20149280. OCBBF20173980, PEBLM20013120, PEBLM20085760, PROST20161950, PUAEN20015260, PUAEN20015860, PUAEN20083140, SMINT20028820, SMINT20049090, SMINT20110660, SPLEN20011410, SPLEN20121750, SPLEN20170310, SPLEN20181810, SPLEN20222270, SPLEN20250170, SPLEN20283650, TESTI20035960, TESTI20288910, TESTI20305540, TESTI20326810, TESTI20369650, TESTI20392250, TESTI20416640, TESTI20432750, TESTI20467320, THYMU20169680, THYMU20172150, THYMU20201980, THYMU20202890, TKIDN20004640, TKIDN20047480, TRACH20057690, UMVEN10001860, UTERU20146310 [0249] The clones predicted to belong to the category of transcription-related protein are the following 144 clones. 3NB6920014590, ADIPS20004250, ASTRO20008010, ASTRO20168470, BLADE20003400, BLADE20003890, BRACE20060890, BRACE20068590, BRACE20257100, BRAMY20210400, BRAMY20260910, BRAMY20270730, BRAWH20028110, BRAWH20075700, BRAWH20096780, BRCAN20280210, BRCQC20144000, BRCQC20178270, BRHIP20095340, BRHIP20096170; BRHIP20119330, BRHIP20191860, BRHIP20195890, BRHIP202222280, BRSSN20039370, BRSSN20046790, BRSSN20176820, CTONG20050280, CTONG20075860, CTONG20085950,

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CTONG20091080, CTONG20092700, CTONG20121010, CTONG20124220, CTONG20133390, CTONG20133520,
D9OST20033970, FCBBF10001710, FCBBF10004370, FCBBF20059090, FCBBF20068820, FCBBF30007680,
FCBBF30010810, FCBBF30018550, FCBBF30025560, FCBBF30057290, FCBBF30083820, FCBBF30129630,
FCBBF30240960, FCBBF30246230, FEBRA20018690, FEBRA20026110, FEBRA20034680, FEBRA20040530,
FEBRA20082010. FEBRA20171380, FEBRA20195820, FEBRA20233770, HCHON20008320, HCHON20009560,
HCHON20035130. HHDPC10000830. HHDPC20030490, HHDPC20031130, KIDNE20027250, KIDNE20027950,
KIDNE20182690. LIVER20055440, NT2NE20010490, NT2NE20089970, NT2NE20142210, NT2NE20184900,
NT2RP60000770. NT2RP70043480, NT2RP70063950, NT2RP70102350, NT2RP70157890, NTONG20070200,
OCBBF10C01850. OCBBF20020830, OCBBF20037440, OCBBF20046120, OCBBF20049300, OCBBF20054200,
OCBBF20066390. OCBBF20071840, OCBBF20080410, OCBBF20108190, OCBBF20125530, OCBBF20148280,
PEBLM20060360. PEBLM20078320, PERIC20003870, PROST10003220, PROST20047390, PROST20066880.
PROST20185830. PROST20189770, PROST20191640, SKNSH20008190, SMINT20001760, SMINT20028820,
SMINT20130320. SMINT20144800, SPLEN20026950. SPLEN20054290, SPLEN20079260, SPLEN20095410,
SPLEN20117660. SPLEN20140800, SPLEN20147390. SPLEN20160450, SPLEN20162680, SPLEN20243830,
SPLEN20250170. SPLEN20252190, SPLEN20267650. STOMA20032890, STOMA20063250, TESTI20039400,
TESTI20041690. TESTI20067200, TESTI20088220. TESTI20130010, TESTI20156100, TESTI20230850,
TESTI20318090 TESTI20320670, TESTI20378190 TESTI20385960, TESTI20409890, TESTI20420620,
TESTI20432820. TESTI20456110, THYMU20247480. TRACH20079690, TRACH20154860, TRACH20163170,
TRACH20164980. TRACH20184490, UTERU20099720. UTERU20116570. UTERU20145480, UTERU20176130
[0250] The clones predicted to belong to the category of disease-related protein are the following 387 clones.
ADIPS20004250 ADRGL10001470, ADRGL20011190. ADRGL20018300, ADRGL20035850, ADRGL20078100,
ASTRO10001550 ASTRO20008010, ASTRO20027430. ASTRO20106150, ASTRO20108190, ASTRO20168470,
BLADE20003400 BLADE20003890, BRACE20038480. BRACE20039540, BRACE20059370, BRACE20108130,
BRACE20108380 BRACE20115920, BRACE20116460. BRACE20232840, BRACE20248260, BRACE20253330,
BRACE20284100 BRALZ20013500, BRALZ20017430. BRALZ20018340, BRAMY20000520, BRAMY20025840,
BRAMY20120910 BRAMY20134140, BRAMY20135900. BRAMY20162510, BRAMY20174550. BRAMY20210400,
BRAMY20211390 BRAMY20242470, BRAMY20245300. BRAMY20266850, BRAMY20285160, BRAWH20016620,
BRAWH20028110 BRAWH20064050, BRAWH20096780. BRAWH20110960, BRAWH20113430, BRAWH20114000,
BRAWH20118230 BRAWH20121640, BRAWH20128270. BRAWH20137480, BRCAN20103740, BRCAN20224720,
BRCAN20279700 BRCAN20280210, BRCAN20283190. BRCOC20001860, BRCOC20006370, BRCOC20027510,
BRCOC20055420 BRCOC20099370, BRCOC20178270, BRCOC20178560, BRHIP20003120, BRHIP20005340,
BRHIP20174040 BRHIP20176420, BRHIP20191490. BRHIP20191860, BRHIP20194940, BRHIP20195890,
 BRHIP20222280 BRHIP20249110, BRHIP20285930. BRHIP30004880, BRSSN20013420, BRSSN20038200,
 BRSSN20039370 BRSSN20046790, BRSSN20066110. BRSSN20101100, BRSSN20120810, BRSSN20187310,
 BRTHA2004629C CD34C30004240, COLON10001350. CTONG20004690, CTONG20052650, CTONG20099550,
 CTONG20124220 CTONG20125640, CTONG20128430. CTONG20131560, CTONG20133390, CTONG20153300,
 CTONG20:53580 CTONG20158040, CTONG20159530. D6OST20003580, D9OST20023970, DFNES20001530,
 DFNES20C37420 FCBBF10001210, FCBBF10001710. FCBBF10003770, FCBBF20059090, FCBBF20064520,
 FCBBF20068820. FCBBF30010810, FCBBF30024750. FCBBF30025560, FCBBF30039020, FCBBF30049550,
 FCBBF30057290. FCBBF30083620, FCBBF30129630, FCBBF30190850, FCBBF30238870, FCBBF30240960,
 FCBBF30243640. FCBBF30279030, FCBBF30281880. FCBBF40001730, FEBRA10001880, FEBRA20004620,
 FEBRA2001012C FEBRA20018690, FEBRA20082010, FEBRA20097310, FEBRA20130190, FEBRA20132740,
 FEBRA2014417C FEBRA20195820, FEBRA20223220, FEBRA20233770, FEBRA20235500, FEHRT20003250,
 HCHON1000176 HCHON20007380, HCHON20008320, HCHON20009560, HCHON20015230, HCHON20015980,
 HCHON20016040 HCHON20035130, HCHON20036420, HCHON20064590, HCHON20067700, HCHON20086720,
 HCHON2010C740 HEART20003060, HEART20017730, HEART20025980, HEART20049410, HHDPC20014320,
 HHDPC20030490 HHDPC20084140, HHDPC20091140, HHDPC20091780, HHDPC20092080, HLUNG20033780,
 IMR3220002430 KIDNE20007770, KIDNE20020150, KIDNE20021680, KIDNE20022620, KIDNE20024830,
 KIDNE20027950. KIDNE20101370, KIDNE20101510, KIDNE20182690, LIVER20002160, LIVER20055200,
 LIVER20055440. LIVER20059810, LIVER20064690, MESAN20101140, MESAN20125860, MESAN20130220,
 MESAN20154010 MESAN20174170, NOVAR10000910, NT2NE20010490, NT2NE20118960, NT2NE20157470,
 NT2RI20040990. NT2RI20041880, NT2RI20048840, NT2RI20050960, NT2RI20240080, NT2RP60000770,
 NT2RP70027380. NT2RP70032610, NT2RP70037240, NT2RP70192730, NT2RP70198350, NTONG20013620,
 NTONG20015870 NTONG20028070, NTONG20067830, NTONG20070200, NTONG20090600, NTONG20092330,
 OCBBF20006770 OCBBF20037440, OCBBF20046120, OCBBF20049300, OCBBF20053490, OCBBF20053730,
 OCBBF20054760 OCBBF20071840, OCBBF20072240, OCBBF20078920, OCBBF20108430, OCBBF20108580,
 OCBBF20127140 OCBBF20129360, OCBBF20145760, OCBBF20153350, OCBBF20173980, OCBBF20178880,
 PEBLM10C00710 PEBLM20013120, PERIC10000250. PLACE60060420, PLACE60177140, PROST20100460,
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PROST20159240, PROST20169800, PROST20176170, PUAEN20018820, PUAEN20030180, PUAEN20055020,
PUAEN20083140, SKMUS20018230, SKMUS20018500, SKMUS20021530, SKMUS20024750, SKMUS20029200,
SKMUS20048970. SKMUS20049030. SKNSH20008190. SKNSH20089400. SMINT20001760. SMINT20026890,
SMINT20028820, SMINT20050750, SMINT20073650, SMINT20105330, SMINT20112730, SMINT20121220,
SMINT20127350. SMINT20127930. SMINT20136130, SMINT20138900, SMINT20153260, SMINT20155180,
SMINT20179740. SMINT20190170. SMINT20191420, SPLEN20006070. SPLEN20011410. SPLEN20026950,
SPLEN20027440, SPLEN20039240, SPLEN20079260, SPLEN20095410. SPLEN20146450. SPLEN20147390.
SPLEN20151210, SPLEN20160450, SPLEN20170310, SPLEN20179180, SPLEN20186430, SPLEN20212730,
SPLEN20243830, SPLEN20245300, SPLEN20250390, SPLEN20252190, SPLEN20267650, SPLEN20305620,
STOMA20001830, STOMA20005390, STOMA20008880, STOMA20010250, STOMA20034770, STOMA20046680,
STOMA20056670, STOMA20064470, STOMA20077450, STOMA20080500, STOMA20083610, STOMA20088380,
SYNOV20001520, SYNOV20001730, SYNOV20002790, SYNOV20002970, SYNOV20007000, SYNOV20008240,
SYNOV20009230, SYNOV20010880, SYNOV20011110, TBAES20003770, TESOP20004000, TESOP20005270,
TESTI20031270, TESTI20036380,
                               TESTI20044310,
                                               TESTI20067200,
                                                               TESTI20116830,
                                                                               TESTI20121550,
                                TESTI20208400,
                                               TESTI20215990,
                                                               TESTI20231940,
                                                                               TESTI20234360,
TESTI20156100.
               TESTI20168480,
                               TESTI20239510,
                                               TESTI20249990,
                                                               TESTI20266740,
                                                                               TESTI20316870.
TESTI20237520.
               TESTI20238610,
               TESTI20335050,
                               TESTI20335200,
                                               TESTI20343570,
                                                               TESTI20352620,
                                                                               TESTI20368330,
TESTI20318090.
TESTI20369650, TESTI20385960,
                               TESTI20392250,
                                               TESTI20400940,
                                                               TESTI20404240.
                                                                               TESTI20420620,
                                               TESTI20442760, TESTI20443090,
TESTI20436560, TESTI20438570,
                               TESTI20441940,
                                                                               TFSTI20449200.
TESTI20455090, TESTI20455620, TESTI20456110, TESTI20463580, TESTI20465350,
                                                                               TESTI20465690,
TESTI20467210. THYMU20122730, THYMU20126900, THYMU20130890, THYMU20159430, THYMU20169680,
THYMU20:72150. THYMU20180280, THYMU20193640, THYMU20209590, THYMU20232090. THYMU20247480,
TKIDN1000010. TKIDN2004640, TKIDN20047480, TRACH20016210, TRACH20019960, TRACH20050040,
TRACH20C57690, TRACH20067620, TRACH20077540, TRACH20079690, TRACH20096610, TRACH20105870,
TRACH20121380, TRACH20154860, TRACH20162860, TRACH20163170, TRACH20164980, TRACH20190240,
TSTOM20005590. TUTER20002830, UTERU20030570, UTERU20116570, UTERU20144640, UTERU20151980,
UTERU20158800. UTERU20183640, UTERU20185230
[0251] In particular, hit data of the following 386 clones for Swiss-Prot, or GenBank, UniGene, or nr corresponded
to genes or proteins which had been deposited in the Online Mendelian Inheritance in Man (OMIM), which is the human
gene and disease database, (the OMIM Number is shown in the parenthesis after the Clone Name).
ADIPS20004250 (601505), ADRGL10001470 (202010;103900), ADRGL20011190 (182790), ADRGL20018300
:600025) ADRG_20035850 (202110), ADRGL20078100 (103270), ASTRO10001650 (126660), ASTRO20008010
(602537), ASTRO20027430 (179555), ASTRO20106150 (602537), ASTRO20108190 (191092), ASTRO20168470
(604077) BLADE20003400 (601276), BLADE20003890 (604077), BRACE20038480 (601504), BRACE20039540
         BRACE20059370 (130500;266140), BRACE20108130 (605413), BRACE20108880 (603758),
BRACE20115920 (300023),
BRACE2011646C (603150), BRACE20232840 (601213), BRACE20248260 (600813), BRACE20253330 (604990),
BRACE20284100 (602415), BRALZ20013500 (602470), BRALZ20017430 (600658), BRALZ20018340 (600547),
BRAMY20000520 (164020), BRAMY20025840 (602327), BRAMY20120910 (600188), BRAMY20134140 (603931),
BRAMY20:35900 (601342), BRAMY20162510 (300098), BRAMY20174550 (605464), BRAMY20210400 (603809).
BRAMY20211390 (602212), BRAMY20242470 (605000), BRAMY20245300 (605367), BRAMY20266850 (605609).
BRAMY20285160 (120700), BRAWH20016620 (605762), BRAWH20028110 (602330), BRAWH20064050 (135820),
BHAWH20096780 (602277), BRAWH20110960 (603481), BRAWH20113430 (602649), BRAWH20114000 (138130),
BRAWH20118230 (112267), BRAWH20121640 (604437), BRAWH20128270 (601997), BRAWH20137480 (602330),
BRCAN20103740 (602566), BRCAN20224720 (600923;176200), BRCAN20279700 (604205), BRCAN20280210
(194538) BRCAN20283190 (602118), BRCOC20001860 (604346), BRCOC20006370 (603784), BRCOC20027510
(179555) BRCOC20055420 (603801), BRCOC20099370 (606045), BRCOC20178270 (194558), BRCOC20178560
(602567) BRHIP20003120 (604249), BRHIP20005340 (147586), BRHIP20174040 (602658), BRHIP20176420
(154020) BRHIP20191490 (600009), BRHIP20191860 (602272), BRHIP20194940 (604696), BRHIP20195890
(602211). BRHIP20222280 (603899), BRHIP20249110 (142600), BRHIP20285930 (602626), BRHIP30004880
(188840). BRSSN20013420 (300272). BRSSN20038200 (602306), BRSSN20039370 (194531), BRSSN20046790
(604077). BRSSN20066110 (605248), BRSSN20101100 (600188), BRSSN20120810 (142440), BRSSN20187310
(182900). BRTHA20046290 (602644), COLON10001350 (146900), CTONG20004690 (600019), CTONG20052650
(603871). CTONG20099550 (190370). CTONG20124220 (184756), CTONG20125640 (180510), CTONG20128430
(601797). CTONG20131560 (103390). CTONG20133390 (604077), CTONG20153300 (604334), CTONG20153580
(605652). CTONG20158040 (602862), CTONG20159530 (600395), D6OST20003580 (602443), D9OST20023970
(601525). DFNES20001530 (164500), DFNES20037420 (139259), FCBBF10001210 (602461), FCBBF10001710
(194558). FCBBF10003770 (604597), FCBBF20059090 (194542), FCBBF20064520 (164020), FCBBF20068820
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(194558), FCBBF30010810 (603899), FCBBF30024750 (603706), FCBBF30025560 (600494), FCBBF30039020
(602835), FCBBF30049550 (106410), FCBBF30057290 (194556), FCBBF30083620 (300022), FCBBF30129630
(603899), FCBBF30190850 (131210). FCBBF30238870 (602320), FCBBF30240960 (604078), FCBBF30243640
(601961), FCBBF30279030 (605208), FCBBF30281880 (602517), FCBBF40001730 (176981), FEBRA10001880
(605451), FEBRA20004620 (600278), FEBRA20010120 (600368), FEBRA20018690 (194542), FEBRA20082010
(602187), FEBRA20097310 (602895), FEBRA20130190 (605863), FEBRA20132740 (602654), FEBRA20144170
(601685), FEBRA20195820 (604074), FEBRA20223220 (604633), FEBRA20233770 (603347), FEBRA20235500
(312090), FEHRT20003250 (600286), HCHON10001760 (605315), HCHON20007380 (600833), HCHON20008320
(604077), HCHON20009560 (194548), HCHON20015230 (604646), HCHON20015980 (604789), HCHON20016040
(146732), HCHON20035130 (194529), HCHON20036420 (603434), HCHON20064590 (103950), HCHON20067700
(603054), HCHON20086720 (146732), HCHON20100740 (602281), HEART20003060 (109480), HEART20017730
(106410), HEART20025980 (602127), HEART20049410 (603777), HHDPC20014320 (602714), HHDPC20030490
(603795), HHDPC20084140 (605184). HHDPC20091140 (603054), HHDPC20091780 (227400), HHDPC20092080
(146732), HLUNG20033780 (600888), IMR3220002430 (602923), KIDNE20007770 (114890), KIDNE20020150
(140550;603012), KIDNE20021680 (601609), KIDNE20022620 (603590), KIDNE20024830 (604205),
KIDNE20027950 (194531), KIDNE20101370 (602580), KIDNE20101510 (191845), KIDNE20182690 (605226),
LIVER20002160 (600816), LIVER20055200 (604814), LIVER20055440 (605277), LIVER20059810 (230350),
LIVER20064690 (601841), MESAN20101140 (602567), MESAN20125860 (155750), MESAN20130220 (603778),
MESAN20154010 (180480), MESAN20174170 (602516), NOVAR10000910 (159350), NT2NE20010490 (603899),
NT2NE20118960 (180490), NT2NE20157470 (217000), NT2RI20040990 (106410), NT2RI20041880 (160775),
NT2RI20048840 (139360), NT2RI20050960 (606103), NT2RI20240080 (603419), NT2RP60000770 (603044),
NT2RP70027380 (118423), NT2RP70032610 (172430), NT2RP70037240 (604108), NT2RP70192730 (278000),
NT2RP70198350 (300043), NTONG20013620 (604125), NTONG20015870 (123940), NTONG20028070 (602369),
NTONG20067830 (182900), NTONG20070200 (194558), NTONG20090600 (313440), NTONG20092330 (153700),
 OCBBF20006770 (154500), OCBBF20037440 (602290), OCBBF20046120 (601262), OCBBF20049300 (602277),
 OCBBF20053490 (154550;602579), OCBBF20053730 (603604), OCBBF20054760 (603453), OCBBF20071840
 (604077). OCBBF20072240 (604331). OCBBF20078920 (602120), OCBBF20108430 (139360), OCBBF20108580
 (300103). OCBBF20127140 (139380). OCBBF20129360 (602142), OCBBF20145760 (600395), OCBBF20153350
 (601935), OCBBF20173980 (603524), OCBBF20178880 (601617), PEBLM10000710 (601007), PEBLM20013120
 (602288). PERIC10000250 (603582), PLACE60060420 (180469), PLACE60177140 (600022), PROST20100460
 (158374). PROST20159240 (606019). PROST20169800 (604426), PROST20176170 (605903), PUAEN20018820
 (164740). PUAEN20030180 (603263). PUAEN20055020 (604677), PUAEN20083140 (604762), SKMUS20018230
 (603768), SKMUS20018500 (601402), SKMUS20021530 (606045), SKMUS20024750 (179555), SKMUS20029200
 (605758), SKMUS20048970 (102610), SKMUS20049030 (161650), SKNSH20008190 (604075), SKNSH20089400
 (603070), SMINT20001760 (194558), SMINT20026890 (602127) SMINT20028820 (604719), SMINT20050750
 (182120) SMINT20073650 (146900), SMINT20105330 (230500;230600;230650;253010), SMINT20112730
 (146900). SMINT20121220 (160776), SMINT20127350 (180740), SMINT20127930 (146900), SMINT20136130
 (147220), SMINT20138900 (125660;601419), SMINT20153260 (602201), SMINT20155180 (603004),
 SMINT20179740 (147020), SMINT20190170 (146900), SMINT20191420 (102770),
 SPLEN20006070 (182900), SPLEN20011410 (602732), SPLEN20026950 (600014), SPLEN20027440 (106410),
 SPLEN20039240 (140550:603012), SPLEN20079260 (604074), SPLEN20095410 (602277), SPLEN20146450
 (602861), SPLEN20147390 (604078), SPLEN20151210 (600267), SPLEN20160450 (604375), SPLEN20170310
  (605216), SPLEN20179180 (605890), SPLEN20186430 (600052), SPLEN20212730 (114230), SPLEN20243830
  (601796), SPLEN20245300 (606004), SPLEN20250390 (114220), SPLEN20252190 (604077), SPLEN20267650
  (602277). SPLEN20305620 (126064), STOMA20001830 (146900), STOMA20005390 (146900), STOMA20008880
  (601652;137750). STOMA20010250 (605786), STOMA20034770 (146900), STOMA20046680 (164772),
  STOMA20056670 (146900). STOMA20064470 (173320), STOMA20077450 (314370), STOMA20080500 (605414),
  STOMA20083610 (146900), STOMA20088380 (146900), SYNOV20001520 (147200), SYNOV20001730 (147120),
  SYNOV20002790 (147120), SYNOV20002970 (147120), SYNOV20007000 (147120), SYNOV20008240 (147120),
  SYNOV20009230 (146900), SYNOV20010880 (147120), SYNOV20011110 (147120), TBAES20003770 (118990),
  TESOP20004000 (116810), TESOP20005270 (600641), TESTI20031270 (191161), TESTI20036380 (126650;
  214700), TESTI20044310 (179555), TESTI20067200 (176312), TESTI20116830 (603142), TESTI20121550 (600862),
  TESTI20156100 (602253), TESTI20168480 (188840), TESTI20208400 (164031), TESTI20215990 (605652),
  TESTI20231940 (604200), TESTI20234360 (601052), TESTI20237520 (604212), TESTI20238610 (300097),
  TESTI20239510 (604334);
  TESTI20249990 (164500), TESTI20266740 (605198), TESTI20316870 (605497), TESTI20318090 (604077),
  TESTI20335050 (605209), TESTI20335200 (109770), TESTI20343570 (190470), TESTI20352620 (176801;249900),
  TESTI20368330 (157680), TESTI20369650 (602052), TESTI20385960 (605970), TESTI20392250 (605541),
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TESTI20400940 (117143), TESTI20404240 (602725), TESTI20420620 (602955), TESTI20436560 (150330), TESTI20438570 (603577), TESTI20441940 (604119), TESTI20442760 (603491), TESTI20443090 (602954), TESTI20449200 (604101). TESTI20455090 (148070). TESTI20455620 (140560), TESTI20456110 (109092), TESTI20463580 (603486), TESTI20465350 (123830), TESTI20465690 (605468), TESTI20467210 (600833), THYMU20122730 (604700), THYMU20126900 (603370), THYMU20130890 (603675), THYMU20159430 (146900), THYMU20169680 (601441), THYMU20172150 (605000), THYMU20180280 (600549), THYMU20193640 (603083;164021), THYMU20209590 (602378), THYMU20232090 (601717), THYMU20247480 (604077), TKIDN10000010 (605034), TKIDN20004640 (137028), TKIDN20047480 (602399), TRACH20016210 (136836), TRACH20019960 (182310). TRACH20050040 (603784), TRACH20057690 (164731), TRACH20067620 (600429;110800), TRACH20077540 (300080), TRACH20079690 (604078), TRACH20096610 (150330), TRACH20105870 (600495), TRACH20121380 (602513). TRACH20154860 (180240), TRACH20162860 (603845), TRACH20163170 (601739), TRACH20164980 (602277), TRACH20190240 (604633), TSTOM20005690 (605775), TUTER20002830 (602719), UTERU20030570 (602023: 241200), UTERU20116570 (602330), UTERU20144640 (228000), UTERU20151980 (602038), UTERU20158800 (600738), UTERU20183640 (601281), UTERU20185230 (605333) [0252] The clones predicted to belong to the category of enzyme and/or metabolism-related protein are the following 206 clones. 3NB6910001910, ADRGL10001470, ADRGL20035850, ADRGL20078100, ASTRO20105820, ASTRO20106150, ASTRO20130500, ASTRO20145760, BRACE20027620, BRACE20038000, BRACE20062640, BRACE20096200, BRACE20107530, BRACE20108130, BRACE20108880, BRACE20116460, BRACE20148240, BRACE20185680, BRACE20253160, BRALZ20017430, BRALZ20018340, BRAMY20104640, BRAMY20134140, BRAMY20153110, BRAMY20213100, BRAMY20252720, BRAWH20016620, BRAWH20105840, BRAWH20112940. BRAWH20114000, BRAWH20117950, BRAWH20125380, BRAWH20132190, BRAWH20171030, BRCAN20054490, BRCAN20224720, BRCAN20280360, BRCAN20283190, BRCAN20283380, BRCOC20001860, BRCOC20031250, BRCOC20055420, BRCOC20091960. BRCOC20144000. BRHIP10001290, BRHIP20005530, BRHIP20096850, BRHIP20103090, BRHIP20174040, BRHIP20249110, BRSSN20013420, BRSSN20015790, BRSSN20120810, BRSSN20146100, CTONG20095340, CTONG20106520, CTONG20118250, CTONG20127450, CTONG20140580, CTONG20153300, CTONG20158040, D3OST20006180, D6OST20003580 DFNES20031920, DFNES20071130, FCBBF10001820, FCBBF10003670, FCBBF30012350, FCBBF30012810, FCBBF30175310, FCBBF30243640, FEBRA10001880, FEBRA20007620. FEBRA20130190, FEBRA20144170, FEBRA20167390, FEBRA20196630. FEHRT20003250. HCHON10001760. HCHON20003220. HCHON20015350, HEART20034320, HEART20090000. HHDPC20014320; KIDNE20002520. KIDNE20008010. KIDNE20021680, KIDNE20022620, KIDNE20028390, KIDNE20028720, KIDNE20107620, LIVER20059810, MESAN20154010, NT2NE20118960, NT2NE20157470, NT2RI20005750, NT2RI20244600, NT2RI20273230, NT2RP70032610, NT2RP70045590, NT2RP70192730, NT2RP70195430, NTONG20009770, NTONG20013620, NTONG20046140, OCBBF20028650, OCBBF20030910, OCBBF20046690, OCBBF20050770, OCBBF20053430, OCBBF20053490, OCBBF20053730, OCBBF20054760, OCBBF20078920, OCBBF20124360, OCBBF20129360, OCBBF20178880, PEBLM20044520, PEBLM20052820, PEBLM20060490, PERIC10000250, PLACE50000660, PROST20083600, PROST20169800, PUAEN20015260, PUAEN20030180, SKMUS20018230, SMINT20028820, SMINT20049090, SMINT20102780, SMINT20105330, SMINT20106290, SMINT20110660, SMINT20152940, SMINT20191420, SMINT20191530, SPLEN20021660, SPLEN20026950, SPLEN20121750, SPLEN20145720, SPLEN20149240, SPLEN20150940, SPLEN20151210, SPLEN20173510, SPLEN20212730, SPLEN20250390, SPLEN20305620, STOMA20006860, STOMA20077450, TBAES20002550, TBAES20003150. TESOP20004000, TESOP20005270, TESTI20001000, TESTI20002720, TESTI20002780, TESTI20060400. TESTI20066670, TESTI20082330, TESTI20083200, TESTI20108720, TESTI20116830, TESTI20143390, TESTI20148000, TESTI20216370, TESTI20232140, TESTI20234360, TESTI20237520, TESTI20239510, TESTI20266740, TESTI20314180, TESTI20334410, TESTI20343570, TESTI20352620, TESTI20355020, TESTI20366910, TESTI20368330, TESTI20369650, TESTI20375340, TESTI20397760, TESTI20416640, TESTI20432750, TESTI20463580, TESTI20465350, TESTI20471410, TESTI20473830, THYMU20023380, THYMU20111830, THYMU20126900, THYMU20169680, THYMU20202890, TKIDN20004640, TKIDN20047480, TRACH20003590, TRACH20016210, TRACH20019960, TRACH20041830, TRACH20057690, TRACH20067620, TRACH20084720, TRACH20085830, TRACH20162860, UTERU20064860, UTERU20144640, UTERU20146310, UTERU20151980 [0253] The clones predicted to belong to the category of cytoskeleton-related protein are the following 75 clones. ADRGL20011190, ADRGL20018300, ASTRO10001650, ASTRO20055750, BRACE20003070, BRACE20059370, BRACE20163350, BRAMY20121620, BRAMY20157820, BRAMY20242470, BRAWH20028110, BRAWH20137480, BRCAN20003460, BRCOC20008160. BRCOC20059510, BRHIP20115080, BRHIP20137230, BRHIP20167880,

BRHIP20283030, BRHIP20285830, BRSSN20187310, CTONG10002770, CTONG20052900, CTONG20121580,

FCBBF10001150, FCBBF30013770, FCBBF30015940. FCBBF30049550, FEBRA2024100, FEBRA20237640, HCHON20015980, HCHON20068410. HEART20017730, HEART20025980, HEART20061950, HEART20077670, HLUNG20016330. KIDNE20118580, MESAN20004570. NT2RI20040990, NT2RI20041880, NT2RP70037240, NT2RP70062230, NTONG20015870, NTONG20056570, NTONG20067830, NTONG20090600, OCBBF20107090, OCBBF20155060, PLACE60079250, PUAEN20040670, SKMUS20001980, SKMUS20016220, SKMUS20048970, SKMUS20049030, SMINT20024570, SMINT20026890, SMINT20121220, SMINT20138900, SPLEN2006070, SPLEN20027440, SPLEN20142100, TESTI20063830, TESTI20094230, TESTI20278400, TESTI20371030, TESTI20417300, TESTI20436560. TESTI20455090, THYMU20105190, THYMU20172150, THYMU20209590, TRACH20096610, UMVEN10001560, UTERU20116570

- [0254] The clones predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein are the following 65 clones.
  - BRACE20057190, BRACE20064880, BRACE20248260, BRACE20253160, BRAMY20000520, BRAMY20120910, BRAWH20113430, BRAWH20171030, BRCAN10001490, BRCAN20283190, BRCOC20037320, BRCOC20178560, BRHIP20106100, BRHIP20176420, BRHIP20243470, BRSSN20101100, CTONG20114290, CTONG20125540, CTONG20131560, CTONG20140580, DFNES20001530, FCBBF20064520, FEBRA20007620, FEBRA20010120, FEBRA20097310, FEBRA20144170, FEBRA20174410, FEBRA20215500, IMR3220002430, MESAN20101140, NT2RI20273230, OCBBF20028650, OCBBF20030910, OCBBF20078920, PROST20104000, PUAEN20018820, SKMUS20007010, SMINT20127350, SMINT20177360, SMINT20191530, SPLEN20008740, SPLEN20146450, STOMA20046680, TESTI20082330, TESTI20094470, TESTI20121550, TESTI20208400, TESTI202349990, TESTI20334410, TESTI20355020, TESTI20368330, TESTI20392760, THYMU20241210, TRACH20096610, TUTER20002830, UTERU20151980, UTERU20176320

[0255] The clones predicted to belong to the category of protein synthesis and/or transport-related protein are the to lowing 62 clones.

- 3NB6910001910. ASTRO20106150, ASTRO20130500, ASTRO20141350, BRACE20038480, BRACE20052160, BRACE20057620. BRACE20106840, BRACE20172980, BRACE20192440, BRAWH20110960, BRCOC20037320, BRHIP20005530. BRSSN20120810, BRSTN20005360, CTONG20009770, CTONG20114290, CTONG20125640, CTONG20153300. D6OST20003580, DFNES20037420, FCBBF30012810, FEBRA20080810, HCHON20064590, HHDPC20014320. HHDPC20084140, HLUNG20017120, LIVER20064690, NT2NE20132170. NT2NE20157470, NT2RP70133740. NTONG2009770, NTONG20075220, NTONG20076930, OCBBF20030910. OCBBF20035930, OCBBF20153340. PLACE60060420. SMINT20152940, SPLEN20008740, SPLEN20103950. SPLEN20118300, SPLEN20212730. SPLEN20250390, STOMA20077450, TBAES20002550, TESOP20004000, TESTI20239510, TESTI20278400. TESTI20314180, TESTI20463580, THYMU20111830, THYMU20122730, THYMU20130890, THYMU20232090. TKIDN10000010, TRACH20084720, TRACH20105870, TRACH20139820, TRACH20149970, UTERU20120310. UTERU20188110
  - [0256] The clones predicted to belong to the category of cellular defense-related protein are the following 15 clones. BRCOC20\*44000 CTONG20092680, KIDNE20020150, LIVER20002160, NT2RI20050960, NT2RP70045590, OCB3F20128120. PLACE60003480, SKNSH20089400, SMINT20106290, SPLEN20039240, TESTI20001000, TESTI20455620 TRACH20028030, UTERU20176320
- [0257] The clones predicted to belong to the category of development and/or differentiation-related protein are the following 13 clones.
  3NB6920014590. BRAMY20211390, CTONG20091080, CTONG20121010, FCBBF30024750, KIDNE20027250, N12NE20142210. OCBBF20054200, PROST10003220, SKMUS20007010, SPLEN20179810, STOMA20063250,
- TESTI20291960
   [0258] The clones predicted to belong to the category of DNA-binding and/or RNA-binding protein are the following
   174 clones
  - 3NB6920014590. ADIPS20004250, ASTRO2008010, ASTRO20168470, BLADE20003400, BLADE20003890, BRACE2057620. BRACE20060890, BRACE20064880, BRACE20068590, BRACE20248260. BRACE20253160, BRAMY20000520. BRAMY20213100, BRAMY20260910, BRAMY20270730, BRAWH20028110, BRAWH20075700, BRAWH20096780, BRAWH20113430, BRCAN10001490, BRCAN20280210, BRCAN20283190, BRCOC20144000, BRCOC20178270. BRCOC20178560, BRHIP20005340, BRHIP20106100, BRHIP20119330, BRHIP20153600, BRHIP20176420. BRHIP20191860, BRHIP20195890, BRHIP20222280, BRSSN20039370, BRSSN20046790, BRSSN20176820, CTONG20050280, CTONG20075860, CTONG20085950, CTONG20091080, CTONG20092700, CTONG20121010, CTONG20124220, CTONG20125540, CTONG20133390, CTONG20133520, CTONG20140580, CTONG20156780. D9OST20033970, FCBBF10001710, FCBBF10004370, FCBBF20059090, FCBBF20064520,
- FCBBF20068820, FCBBF30007680, FCBBF30010810, FCBBF30018550, FCBBF30025560, FCBBF30057290, FCBBF30083820, FCBBF30129630, FCBEF30240960, FCBBF30246230, FEBRA20010120, FEBRA20018690, FEBRA20026110, FEBRA20034680, FEBRA20040530, FEBRA20082010, FEBRA20097310, FEBRA20171380,

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FEBRA20195820, FEBRA20196630, FEBRA20233770, HCHON20008320, HCHON20009560, HCHON20035130,
HHDPC10000830, HHDPC20031130, KIDNE20017130, KIDNE20027250, KIDNE20027950, KIDNE20107390,
KIDNE20182690. LIVER20055440. MESAN20101140, NT2NE20010490, NT2NE20089970, NT2NE20142210.
NT2NE20184900, NT2RP60000770, NT2RP70044280, NT2RP70102350, NT2RP70157890, NTONG20070200,
OCBBF10001850, OCBBF20020830, OCBBF20037440, OCBBF20046120, OCBBF20049300, OCBBF20066390,
OCBBF20071840, OCBBF20078920, OCBBF20080410, OCBBF20108190, OCBBF20125530, OCBBF20148280,
PEBLM20060360, PEBLM20060490, PEBLM20078320, PERIC10000250, PROST10003220, PROST20047390,
PROST20066880, PROST20185830, PROST20189770, PROST20191640, PUAEN20018820, SKNSH20008190,
SKNSH20089400, SMINT20001760, SMINT20127350, SMINT20144800, SMINT20177360, SMINT20191530,
SPLEN20054290, SPLEN20079260, SPLEN20095410, SPLEN20140800, SPLEN20147390, SPLEN20160450,
SPLEN20252190. SPLEN20267650, STOMA20010250, STOMA20032890, STOMA20046680, STOMA20063250,
TESTI20039400, TESTI20067200, TESTI20088220, TESTI20094470, TESTI20121550, TESTI20130010,
TESTI20156100, TESTI20204450, TESTI20230850, TESTI20237520, TESTI20266740, TESTI20318090,
TESTI20320670, TESTI20334410, TESTI20355020, TESTI20378190, TESTI20385960, TESTI20432820,
TESTI20443090, TESTI20456110, THYMU20193640, THYMU20241210, THYMU20247480, TRACH20079690,
TRACH20105870, TRACH20139820, TRACH20154860, TRACH20163170, TRACH20164980, TRACH20184490,
TUTER20002830, UTERU20099720, UTERU20116570, UTERU20145480, UTERU20176130, UTERU20185230
[0259] The clones predicted to belong to the category of ATP binding and/or GTP-binding protein are the following
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3NB6910001910, BRACE20108130, BRACE20148240, BRAMY20134140, BRAMY20157820, BRAMY20174550, BRAWH20164460, BRCAN2003460, BRCAN20054490, BRCAN20283190, BRCOC20059510, BRCOC20144000, BRHIP20103090, BRHIP20115080, BRHIP20167880, BRSTN20005360, CD34C30004240, CTONG20095340, CTONG20121580, CTONG20200310, DFNES20037420, FCBBF20067810, FCBBF30012350, FCBBF30015940, FEBRA20007620, FEBRA20024100, FEBRA20144170, KIDNE20020150, KIDNE20028720, LIVER20002160, LIVER20087060, NT2RI20005750, NT2RI20041880, NT2RI20048840, NT2RI20273230, OCBBF20028650, OCBBF20046690, OCBBF20054760, OCBBF20108430, OCBBF20108630, SMINT20121220, SMINT20183530, SMINT20191530, SPLEN20026950, SPLEN20039240, SPLEN20099700, SPLEN20145720, SPLEN20179180, STOMA20006860, TESTI20035960, TESTI20355020, TESTI20397760, TESTI20400940, TESTI20417300, TESTI20443090, TESTI20455620, THYMU20105190, THYMU20202890, THYMU20209590, TKIDN20004640, TKIDN20047480, TRACH20005400, TRACH20019960, TRACH20057690, TRACH20084720, UTERU20168220, UTERU20176320, UTERU20185230

[0260] Among the clones other than the ones shown above, BRAMY20248490, FCBBF10002800, NTONG20092290, OCBBF20127040, SMINT20163960, THYMU20279750, TRACH20167220, are clones which were predicted to highly possibly belong to the category of secretory protein and/or membrane protein based on the result of domain search by Pfam.

FCBBF10002800, NTONG20092290, OCBBF20127040, SMINT20163960, TESTI20478850, THYMU20279750 [0261] The 6 clones shown above are clones which were predicted to highly possibly belong to the category of glycoprotein-related protein based on the result of domain search by Pfam.

BRACE20060720, BRACE20223330, BRALZ20058880, BRAMY20148130, BRAWH20101360, BRCAN20124080, BRHIP20253660.

CTONG10000620, CTONG20014280, CTONG20124010, KIDNE20109890, MESAN20171520, OCBBF20109310, OCBBF20140640, PROST20079500, PUAEN20078980, SPLEN20077500, SPLEN20143180, TESTI20017950, TESTI20184620.

TESTI20208710, TESTI20211160, TESTI20226230, TESTI20234140, TESTI20258460, TESTI20275030

[0262] The 26 clones shown above are clones which were predicted to highly possibly belong to the category of signal transduction-related protein based on the result of domain search by Pfam.

ADRGL20048330, ASTRO20064750, ASTRO20084250, BRACE20151320, BRALZ20058880, BRHIP20207990, CTONG20093950, FCBBF30195640, FEBRA10001900, FEBRA20090290, FEBRA20214970, FEBRA20222040, KIDNE20109890, LIVER20087510, MESAN20029400, MESAN20031900, MESAN20035290, MESAN20136110, NT2NE20130190, PEBLM20060310, PERIC20004780, PROST20171280, PUAEN20078980, SMINT20115880, SPLEN20095550, TESTI20023510, TESTI20083940, TESTI20152460, TESTI20185650, TESTI20189410, TESTI20200710, TESTI20308600, TESTI20343070, TESTI20369690, TESTI20381040, UTERU20050690

[0263] The 36 clones shown above are clones which were predicted to highly possibly belong to the category of transcription-related protein based on the result of domain search by Pfam.

BGGI120006160, BRACE20053480, BRACE20190040, BRACE20223330, BRAWH20101360, BRAWH20185060, BRCOC20023230, BRHIP20252450, BRSSN20105870, BRSSN20117990, BRTHA20000570, CTONG20098440, CTONG20129960, CTONG20146300, CTONG20155180, FEBRA20025270, HEART20083640, KIDNE20009470, LIVER20035680, MESAN20029400, MESAN20031900, MESAN20186700, NOVAR10000150, NTONG20029480,

OCBBF20079310, OCBBF20082830, PEBLM20042900, PLACE60136500, PLACE60136720, PRCST20114390, SKNSH20020540, SMINT20013480, SMINT20174360, SPLEN20077500, SPLEN20119810, SPLEN20126190, SPLEN20174260, SPLEN20211220, TESTI20046750, TESTI20057750, TESTI20061110, TESTI20197940, TESTI20211160, TESTI20226230, TESTI20255820, TESTI20317600, TESTI20377230, THYMU20111180, THYMU20115850, THYMU20143270, THYMU20240710, UTERU20055330, UTERU20055930, UTERU20064000, UTERU20119060

[0264] The 55 clones shown above are clones which were predicted to highly possibly belong to the category of enzyme and/or metabolism-related protein based on the result of domain search by Pfam.

TESTI20127760, TESTI20392270

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[0265] The 2 clones shown above are clones which were predicted to highly possibly belong to the category of cell division and/or cell proliferation-related protein based on the result of domain search by Pfam. FCBBF30262510, MESAN20031900, NT2NE20125050, SMINT20068010, SPLEN20163560, STOMA20092890, TESTI20382750

[0266] The 7 clones shown above are clones which were predicted to highly possibly belong to the category of cytoskeleton-related protein based on the result of domain search by Pfam.

[0267] The clone shown above is clone which were predicted to highly possibly belong to the protein and/or RNA synthesis-related protein based on the result of domain search by Pfam.

BRACE20053480, BRACE20240740, KIDNE20009470, OCBBF20140890, SMINT20035690, UTERU20064000

[0268] The 6 clones shown above are clones which were predicted to highly possibly belong to the category of protein synthesis and/or transport-related protein based on the result of domain search by Pfam.

ADRGL20048330, ASTRO20064750, ASTRO20084250, BRACE20151320, BRACE20190040, BRACE20223330, BRALZ20058880, BRAMY20103570, BRCOC20023230, BRHIP20207990, BRTHA20000570, CTONG20093950, CTONG20129960, CTONG20146300, CTONG20155180, CTONG20160560, FCBBF10004120, FCBBF30195640,

FEBRA10001900, FEBRA20090290, FEBRA20214970, FEBRA20222040, HCHON20008150, HEART20083640, KIDNE20109890, LIVER20035680, LIVER20087510, MESAN20029400, MESAN20031900, MESAN20035290, MESAN20136110, MESAN20186700, NT2NE20130190, NT2RI20025640, NTONG20029480, PEBLM20060310, PERIC20004780, PROST20114390, PROST20171280, PUAEN20078980, SMINT20115880, SPLEN20119810, TESTI20023510, TESTI20057750, TESTI20083940, TESTI20152460, TESTI20185650,

TESTI20189410, TESTI20200710, TESTI20308600, TESTI20343070, TESTI20369690, TESTI20381040, THYMU20115850, UTERU20050690, UTERU20055330

[0269] The 57 clones shown above are clones which were predicted to highly possibly belong to the category of DNA-binding and/or RNA-binding protein based on the result of domain search by Pfam. PLACE60136720

[0270] The clone shown above is a clone which was predicted to highly possibly belong to the category of ATP-binding and/or GTP-binding protein based on the result of domain search by Pfam.

[0271] The 213 clones shown below are clones which were unassignable to any of the above-mentioned categories, but have been predicted to have some functions based on homology search for their full-length nucleotide sequences and motif search in their deduced ORFs. Clone Name, Definition in the result of homology search or Motif Name in the motif search, demarcated by a double slash mark (//), are shown below.

ADRGL20028570//Rattus norvegicus MG87 mRNA, complete cds.

ADRGL20061930//transposon-derived Buster1 transposase-like protein

ASTRO20012490//Eukaryotic initiation factor 1A

ASTRO20072210//PERIAXIN.

ASTRO20114370//Mus musculus SMAR1 mRNA, complete cds.

ASTRO20125520//dnaj protein [Schizosaccharomyces pombe]

ASTRO20143630//KH domain// Bacterial regulatory proteins, crp family

ASTRO20155290//TPR Domain// TPR Domain// TPR Domain

ASTRO20181690//oocyte-specific protein P100

BGGI110001930//UBX domain

BRACE20011070//Mus musculus F-box protein FBX15 mRNA, partial cds.

BRACE20039440//Drosophila melanogaster CHARYBDE (charybde) mRNA, complete cds.

BRACE20050900//TPR Domain// TPR Domain// TPR Domain// TPR Domain

BRACE20053280//Mus musculus Pdz-containing protein (Pdzx) mRNA, complete cds.

BRACE20057730//toxin sensitivity protein KTI12 homolog

BRACE20058580//Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds.

BRACE20063780//NOL1/NOP2/sun family

BRACE20269200//Heat-labile enterotoxin alpha chain BRACE20276430//Homo sapiens retinoblastoma-associated protein RAP140 mRNA, complete cds. BRACE20286360//Alpha adaptin carboxyl-terminal domain BRAMY10001300//Homo sapiens MAGE-E1b mRNA, complete cds. BRAMY20045240//Flagellar L-ring protein BRAMY20054880//Rattus norvegicus KPL2 (Kpl2) mRNA, complete cds. BRAMY20167060//Collagen triple helix repeat (20 copies) BRAMY20184670//Homo sapiens mRNA for ALEX1, complete cds. BRAMY20217460//Homo sapiens cardiac voltage gated potassium channel modulatory subunit mRNA, complete cds. alternatively spliced. BRAMY20240040//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds. BRAMY20247110//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds. BRAWH20004600//Mus musculus mRNA for NAKAP95, complete cds. BRAWH20011710//cytoplasmic linker 2 BRAWH20012390//Trichomonas vaginalis mRNA for centrin (ce1 gene). BRAWH20017010//Homo sapiens testes development-related NYD-SP22 mRNA, complete cds. BRAWH20029630//Homo sapiens bet3 (BET3) mRNA, complete cds. BRAWH20138660//Homo sapiens stonin 2 mRNA, complete cds. BRCOC20008500//Human ras inhibitor mRNA, 3' end. BRCOC20026640//Gag P30 core shell protein BRCOC20035130//14-3-3 PROTEIN EPSILON (MITOCHONDRIAL IMPORT STIMULATION, FACTOR L SUBU-NIT) (PROTEIN KINASE C INHIBITOR PROTEIN-1) (KCIP-1) (14-3-3E). BRCOC20074760//CDC4-LIKE PROTEIN (FRAGMENT). BRCOC20110100//Integrase core domain BRCOC20176520//Rattus norvegicus mRNA for type-II brain 4.1. complete cds. BRHIP20001630//Protein of unknown function DUF16 BRHIP20132860//Homo sapiens rhophilin-like protein mRNA, complete cds. BRHIP20143730//MYND finger BRHIP20175420//Mus musculus partial mRNA for stretch responsive protein 278 (sr278 gene). BRHIP20236950//Outer Capsid protein VP4 (Hemagglutinin) BRSSN20014260//RIBONUCLEASE INHIBITOR. BRSSN20018690//Homo sapiens NY-REN-25 antigen mRNA, partial cds. BRSSN20021600//RING CANAL PROTEIN (KELCH PROTEIN). BRSSN20177570//Phosducin BRSTN10000830//Kelch motif// Kelch motif// Kelch motif// Kelch motif/ CTONG10000220//Mus musculus cerebellar postnatal development protein-1 (Cpd1) mRNA, partial cds. CTONG10000930//Armadillo/beta-catenin-like repeats CTONG20027090//Glypican// Leucine Rich Repeat// Leucine Rich Repeat CTONG20076130//ZINC FINGER PROTEIN 185 (LIM-DOMAIN PROTEIN ZNF185) (P1-A). CTONG20096750//Disintegrin CTONG20100240//Mus musculus radial spokehead-L protein (Rshl1) mRNA, complete cds. CTONG20139860//Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16 mRNA, complete cds. CTONG20143690//MYND finger CTONG20149460//RING CANAL PROTEIN (KELCH PROTEIN). CTONG20165050//Keratin, high sulfur B2 protein CTONG20186320//RING CANAL PROTEIN (KELCH PROTEIN). D3OST20013280//ARP2/3 COMPLEX 16 KDA SUBUNIT (P16-ARC). D3OST20024360//Homo sapiens neuroendocrine differentiation factor mRNA, complete cds. D9OST20031370//Homo sapiens mRNA for partial putative TCPTP-interacting protein (ptpip5 gene). DFNES20014040//TRICHOHYALIN. FCBBF10000630//Homo sapiens huntingtin interacting protein HYPB mRNA, partial cds. FCBBF10000770//Homo sapiens REC8 mRNA, partial cds. FCBBF10005060//CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP). FCBBF10005500//Keratin, high sulfur B2 protein FCBBF20014270//ACYL-COA-BINDING PROTEIN (ACBP) (DIAZEPAM BINDING INHIBITOR) (DBI) (EN-DOZEPINE) (EP).

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FCBBF20042170//Homo sapiens NIBAN mRNA, complete cds.

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NT2RP70105210//Myc amino-terminal region NT2RP70188710//Yeast PIR proteins

FCBBF30016320//SecA protein, amino terminal region FCBBF30033050//Sm protein FCBBF30054440//PLAT/LH2 domain FCBBF30225660//Ank repeat// Ank repeat// Ank repeat// K+ channel tetramerisation domain// BTB/POZ domain FCBBP30233680//G10 protein FCBBF30246630//H. sapiens mRNA for ZYG homologue. FCBBF30250730//TRICHOHYALIN. FCBBF30252520//Homo sapiens bicaudal-D (BICD) mRNA, alternatively spliced, partial cds. FCBBF30252800//NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN FCBBF30252850//Mus musculus peripherial benzodiazepine receptor associated protein (Pap7) mRNA, complete FCBBF30285280//Keratin, high sulfur B2 protein// Bacterial regulatory proteins, gntR family FEBRA20088360//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KDA COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN AL-PHA C SUBUNIT). FEBRA20184330//Rattus norvegicus glutamate receptor interacting protein 2 (GRIP2) mRNA, complete cds. FEBRA20192420//Cyclin-dependent kinase inhibitor// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif FEBRA20196370//Cyclin-dependent kinase inhibitor// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif FEBRA20225040//high-glucose-regulated protein 8 HCHON20001560//TRANSCRIPTION FACTOR-LIKE PROTEIN MORF4. HCHON20003440//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds. HCHON20010990//TPR Domain HCHON20059870//Hypothetical protein. HHDPC20034390//Cereal trypsin/alpha-amylase inhibito HHDPC20057420//Mus musculus proline-rich protein (Bprp) mRNA, complete cds. HHDPC20064600//SUPPRESSOR PROTEIN SRP40. HLUNG20023340//Mus musculus SLM-1 (S1m1) mRNA, complete cds. KIDNE20007210//Xenopus laevis mRNA for RPA interacting protein alpha (ripalpha gene). KIDNE20028830//K-box region KIDNE20115080//Homo sapiens mRNA for hNBL4, complete cds. KIDNE20124400//Homo sapiens mRNA for ALEX1, complete cds. KIDNE20127100//Drosophila melanogaster Diablo (dbo) mRNA, complete cds. KIDNE20127750//Homo sapiens partial mRNA for transport-secretion protein 2.1 (TTS-2.1 gene). KIDNE20190740//Rattus norvegicus SNIP-b mRNA, complete cds. LIVER10004790//EF hand LIVER20011130//Homo sapiens F-box protein FBL9 mRNA, partial cds. LIVER20064100//Ciona intestinalis mRNA for myoplasmin-C1, complete cds. LIVER20080530//Drosophila melanogaster forked mRNA for large Forked protein, complete cds. MAMGL10000830//Drosophila melanogaster L82B (L82) mRNA, complete cds. MESAN20036460//Corticotropin-releasing factor family MESAN20127350//myelin expression factor-3 MESAN20141920//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds. NT2NE20010400//Homo sapiens GL013 mRNA, complete cds. NT2NE20122430//GLYOXYLATE-INDUCED PROTEIN. NT2NE20158600//erythroid ankyrin - Synechocystis sp. (strain PCC 6803). NT2RI20001330//Homo sapiens KE03 protein mRNA, partial cds. NT2RI20009870//lunatic fringe precursor [Mus musculus] NT2RI20046080//recA bacterial DNA recombination proteins NT2RI20091730//Molluscan rhodopsin C-terminal tail NT2RP60000850//Bos taurus RPGR-interacting protein-1 (RPGRIP1) mRNA, complete cds. NT2RP70080850//SPRY domain// Adenovirus EB1 55K protein / large t-an

NT2RP70194450//Bacterial regulatory proteins, crp family NTONG20052650//Gallus gallus Xin mRNA, complete cds. NTONG20064400//REPETIN. NTONG20064840//Mus musculus s1p1 mRNA for synaptotagmin-like protein 1, complete cds. NTONG20066460//Mus musculus Gd mRNA for gasdermin, complete cds. NTONG20067090//Mus musculus mRNA for Sh3yl1, complete cds. NTONG20070340//collagen alpha 1(IX) chain NTONG20083650//TPR Domain// TPR Domain// TPR Domain// PPR repeat// TPR Domain// PPR repeat// TPR NTONG20088620//Homo sapiens genethonin 3 mRNA, partial cds. OCBBF10000540//Mus musculus rjs (rjs) mRNA, complete cds. OCBBF20019380//seizure related gene 6 OCBBF20022900//Homo sapiens SCHIP-1 mRNA, complete cds. OCBBF20030280//Rattus norvegicus hfb2 mRNA, complete cds. OCBBF20046470//ARFAPTIN 1. OCBBF20049840//Homo sapiens mRNA for neurabin II protein. OCBBF20068490//Mus musculus RW1 protein mRNA, complete cds. OCBBF20071960//Coturnix coturnix japonica qMEF2D gene. OCBBF20073540//Homo sapiens p30 DBC mRNA, complete cds. OCBBF20121390//RING CANAL PROTEIN (KELCH PROTEIN). OCBBF20127550//Outer Capsid protein VP4 (Hemagglutinin) OCBBF20148730//RING CANAL PROTEIN (KELCH PROTEIN). . OCBBF20178150//Plasmodium falciparum ADA2-like protein gene, partial cds. PEBLM10000240//Domain found in Dishevolled, Eg1-10, and Ple PROST20047270//CRAL/TRIO domain. PROST20112970//Sterile alpha motif (SAM)/Pointed domain// SAM domain (Sterile alpha motif) PUAEN10000850//Uncharacterized protein family UPF0025// Secl family PUAEN20011880//Mus musculus mRNA for MIWI (piwi), complete cds. PUAEN20051100//Mus musculus otogelin mRNA, complete cds. PUAEN20108240//Drosophila melanogaster ankyrin 2 (Ank2) mRNA, complete cds. SKMUS20084740//Syndecan domain SMINT20053300//Homo sapiens hepatocellular carcinoma-associated antigen 59 mRNA, complete cds. SMINT20071400//NOL1/NOP2/sun family SMINT20101440//Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds. SMINT20110330//pKID domain SMINT20122910//Mus musculus StAR-related protein 1-4E mRNA, partial cds. SMINT20131810//ENV polyprotein (coat polyprotein) SMINT20168570//Homo sapiens mRNA for stabilin-1 (stab1 gene). SPLEN20008390//Human placenta (Diff48) mRNA, complete cds. SPLEN20084600//RING CANAL PROTEIN (KELCH PROTEIN). SPLEN20128000//Xenopus laevis XMAB21 (Xmab-21) mRNA, complete cds. SPLEN20149110//Dishevelled specific domain SPLEN20171470//Keratin, high sulfur B2 protein SPLEN20194050//Homo sapiens HOTTL protein mRNA, complete cds. SPLEN20214580//Mus musculus mdg1-1 mRNA, complete cds. STOMA20057820//Uncharacterized protein family UPF0024 STOMA20063980//Collagen triple helix repeat (20 copies) STOMA20069040//Keratin, high sulfur B2 protein SYNOV20017080//UBX domain TBAES20000590//Cytochrome P450// Cytochrome P450 TESTI20001170//HORMA domain TESTI20031810//Bacterial luciforase// Domain of unknown function DUF28 TESTI20044230//Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds. TESTI20098350//VAT-Nn domain TESTI20157520//K+ channel tetramerisation domain// K+ channel tetramerisation domain TESTI20170350//Cystine-knot domain

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TESTI20199750//TRICHOHYALIN.

TESTI20192800//Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16 mRNA, complete cds.

TESTI20202650//Repeat in HS1/Cortactin

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TESTI20229600//Drosophila melanogaster SP2353 mRNA, complete cds.
  TESTI20231920//Gag P30 core shell protein
  TESTI20242830//E2 (early) protein, C terminal// Syndecan domain
  TESTI20254540//Homo sapiens hepatocellular carcinoma-associated antigen 59 mRNA, complete cds.
  TESTI20320440//THIOREDOXIN.
  TESTI20327680//EF hand// EF hand
  TESTI20328280//KE2 family protein// Troponin
  TESTI20351830//K-box region
  TESTI20370020//Bleomycin resistance protein
  TESTI20391210//IQ calmodulin-binding motif
  TESTI20408150//Keratin, high sulfur B2 protein
  TESTI20451990//SAP domain
  TESTI20467970//Neurohypophysial hormones. N-terminal Domain// Neurohypophysial hormones, N-terminal Do-
  main// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neu-
  rohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypophy-
  sial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hor-
  mones, N-terminal Domain
  THYMU20108310//Mouse NCBP-29 mRNA for PW29, complete cds.
  THYMU20142040//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).
  THYMU20194360//Kelch motif
  THYMU20239000//collagen alpha 1(XI) chain
  TOVAR20004760//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
  TRACH20005020//Ank repeat// MutT-like domain
  TRACH20007020//TRICHOHYALIN.
   TRACH20048450//PROTEIN K4 (PROTEIN K3).
   TPACH20068700//Homo sapiens adaptor protein CIKS mRNA, complete cds.
   TRACH20076760//Keratin, high sulfur B2 protein
   TRACH20135520//TBC domain// Rhodanese-like domain
   TRACH20141240//Mus musculus G21 protein mRNA, complete cds.
   TRACH20183170//Rattus norvegicus Sprague-Dawley SM-20 mRNA. complete cds.
   UTERU20000740//Human fusion protein mRNA, complete cds.
   UTERU20004240//CGI-96 protein
   UTERU20006960//endoplasmic reticulum resident protein 58
   UTERU20022940//Human (p23) mRNA, complete cds.
   UTERU20046640//Mus musculus idiBp (LDLB) mRNA, complete cds.
   UTERU20065930//GTP-RHO BINDING PROTEIN 1 (RHOPHILIN).
   UTERU20115740//Human PMS2 related (hPMSR3) gene, complete cds.
   UTERU20179880//TPR Domain// TPR Domain// TPR Domain// TPR Domain
[0272] With respect to the remaining 882 clones, there are so far no information available for estimating their func-
tions. However, there is the possibility that the functions of these clones will be revealed in future. Their Clone Names
are indicated below.
3NB6920014080, ADRGL2000640, ADRGL20012870, ADRGL20013010, ADRGL20044590, ADRGL20067670,
ADRGL20068170, ADRGL20068460, ADRGL20073570, ADRGL20076360. ADRGL20083310, ASTRO20032120,
ASTRO20100720, ASTRO20111490, ASTRO20114G10, ASTRO20136710. ASTRO20138020, ASTRO20152140,
ASTRO20166810, ASTRO20173480, BLADE20004630, BRACE20019540, BRACE20037660, BRACE20038850,
BRACE20051690, BRACE20054500, BRACE20055180, BRACE20056810. BRACE20057420, BRACE20058810,
BRACE20060840, BRACE20061740, BRACE20062400, BRACE20062740. BRACE20063800, BRACE20063930,
BRACE20082950, BRACE20090440, BRACE20096540, BRACE20097320. BRACE20099570, BRACE20106690,
BRACE20109370, BRACE20109830, BRACE20111830, BRACE20114780. BRACE20115450, BRACE20118380,
BRACE20121850, BRACE20136240, BRACE20141080, BRACE20142320, BRACE20142570, BRACE20148210,
BRACE20150310, BRACE20152870, BRACE20163150, BRACE20165830. BRACE20171240, BRACE20175870,
BRACE20190440, BRACE20220300, BRACE20223280, BRACE20229280. BRACE20230700, BRACE20235400,
BRACE20262930, BRACE20262940, BRACE20266750, BRACE20267250. BRACE20269710, BRACE20283920,
BRACE20287410, BRALZ20014450, BRALZ20019660, BRALZ20059500. BRALZ20065600, BRALZ20075450,
BRALZ20075760, BRALZ20080310, BRALZ20088690, BRAMY10001570. BRAMY20004110, BRAMY20011140,
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BRAMY20071850, BRAMY20102080, BRAMY20110640, BRAMY20116790. BRAMY20121190, BRAMY20137560,

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BRAMY20147540, BRAMY20160700, BRAMY20163250, BRAMY20163270, BRAMY20167710, BRAMY20168920,
BRAMY20170140, BRAMY20178640, BRAMY20182730, BRAMY20183080, BRAMY20196000, BRAMY20204450,
BRAMY20205740, BRAMY20229840, BRAMY20230600, BRAMY20250240, BRAMY20250320, BRAMY20261680,
BRAMY20267130, BRAMY20268990, BRAMY20277140, BRAMY20280720, BRAMY20285930. BRAMY20286820,
BRAWH10000930, BRAWH20012410, BRAWH20014920, BRAWH20016660, BRAWH20100690, BRAWH20103180,
BRAWH20106180, BRAWH20107540, BRAWH20110660, BRAWH20111550, BRAWH20122770, BRAWH20126190,
BRAWH20126980, BRAWH20139410, BRAWH20142340, BRAWH20147290, BRAWH20155950, BRAWH20158530,
BRAWH20160280, BRAWH20162690, BRAWH20166790, BRAWH20173050, BRAWH20182060, BRCAN20006200,
BRCAN2006390, BRCAN20060190, BRCAN20126130, BRCAN20143700, BRCAN20147880, BRCAN20216690,
BRCAN20237240, BRCAN20263400, BRCAN20273100, BRCAN20273340, BRCAN20275130. BRCAN20280400,
BRCAN20284600, BRCOC20004870, BRCOC20020850, BRCOC20031000, BRCOC20031870. BRCOC20037400,
BRCOC20093800, BRCOC20105100, BRCOC20117690, BRCOC20119960, BRCOC20122290, BRCOC20128130,
BRCOC20135730, BRCOC20147480, BRCOC20148330, BRCOC20155970, BRCOC20158240, BRHIP10001740,
BRHIP20104440, BRHIP20105710, BRHIP20107440, BRHIP20110800, BRHIP20115760, BRHIP20123140,
BRHIP20129720, BRHIP20139720, BRHIP20140630, BRHIP20142850, BRHIP20143860, BRHIP20149540,
BRHIP20153560, BRHIP20169680, BRHIP20169900, BRHIP20170100, BRHIP20173150, BRHIP20180140,
BRHIP20186120, BRHIP20186500, BRHIP20190070, BRHIP20196410, BRHIP20205090, BRHIP20208420,
BRHIP20214950, BRHIP20227080, BRHIP20230710, BRHIP20232290, BRHIP20238690, BRHIP20240460,
BRHIP20254480, BRHIP20277620, BRHIP20284800, BRHIP30001110, BRSSN10000920, BRSSN20006340,
BRSSN20015030, BRSSN20028570, BRSSN20038410, BRSSN20046570, BRSSN20046860. BRSSN20097020,
BRSSN20105960, BRSSN20108300, BRSSN20121030, BRSSN20152380, BRSSN20159070. BRSSN20159820,
BRSTN20000580, BRTHA20046390, CD34C30001250, CD34C30003140, CD34C30004940, COLON20043180,
CTONG20002180, CTONG20028410, CTONG20038890, CTONG20049410, CTONG20077790, CTONG20082690,
CTONG20091320, CTONG20095270, CTONG20095290, CTONG20096430, CTONG20097660. CTONG20099630,
CTONG20101480, CTONG20105660, CTONG20106230, CTONG20108210, CTONG20124470, CTONG20126070,
CTONG20128470, CTONG20136300, CTONG20138030, CTONG20139070, CTONG20140320. CTONG20141650,
CTONG20146970, CTONG20147050, CTONG20150910, CTONG20158150, CTONG20162170, CTONG20163550,
CTONG20164990, CTONG20265130, CTONG20273610, D3OST10002670, D3OST10002700, D3OST20006540,
D3OST20007340. D3OST20024170, D3OST20024520, D3OST20037970, D3OST30002910, D6OST20004450,
D9OST20000310, D9OST20035800, DFNES10000030, DFNES10001850, DFNES20010910, DFNES20055270,
DFNES20082800, FCBBF10003740, FCBBF20006780, FCBBF20023700, FCBBF20035280, FCBBF20054280,
FCBBF20056370. FCBBF20071860, FCBBF20072650, FCBBF20075560, FCBBF20076330, FCBBF30001840.
FCBBF30016570, FCBBF30019120, FCBBF30028180, FCBBF30052180, FCBBF30062880, FCBBF30070770,
FCBBF30071520, FCBBF30170590, FCBBF30178730, FCBBF30189490, FCBBF30199610, FCBBF30240020,
FCBBF30242250. FCBBF30262360, FCBBF30266780, FCBBF30266920, FCBBF30278630, FCBBF30284720,
FCBBF40001420, FCBBF40005480, FEBRA20003210, FEBRA20017050, FEBRA20018280, FEBRA20025520,
FEBRA20026280. FEBRA20027810, FEBRA20034360, FEBRA20037500, FEBRA20042190, FEBRA20052910,
FEBRA20060610, FEBRA20072120, FEBRA20079310, FEBRA20082100, FEBRA20095140, FEBRA20098460,
FEBRA20161120, FEBRA20166540, FEBRA20176800, FEBRA20197110, FEBRA20204000, FEBRA20204060,
FEBRA20216360, FEBRA20226010, FEBRA20229560, FEBRA20232850, FELNG20002410, HCHON20002260,
HCHON20008980, HCHON20009350, HCHON20011160, HCHON20014970, HCHON20022470, HCHON20036760,
HCHON20043590, HCHON20067220, HCHON20074820, HCHON20076500, HEART20021840, HEART20037810,
HEART20049400. HEART20063340. HEART20067870, HEART20067890, HEART20074430, HEART20089940,
HEART20095990. HHDPC10000650, HHDPC20006920, HHDPC20057940, HHDPC20095280. HLUNG20016770,
HLUNG20084390, KIDNE20006780, KIDNE20011170, KIDNE20013730, KIDNE20018730, KIDNE20018970,
KIDNE20021980. KIDNE20029800, KIDNE20067330, KIDNE20079440, KIDNE20096280, KIDNE20096470,
KIDNE20100840, KIDNE20102650, KIDNE20104300, KIDNE20106740, KIDNE20107500, KIDNE20112000,
KIDNE20120090, KIDNE20122910, KIDNE20132180, KIDNE20138010, KIDNE20141190, KIDNE20144890,
KIDNE20148900, KIDNE20163880, KIDNE20180710, KIDNE20186780, LIVER10001260, LIVER20011910,
LIVER20028420, LIVER20038540, LIVER20084730, LIVER20085800, MESAN20106640, MESAN20121130,
MESAN20132110, MESAN20138450, MESAN20157080, MESAN20161590, MESAN20164090, MESAN20182090,
NESOP10001080, NOVAR10001020, NOVAR20003520, NT2NE20003740, NT2NE20010210, NT2NE20015240,
NT2NE20043780, NT2NE20053580, NT2NE20072200, NT2NE20074250, NT2NE20089610, NT2NE20108540,
NT2NE20110360, NT2NE20146810, NT2NE20152750, NT2NE20172590, NT2NE20174800, NT2NE20174920,
NT2NE20187390, NT2RI20022600, NT2RI20023160, NT2RI20023590, NT2RI20036670, NT2RI20055790,
NT2RI20069730, NT2RI20198260, NT2RI20203900, NT2RI20207030, NT2RI20216250, NT2RI20244960,
NT2RI20250750, NT2RI20252550, NT2RP70010740, NT2RP70056750, NT2RP70075240, NT2RP70077660,
NT2RP70085440, NT2RP70110860, NT2RP70111320, NT2RP70130020, NT2RP70137640, NT2RP70143480,
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NT2RP70147210. NT2RP70150800, NT2RP70169110, NT2RP70175670, NT2RP70181970, NT2RP70190640,
NT2RP70203790. NTONG20050620, NTONG20050860, NTONG20065010, NTONG20077560, NTONG20090680,
OCBBF20005230. OCBBF20020150, OCBBF20029800, OCBBF20032460, OCBBF20041680. OCBBF20045330,
OCBBF20047570. OCBBF20048660, OCBBF20051610, OCBBF20060300, OCBBF20061720. OCBBF20062140,
OCBBF20062410. OCBBF20074140, OCBBF20076220, OCBBF20079460, OCBBF20081380. OCBBF20084660,
OCBBF20085200 OCBBF20088220, OCBBF20094240, OCBBF20097720, OCBBF20100400, OCBBF20103130,
OCBBF20104340 OCBBF20105570, OCBBF20107920, OCBBF20111770, OCBBF20118970, OCBBF20126780,
OCBBF2013011C OCBBF20139260, OCBBF20151150, OCBBF20164050, OCBBF20164670, OCBBF20170690,
OCBBF20173060 OCBBF20173250, OCBBF20178990, OCBBF20186870, OCBBF20189560, PEBLM20024550,
PEBLM20071880 PEBLM20072960, PERIC20002140, PERIC20003860, PLACE60004630, PLACE60119750,
PLACE60138830 PLACE60153220, PLACE60155130, PLACE60169420, PLACE60181070, PLACE60187690,
PLACE60188340. PROST10004800, PROST20005670, PROST20021010, PROST20024890, PROST20029270,
PROST20052280. PROST20057930, PROST20059040. PROST20087700, PROST20097950, PROST20111050,
PROST20120050. PROST20121900, PROST20123530. PROST20127400, PROST20130530, PROST20132600,
PROST20133270. PROST20144220, PROST20149160. PROST20149250, PROST20151240, PROST20152460,
PROST20153320 PROST20166680, PROST20168290. PROST20178360, PUAEN20025680, PUAEN20027580,
PUAEN20C44000 PUAEN20045110, PUAEN20045250. PUAEN20052470, PUAEN20081230, PUAEN20085150,
RECTM10001410 RECTM20003490, RECTM20005100. SKMUS20012010, SKMUS20031680, SKMUS20046670,
SKNMC20006220 SKNSH20034660, SKNSH20062340. SKNSH20080430, SKNSH20087770. SKNSH20091970,
SMINT20005410 SMINT20008240, SMINT20011140. SMINT20011580, SMINT20014580, SMINT20015590,
                SMINT20033170, SMINT20033400. SMINT20042990, SMINT20047810, SMINT20056210,
SMINT20023280
                SMINT20060780, SMINT20065960. SMINT20076470, SMINT20080540, SMINT20089170,
SMINT20058C00
                                               SMINT20103690, SMINT20105000, SMINT20108530,
                SMINT20092720, SMINT20098320.
SMINT20092330
                                               SMINT20153530, SMINT20158100, SMINT20161220,
                SMINT20122850, SMINT20132280.
SMINT20109970
                SMINT20164400, SMINT20164770. SMINT20173190, SPLEN10000830, SPLEN20000640,
SMINT20162860
                SPLEN20008820, SPLEN20013540. SPLEN20016260, SPLEN20019450, SPLEN20020070,
SPLEN20002220
SPLEN20022230 SPLEN20023140, SPLEN20031600. SPLEN20032040. SPLEN20032190, SPLEN20033960,
                SPLEN20076530, SPLEN20101190 SPLEN20106250, SPLEN20129610, SPLEN20146690,
SPLEN20040600
SPLFN20149:40 SPLEN20152610, SPLEN20157300 SPLEN20158900, SPLEN20158990, SPLEN20160690,
SPLEN20150980 SPLEN20166270, SPLEN20171210. SPLEN20176200, SPLEN20193110, SPLEN20198110,
SPLEN20204*70 SPLEN20212950, SPLEN20214400. SPLEN20225220. SPLEN20242320, SPLEN20242730,
 SPLEN20249560 SPLEN20261440, SPLEN20264110 SPLEN20279950, SPLEN20280660, SPLEN20303970,
 STOMA20013890 STOMA20026880, STOMA20036460. STOMA20048520, STOMA20048840, STOMA20062290,
 STOMA20067800 STOMA20072690, STOMA20076800. STOMA20086140, STOMA20092560, SYNOV20003970,
               TESOP20000900, TESOP20003120. TESTI10000940, TESTI20004890, TESTI20011200,
 TCOLN20C01390
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                TESTI20029930, TESTI20030310. TESTI20030890,
                                                               TEST120038270,
 TESTI20018230
                                                               TEST120098530,
                                                                               TESTI20102800,
                                TESTI20087620.
                                               TESTI20094020.
 TESTI20076850
                TESTI20086210.
                                                               TESTI20122310,
                                                                               TESTI20129150,
                                TESTI20114070.
                                               TESTI20116650.
 TESTI20105720
                TESTI20112940.
                                                               TESTI20137370,
                                                                               TESTI20137670,
                                                TESTI20136990,
 TESTI20129220
                TESTI20130120.
                                TESTI20135660.
                                                                               TESTI20161970,
                                                TESTI20157100,
                                                               TESTI20159140,
                                TEST120155900.
 TESTI20143240
                TESTI20143620,
                                                               TESTI20178160,
                                                                               TESTI20179320,
                                                TESTI20171020,
                                TESTI20169960.
                TESTI20168960,
 TESTI20168630
                                                                               TESTI20199170,
                                                TESTI20194300,
                                                               TESTI20194810,
 TESTI20183370
                                TESTI20192280.
                TESTI20185810.
                                                                               TESTI20213580,
                                                                TESTI20213150.
                                                TESTI20211240,
                                TESTI20209460.
                TEST120203440.
 TEST1202C0260
                                                                               TESTI20238000,
                                                TESTI20226490,
                                                                TESTI20234270,
                                TESTI20224620.
                TESTI20220650,
 TESTI20220100
                                                               TESTI20244760,
                                                                               TESTI20262330,
                                                TESTI20241920,
                TESTI20240090,
                                TESTI20241530.
 TESTI20239470
                                                               TESTI20272060,
                                                                               TESTI20272390,
                                                TESTI20269570,
                                TESTI20265370,
                 TEST120265250,
 TESTI20262910
                                                                TESTI20282540,
                                                                               TESTI20285830,
                                                TESTI20280980,
                                TESTI20278200,
                 TEST120277360,
 TESTI20275620
                                                TESTI20294700,
                                                                TESTI20297850,
                                                                               TESTI20301360,
                 TESTI20289850,
                                TESTI20291620,
 TESTI20288110
                                                                TESTI20319190,
                                                                               TESTI20327740.
                                                TESTI20311290,
                                TESTI20310070,
                 TESTI20307540,
 TEST120305560
                                                                TESTI20342430,
                                                                               TESTI20345060,
                                TESTI20336410,
                                                TESTI20337100,
                 TESTI20333950,
 TESTI20330310
                                                                                TESTI20367360,
                                                                TESTI20361140,
                                 TESTI20357750,
                                                TESTI20357930,
                 TESTI20347770,
 TESTI20347740
                                                                                TESTI20380650,
                                                                TESTI20378450,
                                 TESTI20370550,
                                                TESTI20371060,
                 TESTI20369220,
 TESTI20369130
                                                                TESTI20392090,
                                                                                TESTI20401430,
                                 TESTI20388580,
                                                TESTI20391130,
 TESTI20386230
                 TEST120386440,
                                                                                TESTI20423020,
                                                                TESTI20419560,
                                 TESTI20413300,
                                                TESTI20415640,
 TESTI204C6420
                 TESTI20409440,
                                                                                TESTI20429280,
                                                                TESTI20428060,
                                 TESTI20425070,
                                                TESTI20427830.
                 TESTI20424730,
 TESTI20424000
                                                                                TESTI20458190,
                                                TESTI20447540,
                                                                TESTI20451710,
                                 TESTI20438660,
                 TFSTI20433130,
 TESTI20429580
                                                                                TESTI20473420,
                                                TESTI20471530.
                                                                TESTI20472120,
                                 TESTI20471470,
 TESTI20465520
                 TFSTI20468630;
                TESTI20478010, TESTI20478180, TESTI20479300, THYMU20000570, THYMU20011950,
 TESTI20477920
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THYMU20015210, THYMU20018190, THYMU20029100, THYMU20045120, THYMU20058070. THYMU20061700, THYMU20070360, THYMU20075320, THYMU20095960, THYMU20101610, THYMU20101920, THYMU20111420, THYMU20114470, THYMU20118060, THYMU20119390, THYMU20128070, THYMU20128260, THYMU20142970, THYMU20153160, THYMU20158250, THYMU20186390, THYMU20186730, THYMU20187720. THYMU20195990, THYMU20204160, THYMU20204990, THYMU20215090, THYMU20215970, THYMU20226600. THYMU20228540, THYMU20235760, THYMU20239430, THYMU20246840, THYMU20250420, THYMU20251890. THYMU20253250, THYMU20255570, THYMU20255720, THYMU20259090, THYMU20265300, THYMU20271250. THYMU20272490, THYMU20283790, THYMU20284120, THYMU20286290, THYMU20286320, TKIDN20030590, TKIDN20030620, TOVAR20005750, TRACH20027840, TRACH20032720, TRACH20037360, TRACH20056980, TRACH20060150, TRACH20082780, TRACH20091230, TRACH20092680, TRACH20099340, TRACH20107710, TRACH20115740, TRACH20118940, TRACH20147250, TRACH20153810, TRACH20169800, TRACH20187180, TSTOM10001860, TSTOM20001390, TSTOM20003150, UMVEN20003540, UTERU20006290, UTERU20020010. UTERU20054460, UTERU20056010, UTERU20059050, UTERU20061030, UTERU20067050, UTERU20068990. UTERU20070040, UTERU20070810, UTERU20081300, UTERU20084260, UTERU20095380, UTERU20095400, UTERU20101240, UTERU20114100, UTERU20118110, UTERU20118970. UTERU20119680, UTERU20124070, UTERU20126880, U1ERU20134910, UTERU20143980, UTERU20146680, UTERU20150870, UTERU20164260, UTERU20188810

# EXAMPLE 7

# Expression frequency analysis in silico

[0273] The cDNA libraries derived from various tissues and cells as indicated in Example 1 were prepared, and cDNA clones were selected from each library at random. The 5'-end sequences were determined and the database was constructed based on the data. The database was constructed based on the nucleotide sequences of 1,402,070 clones, and thus the population of the database is large enough for the analysis.

[0274] Then clones having a homologous sequence are categorized into a single cluster (clustering) by searching the nucleotide sequences of respective clones in this database with the program of nucleotide sequence homology search the number of clones belonging to each cluster was determined and normalized for every library; thus, the ratio of a certain gene in each cDNA library was determined. This analysis gave the information of the expression trequency of genes in tissues and cells which were sources of the cDNA libraries.

[0275] Then in order to analyze the expression of a gene containing the nucleotide sequence of the cDNA of the present invention in tissues and cells, the library derived from a tissue or a cell used in the large-scale cDNA analysis was subjected to the comparison of the expression levels between tissues or cells. Namely, the expression frequency was analyzed by comparing the previously normalized values between tissues and/or cells for which the nucleotide sequences of 600 or more cDNA clones had been analyzed. By this analysis, some of the genes were revealed to be involved in the pathology and functions indicated below. Each value in Tables 3 to 51 shown below represents a relative express on frequency; the higher the value, the higher the expression level.

# Ostcoperosis-related genes

[0276] Osteopcrosis is a pathology in which bones are easily broken owing to overall decrease in components of bone. The onset involves the balance between the functions of osteoblast producing bone and osteoclast absorbing bone namely bone metabolism. Thus, the genes involved in the increase of osteoclasts differentiating from precursor colls of monocyte/macrophage line (Molecular Medicine 38, 642-648, (2001)) are genes involved in osteoporosis relevant to bone metabolism.

[0277] A nucleotide sequence information-based analysis was carried out to identify the genes whose expression frequencies are higher or lower in CD34+ cell (cell expressing a glycoprotein CD34) treated with the osteoclast differentiation factor (Molecular Medicine 38, 642-648, (2001)) than in the untreated CD34+ cell, which is the precursor cell of monocyte/macrophage line. The result of comparative analysis for the frequency between the two cDNA libraries prepared from the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D30ST, D60ST or D90ST) showed that the genes whose expression levels were different between the two were the following clones (Table 3).

ASTRO20001410, D3OST10001090, D3OST20036070, THYMU20039810, KIDNE20028720, BRAWH10000930, BRHIP20005340. CTONG20141650, D9OST2000310, D9OST20002780, D9OST20023970, D9OST20026730, D9OST20031370. D9OST20033970, D9OST20035800, D9OST20035940, D9OST20040180. FCBBF30018550, FCBBF30233680, KIDNE20102650, NT2RI20023160, PROST20107820, SKNSH20089400. SMINT20033400, CTONG20108210, D6OST20003580 D6OST20005070, ASTRO20155290, D3OST10002670, D3OST10002700, D3OST20006180, D3OST20006540, D3OST20007340, D3OST20013280, D3OST20024170, D3OST20024360,

D3OST20037970, D3OST30002580, D3OST30002910, FCBBF10004120, NT2RI20001330, NTONG20009770, SPLEN20084600, SPLEN20140800, THYMU20169680, TRACH20141240, CD34C30001250, CD34C30003140, CD34C30004240, CD34C30004940, DFNES10001850, HHDPC20034390, NT2RI20091730, SKMUS20003610, SPLEN20225220, BRCOC20101230

5 [0278] These genes are involved in osteoporosis.

Genes involved in neural cell differentiation .

35

[0279] Genes involved in neural cell differentiation are useful for treating neurological diseases. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in neurological diseases.

[0280] A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed that the genes whose expression

levels were different between the two were the following clones (Table 4). CTONG20027090, CTONG20160560, NT2RP70032610, OCBBF20188730, SPLEN20162680, BRCOC20101230, BRHIP20005340, BRHIP20238880, FCBBF30016320, FEBRA20080810, FEBRA20225040, HCHON20008320, HHDPC20034390, HLUNG10000550, NT2RI20028470, NT2RI20054050, NT2RI20091730, NT2RP70078420, PUAEN20003740, THYMU20271250, BRACE20003070, BRACE20039040, BRAWH20004600, BRAWH20011710, BRCOC20121720, BRHIP20005530, D3OST10002700, HCHON20007380, HEART20072310, KIDNE20121880, MESAN20121130, NT2RI20022600, NT2RI20023160, NT2RI20086220, NT2RI20216250, NT2RP60000850, NT2RP70036880, NT2RP70043480, NT2RP70062230, NT2RP70081610, NT2RP70102350, NT2RP70130020, NT2RP70190640, OCBBF10001850, OCBBF20097720, OCBBF20173980, PEBLM20044520, SPLEN20173510, TRACH20007020, UTERU20065930, HCHON20022470, NT2NE20010490, NT2NE20174800, NT2NE20177520, PROST20087700, PROST20107820, SMINT20028820, TESTI20063830, ASTRO20125520, BRHIP30001110, HCHON20002260, HCHON20008150, KIDNE20002520, NT2NE20130190, NT2NE20158600, NT2RI20001330, NT2RI20025400. NT2RI20036670, NT2RI20048840, SKMUS20020840, BRACE20057190, BRACE20060550, BRACE20267250. BRAWH20107540, BRAWH20118230, CTONG20075860, CTONG20095290, FEBRA20086620, FEBRA20144170. FEBRA20196370, HLUNG20023340, NT2NE20003740, NT2NE20010050. NT2NE20010210, NT2NE20010400. NT2NE20015240, NT2NE20021620, NT2NE20043780, NT2NE20053580, NT2NE20068130, NT2NE20072200. NT2NE20074250, NT2NE20080170, NT2NE20089610, NT2NE20089970, NT2NE20108540, NT2NE20110360, NT2NE20118960, NT2NE20122430, NT2NE20124480, NT2NE20125050, NT2NE20131890, NT2NE20132170. NT2NE20142210, NT2NE20146810, NT2NE20152750, NT2NE20155110, NT2NE20156260, NT2NE20157470, NT2NE20159740, NT2NE20172590, NT2NE20174920, NT2NE20181650, NT2NE20183760, NT2NE20184900, NT2NE20187390, OCBBF20108430, RECTM20005100, SMINT20001760, SPLEN20169720, TESTI20265250. ASTRO10001650, ASTRO20033160, BRACE20011070, BRACE20039440, BRACE20151320, BRAMY20104640, BRAMY20137560, BRAMY20167060, BRAWH20028110, BRCAN20280360, BRCOC20004870, BRHIP20207990, BRHIP20217620, BRHIP20249110, BRSTN10000830, CTONG10000940, CTONG20004690, CTONG20050280, CTONG20105660, CTONG20125640, CTONG20133520, CTONG20186320, FCBBF10000770, FCBBF10002800. FCBBF10003770, FCBBF30018550, FCBBF30123470, FCBBF30246230, FEBRA20018280, FEBRA20095140, FEBRA20192420, HCHON20064590, HHDPC10000830, HLUNG20016770, HLUNG20033780, IMR3220002430, KIDNE20104300, MESAN20004570, MESAN20089360, NOVAR10000910, NT2RI20003480, NT2RI20005750, NT2RI20009870, NT2RI20023590, NT2RI20023910, NT2RI20025640, NT2RI20040930, NT2RI20041880. NT2RI20046080, NT2RI20050960, NT2RI20055790, NT2RI20056700, NT2RI20069730, NT2RI20076290, NT2RI20091940, NT2RI20198260, NT2RI20203900, NT2RI20207030, NT2RI20240080, NT2RI20244600, NT2RI20244960, NT2RI20250750, NT2RI20252550, NT2RI20273230, NTONG20067090, OCBBF10001750, OCBBF20047570, OCBBF20054760, OCBBF20059560, OCBBF20073540, OCBBF20125530, OCBBF20126780, OCBBF20127040, OCBBF20140890, SKMUS20003610, SKNSH20008190, SKNSH20080430, SMINT20144800 SPLEN20027440, SPLEN20095550, SPLEN20140800, TESTI20094020, TESTI20369690, TESTI20391770. TESTI20442760. TRACH20084720, TRACH20107710, TRACH20118940, UTERU20022940, ASTRO20108190, BGGI120006160, BRAMY20136210, BRAWH20016620, BRAWH20164460, BRCOC20144000, BRHIP20132860, BRSSN20146100, CTONG10000100, CTONG20103480, CTONG20108210, CTONG20139070, FCBBF10000240, FCBBF10000630, FCBBF20067810, FCBBF30010810, FCBBF30012810, FCBBF30013770, FCBBF30039020, FCBBF40001420, FEBRA10001880, FEBRA20082010, HHDPC20001040, KIDNE20021910, NT2RP60000770, NT2RP70010740, NT2RP70027380, NT2RP70037240, NT2RP70044280, NT2RP70045590, NT2RP70056750, NT2RP70063950, NT2RP70072690, NT2RP70077660, NT2RP70085440, NT2RP70105210,

NT2RP70110860, NT2RP70111320, NT2RP70122910, NT2RP70125160, NT2RP70133740, NT2RP70134990,

NT2RP70137290, NT2RP70137640, NT2RP70143480, NT2RP70147210, NT2RP70150800, NT2RP70157890, NT2RP70159960, NT2RP70169110, NT2RP70175670, NT2RP70179710, NT2RP70181970, NT2RP70188020, NT2RP70188710, NT2RP70192730, NT2RP70194450, NT2RP70195430, NT2RP70198350, NT2RP70203790, OCBBF20039250, OCBBF20080410, OCBBF20108190, OCBBF20108580, OCBBF20122620, OCBBF20130110, OCBBF20151150, OCBBF20189560, PROST10003220, TESTI2001720, TESTI20121550, TESTI20152460, TESTI20211240, TESTI20234140, UMVEN20003540, UTERU20006960, UTERU20094350, UTERU20164260

[0281] These genes are neurological disease-related genes. Cancer-related genes

[0282] It has been assumed that, distinct from normal tissues, cancer tissues express a distinct set of genes, and thus the expression can contribute to the carcinogenesis in tissues and cells. Thus, the genes whose expression patterns in cancer tissues are different from those in normal tissues are cancer-related genes. Search was carried out for the genes whose expression levels in cancer tissues were different from those in normal tissues.

[0283] The result of comparative analysis of cDNA libraries derived from breast tumor (TBAES) and normal breast (BEAST) showed that the genes whose expression levels were different between the two were the following clones (Table 5).

BRACE20039040, BRAMY20163250, BRCOC20031250, BRHIP20005340, BRHIP20217620, BRHIP30001110, FCBBF10000770, FCBBF30010810, FEBRA20080810, FEBRA20144170, FEBRA20196630, FEBRA20197110, HCHON20002260, HCHON20040020, HHDPC20034390, HLUNG10000550, NOVAR10000910, NT2RI20023160, NT2RI20054050, NT2RI20091730, OCBBF20188730, SMINT20144800, SPLEN20128000, SPLEN20171210, SPLEN20264110, TBAES20000590, TBAES20002550, TBAES20003150, TESTI20334410, TESTI20432750, TRACH20003590, TRACH20084720, UTERU20046640, BEAST20004540, SPLEN20008740

[0284] The result of comparative analysis of cDNA libraries derived cervical tumor (TCERX) and normal cervical duct (CERVX) showed that the genes whose expression levels were different between the two were the following clones (Table 6)

BGGI120006160, BRAMY20063970, BRHIP20218580, FEBRA20002100, SPLEN20162680, TESTI20214250, CTONG20105080, HCHON20015980, PROST20175290, TESTI20254220, THYMU20279750

[0285] The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN) and normal colon (COLON) showed that the genes whose expression levels were different between the two were the following clones (Table 7).

ASTRO20001410, BRAWH20162690, CTONG20132220, HCHON20002260, NT2RI20001330, TCOLN20001390, 3NB6910001910, BRAWH20120910, BRAWH20004600, BRCOC20031250, BRCOC20031870, COLON10001350, COLON20043180. COLON20093370, FEBRA20002100, FEBRA20082010, FEBRA20197110, KIDNE20007770, KIDNE20013730. NT2RP70045590, OCBBF20078920, PROST20083600, SPLEN20011410, TRACH20084720, THYMU20271250

[0286] The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP) and normal esophagus (NESOP) showed that the genes whose expression levels were different between the two were the following clones (Table 8).

ASTRO20033160, ASTRO20125520, BRAMY20266850, BRAWH20164460. BRHIP20005340, BRHIP20191490, CTONG20095290, CTONG20143690, CTONG20161850, DFNES20001530, DFNES20071130, FCBBF30123470, FCBBF30175310, FEBRA20095140, HCHON20016650, MESAN20025190, NT2RI20028470, NT2RI20054050, NT2RP70036880, NTONG2009770, NTONG20064840, NTONG20076930, SMINT20042990, SPLEN20008820, SPLEN20128000, SPLEN20149110, STOMA20013890, TESOP20000900, TESOP20003120, TESOP20004000, TESOP20005270, TESOP20005690, TESTI20334410, THYMU20271250, TRACH20141240, UTERU20022940, NESOP10001080, NT2RI20023160, NTONG20013620, TRACH20077540, NTONG20015870

[0287] The result of comparative analysis of cDNA libraries derived from kidney tumor (TKIDN) and normal kidney (KIDNE) showed that the genes whose expression levels were different between the two were the following clones (Table 9).

ASTRO2008010, ASTRO20181690, BRACE20111830, BRACE20152870, BRACE20237270, BRAMY20147540, BRAMY20286820, BRAWH20015350, BRAWH20096780, BRAWH20132190, BRAWH20182060, BRCAN20060190, BRCOC20004870, BRCOC20176520, BRHIP20000870, BRHIP20198190, BRHIP20233090, BRHIP30001110, BRSSN20015790, BRSTN20000580, CTONG10000940, CTONG20098440, CTONG20150910, CTONG20165050, DFNES20014040, DFNES20037420, FCBBF10000770, FCBBF30083820, FCBBF30247930, FEBRA20037500, FEBRA20072120, FEBRA20080810, FEBRA20086620, FEBRA20140100, FEBRA20144170, FEBRA20176800, HCHON20008320, HCHON20059870, HLUNG10000550, MESAN20106640, NT2RI20025400, NT2RI20076290, NT2RI20091940, OCBBF20019830, OCBBF20022900, OCBBF20039250, OCBBF20080050, OCBBF20097720, OCBBF20125530, OCBBF20130110, OCBBF20140640, OCBBF20173980, PANCR10000910, PROST20087700, PUAEN20044000, SPLEN20144520, SPLEN20160980, TKIDN10000010, TKIDN20004640, TKIDN20005210, TKIDN20030590, TKIDN20030620, TKIDN20047480, TRACH2003590, ASTRO20108190, TRACH20184490, UMVEN20003540, UTERU20004240, UTERU20055930, ASTRO20108190,

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BGGI120006160, BRACE20039040, BRAMY20102080, BRAWH20004600, BRAWH20125380, BRAWH20162690,
BRHIP20115760, BRHIP20205090, CTONG20052650, CTONG20108210, CTONG20128470, CTONG20133480,
CTONG20139070, D9OST20000310, DFNES20001530, FCBBF10001820, FEBRA20002100, HCHON20008980,
HCHON20016650, HLUNG20033780, KIDNE20002520, KIDNE20003940, KIDNE20006780, KIDNE20007210,
KIDNE20007770, KIDNE20008010, KIDNE20009470, KIDNE20011170, KIDNE20011400, KIDNE20013730,
KIDNE20017130, KIDNE20018730, KIDNE20018970, KIDNE20020150, KIDNE20021680, KIDNE20021910,
KIDNE20021980, KIDNE20022620, KIDNE20024830, KIDNE20027250, KIDNE20027950, KIDNE20028390,
KIDNE20028720, KIDNE20028830, KIDNE20029800, KIDNE20067330, KIDNE20079440, KIDNE20096280,
KIDNE20096470, KIDNE20100070, KIDNE20100840, KIDNE20101370, KIDNE20101510, KIDNE20102650,
KIDNE20102710, KIDNE20104300, KIDNE20106740, KIDNE20107390, KIDNE20107500, KIDNE20107620,
KIDNE20109730, KIDNE20109890, KIDNE20112000, KIDNE20115080, KIDNE20118580, KIDNE20120090,
KIDNE20121880, KIDNE20122910, KIDNE20124400, KIDNE20125630, KIDNE20126010, KIDNE20126130.
KIDNE20127100, KIDNE20127450, KIDNE20127750, KIDNE20130450, KIDNE20131580, KIDNE20132180.
KIDNE20137340, KIDNE20138010, KIDNE20141190, KIDNE20144890, KIDNE20148900, KIDNE20163880
KIDNE20180710, KIDNE20181660, KIDNE20182690, KIDNE20186780, KIDNE20190740, LIVER20035110,
MESAN20025190, NT2RP70043480, PROST20107820, PROST20123530, PROST20161950, PUAEN20030180,
SKMUS20003610, SMINT20033400, TBAES20000590, TESTI20044310, TESTI20082330, TRACH20032720,
UTERU20099720
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[0288] The result of comparative analysis of cDNA libraries derived from liver tumor (TLIVE) and normal liver (LIVER) showed that the genes whose expression levels were different between the two were the following clones (Table 10). BRAWH20166790, CTONG20103480, HEART20005410, LIVER10001260, LIVER10004790, LIVER20002160, LIVER20011130. LIVER20011910, LIVER20028420, LIVER20035110, LIVER20035680, LIVER20035680, LIVER20045650. LIVER20055200, LIVER20055440, LIVER20059810, LIVER20062510, LIVER20064100, LIVER20064690. LIVER20075680, LIVER20080530, LIVER20084730, LIVER20085800, LIVER20087510, LIVER20064100, ASTRO20125520. BRACE20152870, BRAMY20167060, BRAMY20181220, BRAMY20285160, BRCOC20001860, FEBRA2014417C. HLUNG10000550, OCBBF20073540, OCBBF20088220, PLACE60169420, SMINT20152940, SPEFN20242320 THYMU20000570, TRACH20077540, UTERU20055930, UTERU20065930

[0289] The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG) and normal lung (FLUNG) showed that the genes whose expression levels were different between the two were the following clones (Table 11)

BRAWH2004600, BRAWH20030250, BRCAN2006390, BRCAN20280360, BRHIP20238880, CTONG10000940. CTONG20103480, CTONG20129960, CTONG20155180, FCBBF10001210, FEBRA20144170, FEBRA20197110. HCHON20002260, HHDPC20034390, HLUNG10000550, HLUNG20016330, HLUNG20016770, HLUNG20017120. HLUNG20023340, HLUNG20033780, HLUNG20084390, IMR3220002430, LIVER20028420, NOVAR20000380. NT2RI20023910, NT2RI20054050, NT2RI20091730, NT2RP70044280, OCBBF20020830, OCBBF20125530 PLACE60004630, PROST20057930, PROST20107820, PROST20185830, PUAEN20030180, SPLEN20176200. SPLEN20179180, SPLEN2008740, SPLEN20054290, SPLEN20128000, SPLEN20157300, SPLEN20179180, SPLEN2011940, STOMA20013890, TBAES20000590, TESTI20094230, TRACH20183170. ASTRO20108190, ASTRO20155290, BRHIP20096850, FEBRA20080810, MESAN20014500, SMINT20028820 SPLEN20162680

[0290] The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVEH) showed the genes whose expression levels were different between the two were the following clones (Table

BGGI120006160. BRHIP20005340, BRHIP20191860, HHDPC20001040, NOVAR10000150, NOVAR10000910, NOVAR10001320. NOVAR20000380, NOVAR20003520, THYMU20271250, ASTRO20141350, BRAMY20157820, BRCOC20001860. HLUNG20016770, NT2RI20054050, NTONG20090600, PROST20087700, PUAEN20015860, SPLEN20029310. TOVAR20004760, TOVAR20005750, TRACH20079690, UTERU20004240

[0291] The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) showed that the genes whose expression levels were different between the two were the following clones (Table 13).

BRACE20060840. FEBRA20052910, HCHON20002260, HLUNG10000550, NTONG20009770, PROST20107820, THYMU20039810, TSTOM10001860, TSTOM20001390, TSTOM20003150, TSTOM20005690, ASTRO20125520, BRACE20039040, BRAMY20124260, BRCOC20031870, BRHIP20191860, CTONG20128470, FEBRA20037500, HCHON20040020, HHDPC10000830, IMR3220002430, KIDNE20007770, NOVAR20000380, NT2RI20054050, NT2RI20091730, PROST20130530, SPLEN20149110, SPLEN20157880, STOMA20001830, STOMA20005390, STOMA20005670, STOMA20006400, STOMA20006780, STOMA20006860, STOMA20008880, STOMA20010250,

EP 1 347 046 A1 STOMA20013890, STOMA20026880, STOMA20032890, STOMA20034770, STOMA20036460, STOMA20046680, STOMA20048520, STOMA20048840, STOMA20051200, STOMA20056640, STOMA20056670, STOMA20057820, STOMA20062130, STOMA20062290, STOMA20063250, STOMA20063980, STOMA20064470, STOMA20067800, STOMA20069040. STOMA20072690, STOMA20076800, STOMA20077450, STOMA20080500. STOMA20083610, STOMA20086140, STOMA20088380, STOMA20092530, STOMA20092560, STOMA20092890, TESTI20184620, TRACH20003590. TRACH20183170, PROST20083600, TRACH20068660 [0292] The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) showed that the genes whose expression levels were different between the two were the following clones DFNES10001850, NT2RI20023910, SMINT20144800, SPLEN20162680, TOVAR20004760, TUTER20002830, ASTRO2008010, ASTRO20033160, ASTRO20058630, ASTRO20105820, ASTRO20108190, BRACE20039040, BRACE20057190, BRACE20060840, BRACE20111830, BRACE20223330, BRAMY20266850, BRAWH20113430, BRAWH20126980, BRCOC20031870, BRCOC20107300, BRCOC20121720, BRCOC20155970, BRHIP20105710, BRHIP20191490, BRHIP20207990, BRHIP20217620, BRHIP20222280, BRHIP20238880, BRHIP20249110, BRSSN20018690, BRTHA20000570, CTONG10000940, CTONG10002770, CTONG20095290, CTONG20099380, CTONG20103480, CTONG20108210, CTONG20118250, CTONG20129960, CTONG20131560, CTONG20139070, CTONG20139340, CTONG20143690, CTONG20160560, D3OST30002580, FCBBF10000240, FCBBF10001820, FCBBF10003670, FCBBF10004120, FCBBF10005740, FCBBF30175310, FCBBF30240020, FCBBF30246230, FCBBF40001420, FEBRA20002100, FEBRA20004620, FEBRA20018280, FEBRA20025270, FEBRA20034360, FEBRA20037500, FEBRA20080810, FEBRA20082100, FEBRA20144170, FEBRA20225040, HCHON20002260, HCHON20007380, HCHON20015980, HCHON20016650, HCHON20022470, HCHON20040020, HCHON20076500, HEART20072310, HHDPC20034390, HLUNG10000550, HLUNG20016770, KIDNE20131580, LIVER20028420, MAMGL10000830, MESAN20171520, NOVAR10000150, NOVAR10000910, NT2NE20053580, NT2NE20159740, NT2NE20174920. NT2RI20023160, NT2RI20041880, NT2RI20054050, NT2RI20076290, NT2RI20273230, NT2RP60000770, NT2RP60000850, NT2RP70036880, NT2RP70043480, NT2RP70045590, NT2RP70056750, NT2RP70062230, NT2RP70081610, OCBBF10001750, OCBBF20006770, OCBBF20032460, OCBBF20039250, OCBBF20047570, OCBBF20054760, OCBBF20059560, OCBBF20068490, OCBBF20080050, OCBBF20094240,

PROST20149160, PROST20159240, PROST20176170, PROST20189770, PUAEN20003740, PUAEN20015860, SKMUS20003610, SKNSH20008190, SKNSH20080430, SMINT20026890, SMINT20029760, SMINT20068010, SMINT20110330, SMINT20121220, SPLEN2008390, SPLEN20011410, SPLEN20054290, SPLEN20128000, SPLEN20140800, SPLEN20145720, SPLEN20169720, SPLEN20179180, SPLEN20193110, SPLEN20194050, SPLEN20211940, SPLEN20212730, SPLEN20225220, TBAES20000590, TESTI20061110, TESTI20116830, TESTI20184620, TESTI20208710, TESTI20211240, TESTI20213580, TESTI20214250, TESTI20334410, TESTI20369130, TESTI20369690, TESTI20391770, THYMU20039810, THYMU20216840, THYMU20240710, TRACH20003590, TRACH20032720, TRACH20033230, TRACH20141240, TRACH20149970, UMVEN10001860, UTERU20000740, UTERU20004240, UTERU2006290, UTERU20020010, UTERU20022940, UTERU20030570, UTERU20040610, UTERU20046640, UTERU20059050, UTERU20050690, UTERU20064000, UTERU20064860, UTERU20064860,

OCBBF20097720, OCBBF20103130, OCBBF20105570, OCBBF20140640, OCBBF20173980, OCBBF20180120, OCBBF20188730, OCBBF20189560, PEBLM20044520, PLACE60060420, PROST20087700, PROST20107820,

UTERU20081300, UTERU20084260, UTERU20094350, UTERU20095380, UTERU20095400, UTERU20097760, UTERU20099720, UTERU20101240, UTERU20114100, UTERU20115740, UTERU20116570, UTERU20118110, UTERU20118970, UTERU20119060, UTERU20119680, UTERU20120310, UTERU20124070, UTERU20126880, UTERU20134910, UTERU20135860, UTERU20143980, UTERU20144640, UTERU20145480, UTERU20146310, UTERU20146680, UTERU20150870, UTERU20151980, UTERU20158300, UTERU20158800, UTERU20161570, UTERU20164260, UTERU20168220, UTERU20176130, UTERU20176320, UTERU20178100, UTERU20179880, UTERU20183640, UTERU20185230, UTERU20186740, UTERU20188810, BRAWH10000930, CTONG20128470, UTERU2006960

UTERU20065930, UTERU20067050, UTERU20068990, UTERU20070040, UTERU20070810, UTERU20076390,

[0293] The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) showed that the genes whose expression levels were different between the two were the following clones (Table 15).

ADRGL20018300, ASTRO20058630, ASTRO20072210, ASTRO20108190, BRACE20003070, BRACE20039040, BRACE20060720, BRACE20061050, BRACE20210140, BRACE20276430, BRAMY20152110, BRAMY20266850, BRAMY20271400, BRAWH10000930, BRAWH20004600, BRCAN20280360, BRCOC20004870, BRHIP20005340, BRHIP20005530, BRHIP20238880, BRSSN20146100, CTONG10000100, CTONG10000220, CTONG10000620, CTONG10000930, CTONG10000940, CTONG10001650, CTONG10002770, CTONG20002180, CTONG20004690, CTONG20009770, CTONG20014280, CTONG20027090, CTONG20028410, CTONG20038890, CTONG20049410,

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CTONG20050280, CTONG20052650, CTONG20052900, CTONG20075860, CTONG20076130, CTONG20077790,
CTONG20082690, CTONG20085950, CTONG20091080, CTONG20091320, CTONG20092570. CTONG20092580,
CTONG20092680, CTONG20092700, CTONG20093950, CTONG20095270, CTONG20095290, CTONG20095340.
CTONG20096430, CTONG20096750, CTONG20097660, CTONG20098440, CTONG20099380, CTONG20099550,
CTONG20099630, CTONG20100240, CTONG20101480, CTONG20103480, CTONG20105080. CTONG20105660,
CTONG20106230, CTONG20106520, CTONG20108210, CTONG20114290, CTONG20114740, CTONG20118150,
CTONG20118250, CTONG20119200, CTONG20120770, CTONG20121010, CTONG20121580, CTONG20124010,
CTONG20124220, CTONG20124470, CTONG20124730, CTONG20125540, CTONG20125640. CTONG20126070,
CTONG20127450, CTONG20128470, CTONG20129960, CTONG20131490, CTONG20131560. CTONG20132220,
CTONG20133390, CTONG20133480, CTONG20133520, CTONG20136300, CTONG20138030, CTONG20139070,
CTONG20139340, CTONG20139860, CTONG20140320, CTONG20140580, CTONG20141650, CTONG20146300,
CTONG20147050, CTONG20149460, CTONG20149950, CTONG20153300, CTONG20153580, CTONG20155180,
CTONG20155400, CTONG20156780, CTONG20158040, CTONG20158150, CTONG20158660, CTONG20159530,
CTONG20160560, CTONG20161850, CTONG20162170, CTONG20163550, CTONG20164990. CTONG20165050,
CTONG20186320, CTONG20200310, CTONG20265130, CTONG20267700, CTONG20273610, FCBBF10000240,
FCBBF10005740, FCBBF30123470, FCBBF30233680, FEBRA20025270, FEBRA20037500, HCHON20002260,
HCHON20007380, HCHON20007510, HCHON20015350, HCHON20040020, HHDPC20034390, HLUNG10000550,
KIDNE20002520, KIDNE20009470, KIDNE20115080, KIDNE20127100, LIVER20028420, MESAN20029400,
NT2RI20023160, NT2RI20023910, NT2RI20091730, NT2RP70043480, NT2RP70078420, NT2RP70081610,
OCBBF20006770, OCBBF20059560, OCBBF20073540, OCBBF20094240, OCBBF20108580, PEBLM20044520,
PEBLM20071880, PROST20107820, PUAEN20030180, SKNSH20008190, SMINT20023280, SMINT20089170,
SPLEN20179180, TESTI20094020, TESTI20094230, TESTI20152460, TESTI20184620, TESTI20211240,
TESTI20442760, THYMU20039810, TRACH20028030, TRACH20141240, TSTOM20003150, UTERU20004240,
UTERU20055930, UTERU20065930, UTERU20119060, UTERU20124070, BRACE20039440, BRACE20068590,
FCBBF30018550, IMR3220002430, KIDNE20028830, NT2RI20028470, NT2RI20054050, NT2RI20086220,
NTONG20009770, NTONG20013620, NTONG20028070, NTONG20029480, NTONG20029700. NTONG20046140,
 NTONG20048060, NTONG20049910, NTONG20050620, NTONG20050860, NTONG20051530. NTONG20052650,
 NTONG20056570, NTONG20061870, NTONG20063010, NTONG20064400, NTONG20064840. NTONG20065010,
NTONG20066460, NTONG20067090, NTONG20067830, NTONG20070200, NTONG20070340, NTONG20075220,
 NTONG20076930, NTONG20077560, NTONG20083650, NTONG20088620, NTONG20090600. NTONG20090680,
 NTONG20092290. NTONG20092330, OCBBF20068490, SKMUS20001980, SMINT20138900, SPLEN20008390,
 SPLEN20162680. UTERU20134910, ASTRO20155290, FEBRA20080810, NT2RP70032610. NT2RP70036880,
 NTONG20015870. OCBBF20188730, SMINT20122910, SPLEN20099700
 [0294] These genes are involved in cancers.
 [0295] Further, there is a method to search for genes involved in development and differentiation: the expression
 frequency analysis in which the expression levels of genes are compared between developing or differentiating tissues
 and/or cells and adult tissues and/or cells. The genes involved in tissue development and/or differentiation are genes
 participating in tissue construction and expression of function, and thus are useful genes, which are available for re-
 generative medicine aiming at convenient regeneration of injured tissues.
 [0296] Search was carried out for the genes whose expression frequencies were different between developing and/
 or differentiating tissues and/or cells, and adult tissues and/or cells, by using the information of gene expression fre-
 quency based on the database of the nucleotide sequences of 1,402,070 clones shown above.
 [0297] The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA or OCBBF) and
 adult brain (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN or BRTHA) showed that
 the genes whose expression levels were different between the two were the following clones (Tables 16 to 48).
 3NB6910001910, ADRGL20018300, ASTRO20001410, ASTRO20033160, ASTRO20058630, ASTRO20064750,
 ASTRO20100720, ASTRO20141350, ASTRO20145760, ASTRO20181690, BGG|120006160, BRACE20006400,
 BRACE20011070, BRACE20019540, BRACE20027620, BRACE20037660, BRACE20038000, BRACE20038470,
 BRACE20038480, BRACE20038850, BRACE20039440, BRACE20039540, BRACE20050900, BRACE20051380,
 BRACE20051690, BRACE20052160, BRACE20053280, BRACE20053480, BRACE20053630. ERACE20054500,
 BRACE20055180, BRACE20057420, BRACE20057620, BRACE20057730, BRACE20058580, BRACE20058810,
 BRACE20060840, BRACE20060890, BRACE20061050, BRACE20061740, BRACE20062400, BRACE20062740,
 BRACE20063630, BRACE20063780, BRACE20063800, BRACE20063930, BRACE20064880, BRACE20068590,
 BRACE20069090, BRACE20081720, BRACE20082950, BRACE20096200, BRACE20096540, BRACE20097320,
 BRACE20101700, BRACE20101710, BRACE20106840, BRACE20107530, BRACE20108130, BRACE20108880,
 BRACE20109370, BRACE20109830, BRACE20114780, BRACE20115450, BRACE20115920, BRACE20116110,
 BRACE20116460, BRACE20118380, BRACE20121850, BRACE20141080, BRACE20142320, BRACE20147800,
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BRACE20148210, BRACE20148240, BRACE20150310, BRACE20151320, BRACE20152870, BRACE20153680,

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BRACE20154120, BRACE20163150, BRACE20163350, BRACE20165830, BRACE20171240, BRACE20172980,
BRACE20175870, BRACE20177200, BRACE20179340, BRACE20185680, BRACE20188470, BRACE20190040,
BRACE20190440, BRACE20192440, BRACE20195100, BRACE20201570, BRACE20220300, BRACE20223280,
BRACE20223330, BRACE20224480, BRACE20224500, BRACE20228480, BRACE20229280. BRACE20230700,
BRACE20232840, BRACE20235400, BRACE20237270, BRACE20238000, BRACE20240740, BRACE20248260,
BRACE20253160, BRACE20253330, BRACE20257100, BRACE20262930, BRACE20262940. BRACE20266750,
BRACE20267250, BRACE20269200, BRACE20269710, BRACE20273890, BRACE20274080, BRACE20283920,
BRACE20284100, BRACE20286360, BRACE20287410, BRALZ20013500, BRALZ20014450, BRALZ20017430,
BRALZ20018340, BRALZ20054710, BRALZ20058880, BRALZ20059500, BRALZ20064740, BRALZ20065600,
BRALZ20069760, BRALZ20073760, BRALZ20075450, BRALZ20075760, BRALZ20077900, BRALZ20077930,
BRALZ20080310, BRALZ20088690, BRAMY10001300, BRAMY10001570, BRAMY20000520, BRAMY20000860,
BRAMY20002770, BRAMY20004110, BRAMY20011140, BRAMY20025840, BRAMY20039260, BRAMY20045240,
BRAMY20054880, BRAMY20060920, BRAMY20063970, BRAMY20071850, BRAMY20102080. BRAMY20104640,
BRAMY20110640, BRAMY20111960, BRAMY20116790, BRAMY20121190, BRAMY20121620, BRAMY20124260,
BRAMY20134140, BRAMY20135900, BRAMY20136210, BRAMY20137560, BRAMY20144620, BRAMY20147540,
BRAMY20148130, BRAMY20152110, BRAMY20153110, BRAMY20157820, BRAMY20160700, BRAMY20163250,
BRAMY20163270, BRAMY20167060, BRAMY20167710, BRAMY20168920, BRAMY20170140, BRAMY20174550,
BRAMY20178640, BRAMY20181220, BRAMY20182730, BRAMY20183080, BRAMY20184670, BRAMY20195090,
BRAMY20204450, BRAMY20205740, BRAMY20210400, BRAMY20211390, BRAMY20211420, BRAMY20213100.
BRAMY20215230, BRAMY20217460, BRAMY20218250, BRAMY20218670, BRAMY20229800. BRAMY20229840,
BRAMY20230600, BRAMY20231720, BRAMY20240040, BRAMY20245300, BRAMY20247110, BRAMY20247280,
BRAMY20248490, BRAMY20250240, BRAMY20250320, BRAMY20252180, BRAMY20252720. BRAMY20260910,
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FEHRT20003250, OCBBF20189560, BRAWH20029630, CTON620150910, HCHON20007510, HEART20003060, HEART20005410, HEART20021840, HEART20025980, HEART20034320, HEART20037810, HEART20049400, HEART20049410, HEART20049800, HEART20061950, HEART20063340, HEART20067870, HEART20067890, HEART20072310, HEART20074430, HEART20077670, HEART20089940, HEART20090000, HEART20095990, HLUNG10000550, HLUNG20017120, KIDNE20028390, KIDNE20028830, NTONG20029480, OCBBF10001750, PROST20127800, SKMUS20001980, SKMUS20003610, SMINT20026890, SMINT20121220, SMINT20122910, SMINT20183530. SPLEN20008740, SPLEN20027440, SPLEN20162680, STOMA20062290, TESTI20254220, THYMU20271250, TRACH20141240, UTERU20004240 [0299] The result of comparative analysis of cDNA libraries derived from fetal kidney (FEKID) and adult kidney (KIDNE) showed that the genes whose expression levels were different between the two were the following clones (Table 50). ASTRO10001650, ASTRO20108190, BGGI120006160, BRACE20039040, BRACE20060550, BRAMY20102080, BRAWH20004600, BRAWH20125380, BRAWH20162690, BRHIP20115760, BRHIP20205090, BRHIP20238880, CTONG20052650, CTONG20108210, CTONG20128470, CTON620133480, CTONG20139070, D9OST20000310 DFNES20001530, FCBBF10001820, FEBRA20002100, HCHON20008980, HCHON20016650, HLUNG20033780, KIDNE20002520, KIDNE20003940, KIDNE20006780, KIDNE20007210, KIDNE20007770, KIDNE20008010, KIDNE20009470. KIDNE20011170, KIDNE20011400, KIDNE20013730, KIDNE20017130, KIDNE20018730, KIDNE20018970, KIDNE20020150, KIDNE20021680, KIDNE20021910, KIDNE20021980, KIDNE20022620, KIDNE20024830, KIDNE20027250, KIDNE20027950, KIDNE20028390, KIDNE20028830, KIDNE20029800, KIDNE20067330, KIDNE20079440, KIDNE20096280, KIDNE20096470, KIDNE20100070, KIDNE20100840, KIDNE20101370, KIDNE20101510, KIDNE20102650, KIDNE20102710, KIDNE20104300, KIDNE20106740, KIDNE20107390, KIDNE20107500, KIDNE20107620, KIDNE20109730, KIDNE20109890, KIDNE20112000, KIDNE20115080, KIDNE20118580, KIDNE20120090, KIDNE20121880, KIDNE20122910, KIDNE20124400, KIDNE20125630, KIDNE20126010, KIDNE20126130, KIDNE20127100, KIDNE20127450, KIDNE20127750, KIDNE20130450, KIDNE20131580, KIDNE20132180, KIDNE20137340, KIDNE20138010, KIDNE20141190, KIDNE20144890, KIDNE20148900, KIDNE20163880, KIDNE20180710. KIDNE20181660, KIDNE20182690, KIDNE20186780, KIDNE20190740, LIVER20035110, MESAN20025190, NOVAR20000380, NT2RI20054050, NT2RP70043480, PROST20107820, PROST20123530, PROST20161950, PUAEN20030180, SKMUS20003610, SMINT20033400. TBAES20000590, TESTI20044310, TESTI20082330, TRACH20032720, UTERU20099720, BRACE20003070, BRCOC20031870, CTONG20125640, FCBBF30016320, HCHON20002260. HLUNG10000550, PROST20130530, SPLEN20169720, SPLEN20194050, KIDNE20028720 [0300] The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) showed that the genes whose expression levels were different between the two were the following clones (Table 51). BRACE20096200, BRAWH20004600, BRAWH20030250, BRCAN20006390. BRCAN20280360, BRHIP20238880, CTONG10000940, CTONG20103480, CTONG20129960, CTONG20155180. FCBBF10001210, FEBRA20144170, FEBRA20197110, HHDPC20034390, HLUNG20016330, HLUNG20016770. HLUNG20017120, HLUNG20023340, HLUNG20033780, HLUNG20084390, IMR3220002430, LIVER20028420. NOVAR20000380, NT2RI20054050, NT2RI20091730, NT2RP70044280, OCBBF20020830, OCBBF20125530. PLACE60004630, PROST20057930, PROST20107820, PROST20185830, PUAEN20030180, SMINT20121220. SPLEN20002220, SPLEN20054290, SPLEN20128000, SPLEN20157300, SPLEN20176200, SPLEN20179180, SPLEN20211940, STOMA20013890, TBAES20000590, TESTI20094230, TESTI20184620, TESTI20334410. THYMU20000570, THYMU20039810, TRACH20007020, TRACH20141240, TRACH20183170, D9OST20033970. FELNG20002410, HCHON20016650, KIDNE20029800, OCBBF20145760, SPLEN20162680, TESTI20214250. TRACH20005400, HCHON20002260,

HLUNG10000550, NT2RI20023910, SPLEN20008740

[0301] These genes are involved in regeneration of tissues and/or cells.

## EXAMPLE 8

## Expression frequency analysis by PCR

[0302] Specific PCR primers were prepared based on the full-length nucleotide sequences, and the expression frequency was analyzed by the ATAC-PCR method (Adaptor-tagged competitive PCR method: Nucleic Acids Research 1997–25(22) 4694-4696; "DNA Micro-array and Advanced PCR Techniques", Cell Technology, supplement, Eds., Muramatsu and Nawa (Shujunsha, 2000): 104-112). Inflammation-related genes can be identified by revealing the genes whose expression levels are altered depending on the presence of an inflammation-inducing factor. Then, by using THP-1 cell line, which is a cell line of monocyte line, and TNF- $\alpha$ , which is inflammation-inducing factor, suitable for this system, the genes whose expression levels are altered depending on the presence of the factors were searched for by the system.

[0303] THP-1 cell line (purchased from DAINIPPON PHARMACEUTICAL) was cultured to be confluent in RPMI1640 medium (sigma) containing 5% fetal calf serum (GIBCO BRL). Then, the medium was changed with the medium containing 10 ng/ml TNF- $\alpha$  (human recombinant TNF- $\alpha$ : Pharmacia Biotech), and the culture was continued at 37°C under 5% CO<sub>2</sub>. After three hours, the cells were harvested, and total RNA was extracted from them by using ISOGEN reagent (Nippon Gene). The extraction was carried out according to the method in the document attached to ISOGEN reagent. In addition, total RNA was also extracted from the cells cultured without stimulation of TNF- $\alpha$ .

[0304] The genes involved in the onset of gastritis and gastroduodenal ulcer induced by the infection of *Helicobacter pylon* to the op thelia of stomach can be identified by revealing the genes whose expression levels are altered depending on co-culturing the cells with *Helicobacter pylori*. A recent study has suggested that various substances derived from *Helicobacter pylori* trigger the inflammation reaction. In particular, the members belonging to the family of genes called "cag pathogenicity island (cag PAI)" contribute to the activation of the NF-8B pathway (Gastroenterology 2000, 119: 97-108) Further it has been found that cag PAI is involved in the onset of gastritis and the like by the study using an animal model. Journal of Experimental Medicine 2000–192:1601-1610). Then, by using co-culture of a gastric cancer cell line with cag PAI-positive *Helicobacter pylori* (TN2), suitable for this system, the genes whose expression levels are altered depending on the presence of *Helicobacter pylori* were searched for by the system. Further, in order to study the involvement of cag PAI in the alterations of gene expression levels depending on the co-culture with *Helicobacter pylori*. The altered expression levels were compared between the cells co-cultured with a strain of *Helicobacter pylori* (TN2). CagE strain) having a mutation in cagE—which is one of the cag PAI genes, and the cag PAI-positive strain (TN2).

18

15

[0305] A gastric cancer cell line MKN45 (provided by the Cell Bank, RIKEN GENE BANK, The Institute of Physical and Chemical Research) was cultured to be confluent in RPMI1640 medium (sigma) containing 10% fetal calf serum (GIBCO BRL). Then, the medium was changed with the medium containing 100-fold excess (in terms of the number of cells or the number of colonies) of *Helicobacter pylori* (cag PAI positive strain (TN2) and cagE mutant (TN2∆cagE): both were provided by Prof. Omata, Faculty of Medicine. The University of Tokyo), as compared with the number of the cancer cells. The culture was continued at 37°C under 5% CO<sub>2</sub>. After three hours, the cells were harvested, and total RNA was extracted from them by using ISOGEN reagent (Nippon Gene). The extraction was carried out according to the method in the document attached to ISOGEN reagent. In addition, total RNA was also extracted from the cells cultured without *Helicobacter pylori*.

[0306] The analysis by the ATAC-PCR method was carried out basically according to "DNA Micro-array and Advanced PCH Techniques". Cell Technology, supplement (Genome Science Series 1, Eds., Muramatsu and Nawa (Shujunsha 2000) 104-112) Adapter ligation to the internal standard sample (sample to make the calibration curve for the clone of interest) and test sample was carried out in the two separate reaction systems indicated below. The combination of 6 types of adapters (AD-1, AD-2, AD-3, AD-4, AD-5 and AD-6; see the sequences indicated below) and the samples are as follows.

#### Reaction system A

## [0307]

AD1 internal standard, 10-fold

AD2 THP-1 cells unstimulated

AD3 internal standard, 3-fold

AD4 THP 1 cells TNF-r stimulation for one hour

AD5\_THP-1 cells. TNF-α stimulation for three hours

AD6; internal standard, 1-fold

```
Reaction system B
```

45

```
[0308]
       AD1; internal standard, 1-fold
       AD2; MKN45 cells, unstimulated
       AD3; internal standard, 3-fold
       AD4; MKN45 cells, co-cultured with TN2 (Helicobacter pylori)
10
       AD5; internal standard, 10-fold
       AD6; MKN45 cells, co-cultured with TN2\(\triangle\) cagE (cagE gene mutant)
    Adapter sequences:
15
    [0309]
       SEQ ID NO: 4887//5'-GTACATATTGTCGTTAGAACGCG-3'
       SEQ ID NO: 4888//3'-CATGTATAACAGCAATCTTGCGCCTAG-5'
20
       AD2;
       SEQ ID NO: 4889//5'-GTACATATTGTCGTTAGAACGCGACT-3'
       SEO ID NO: 4890//3'-CATGTATAACAGCAATCTTGCGCTGACTAG-5'
25
        AD3;
30
        SEQ ID NO: 4891//5'-GTACATATTGTCGTTAGAACGCGCATACT-3'
        SEQ ID NO: 4892//3'-CATGTATAACAGCAATCTTGCGCGTATGACTAG-5'
        AD4;
        SEQ ID NO: 4893//5'-GTACATATTGTCGTTAGAACGCGATCCATACT-3'
35
        SEQ ID NO: 4894//3'-CATGTATAACAGCAATCTTGCGCTAGGTATGACTAG-5'
        AD5;
        SEQ ID NO: 4895//5'-GTACATATTGTCGTTAGAACGCGTCAATCCATACT-3'
40
        SEQ ID NO: 4896//3'-CATGTATAACAGCAATCTTGCGCAGTTAGGTATGACTAG-5'
        AD6;
        SEQ ID NO: 4897//5'-GTACATATTGTCGTTAGAACGCGTACTCAATCCATACT-3'
```

[0310] The internal standard sample used for this assay was a mixture of total RNAs from tissues (or culture cells; all from UNITECH) of Fetal Brain, Testis, Trachea, and Spleen. RNA was prepared according to the standard method. [0311] The sequences of primers specific to the genes and the names of clones of interest in the analysis are as follows. The gene specific primers were designed to produce the PCR products of 70 to 200 bp. which are derived from the adapter-containing cDNA. The sequence of adapter-specific primer (labeled with fluorescence (FAM)) used in the competitive PCR was GTACATATTGTCGTTAGAACGC (22 nucleotides; SEQ ID NO: 4899). PCR was basically carried out with a cycling profile of preheating at 94°C for 3 minutes, and 35 or 40 cycles of denaturation at 94°C for 30 seconds/annealing at 50°C for 60 seconds/extension at 72°C for 90 seconds.

SEQ ID NO: 4898//3'-CATGTATAACAGCAATCTTGCGCATGAGTTAGGTATGACTAG-5'

[0312] The nucleotide sequences of clone specific primers used in the experiments

[0313] Clone name, primer sequence and SEQ ID NO are indicated below in this order. Each is demarcated by a double slash mark (//). For a clone for which a primer used in Reaction system A (THP-1 cells) was different from a primer used in Reaction system B (MKN45 cells), the sequence of each of the primers was shown.

#### 3NB6920014080//GTCCTGAAGGTAGATGCT//SEQ ID NO: 4900

```
ADRGL20013010//GGAGGATAGAGCTTGGAG//SEQ ID NO: 4901
     ADRGL20067670//ATAAAACAGGACCAAGGA//SEQ ID NO: 4902
     ADRGL20083310//AAATAAGGCTAAAATGGAACT//SEQ ID NO: 4903
10
     ASTRO20032120//AGTGCTCCCAATTATCCG//SEQ ID NO: 4904
     ASTRO20084250//TAGAAAATATGCTGGGTG//SEQ ID NO: 4905
     ASTRO20152140//TCATTCTTCTCCCACAGC//SEQ ID NO: 4906
     ASTRO20166810//AGTTTTATTTCCAGGCTATC//SEQ ID NO: 4907
     ASTRO20181690//ATGGAGAACAGGACAGCT//SEQ ID NO: 4908
     BLADE20004630//CAAACATCAACCAGAGAA//SEQ ID NO: 4909
     BRACE20006400//TCCCAATCAGCTAAGGTC//SEQ ID NO: 4910
20
     BRACE20019540//CAGGTTATCGAGAGTTACAT//SEQ ID NO: 4911
     BRACE20038480//TCTGGTTGGATTTTGTGC//SEQ ID NO: 4912
     BRACE20039040//TGAACTTTGTGGTCTGGT//SEQ ID NO: 4913
25
     BRACE20039440//TGAACAGTGACATTTTAGG//SEQ ID NO: 4914
     BRACE20052160//AAGAATAAAAGGGACGAG//SEQ ID NO: 4915
     BRACE20053630//GTTTGATACAGATGATTAGGTTA//SEQ ID NO: 4916
     BRACE20057620//GGACAGGTAAGAACTAGGC//SEQ ID NO: 4917
     BRACE20058810//ATCATCTTTCCAATCCAG//SEQ ID NO: 4918
     BRACE20060720//GTACCACCTGACCTTCTG//SEQ ID NO: 4919
     BRACE20060840//AGAAGTTTTATCCCACATTT//SEQ ID NO: 4920
     BRACE20061740//(Reaction system A)//TAACATAACCCTCCCGTC//SEQ ID
35
     //(Reaction system B)//ATAGTGGTGACGTTCCCC//SEQ ID NO: 4922
     BRACE20062640//TCTGTTGCTGAAGGAAAA//SEQ ID NO: 4923
     BRACE20063780//TCCTGTGTGCTATTTGAA//SEQ ID NO: 4924
     BRACE20067430//AATAACAGCAACTCCAGA//SEQ ID NO: 4925
     BRACE20090440//CCCAACATTACCAAAAGT//SEQ ID NO: 4926
     BRACE20101700//CAACATTTTCAAGCACTG//SEQ ID NO: 4927
45
     BRACE20114780//GATGTTGGGGTTTGGAAG//SEQ ID NO: 4928
     BRACE20151320//ACCAGCTGCCCATAGAAG//SEQ ID NO: 4929
     BRACE20152870//GAAGGCAAGATGGTAAGT//SEQ ID NO: 4930
     BRACE20163150//CATAGAGAAAGCGGGGAA//SEQ ID NO: 4931
     BRACE20165830//(Reaction system A)//TCTCCCTGTTCTCTTT//SEQ ID
     NO: 4932
     //(Reaction system B)//TATGACCCAAACGCCTAG//SEQ ID NO: 4933
55
     BRACE20201570//CCTTCTCATCTAGCTTGC//SEQ ID NO: 4934
```

```
BRACE20210140//TACTGATTGGGAAGCACT//SEQ ID NO: 4935
      BRACE20223330//GTTGAAATGCTTGAGCAC//SEQ ID NO: 4936
      ERACE20224500//ATTTAGAGCGCCATCCTT//SEQ ID NO: 4937
      BRACE20229280//CTGAGGGTAAAGGAAGGG//SEQ ID NO: 4938
      BRACE20235400//TTTTACGATTGCCTTTGC//SEQ ID NO: 4939
      BRACE20266750//TTAGGAGTGAAGACAGGA//SEQ ID NO: 4940
      BRACE20267250//GTGCAGTGATAAGTGGCT//SEQ ID NO: 4941
      BRACE20269710//AGGCAGGGAAAGTAGGGT//SEQ ID NO: 4942
      BRALZ20C18340//AGGAGAGGCTTGAGGACT//SEQ ID NO: 4943
15
      BRALZ20058880//AAGGGACCAAAATGAGAG//SEQ ID NO: 4944
      BRALZ20059500//AACAGCCCTCTAATGAAA//SEQ ID NO: 4945
      BRALI20064740//ACTCATGTTGCTCCACCT//SEQ ID NO: 4946
      BRAL220069760//TATGTATGGCTTTGAGCA//SEQ ID NO: 4947
20
      BRALZ20075450//GCTGAAGAAATGTGCTGC//SEQ ID NO: 4948
      BRALZ20088690//ATCATAGTTGTACATACTTTGGG//SEQ ID NO: 4949
      BRAMY200C2770//TTCTTTCCTGTAATAGTTGG//SEQ ID NO: 4950
25
      BRAMY200C4110//AGCTATCTGTGAAAGTCCT//SEQ ID NO: 4951
      BRAMY20060920//(Reaction system A)//TGCTGTCTCGTGATAAAG//SEQ ID
      NO: 4952
      //(Reaction system B)//TTTCTAATGGTTTGGCAC//SEQ ID NO: 4953
      BRAMY20103570//(Reaction system A)//TCAACAGTGCTTTTCCTT//SEQ ID
      NO: 4954
      //(Reaction system B)//GACTCTTCTCCAGGGTGC//SEQ ID NO: 4955
35
      BRAMY20144620//CACGCCATTCTGTTAAAA//SEQ ID NO: 4956
      BRAMY20152110//AATGGGCTAAATATTGCT//SEQ ID NO: 4957
      BRAMY20152510//GCAAATACAGGTAAATGACAG//SEQ ID NO: 4958
      BRAMY20163250//CAAGAGAAATTAAAGAAGACC//SEQ ID NO: 4959
40
      BRAMY20153270//(Reaction system A)//TGCTTTCAACTGTCATTT//SEQ ID
      NO: 4960
      //(Reaction system B)//GAATGATGCCCGATGTAG//SEQ ID NO: 4961
45
      BRAMY20168920//GAATATCCCTGTGGAGTC//SEQ ID NO: 4962
      BRAMY20178640//AGTCTCACTCTATTGCCA//SEQ ID NO: 4963
      BRAMY20184670//AACGAATAGCAGGGTAGC//SEQ ID NO: 4964
 50
      BRAMY20204450//GGTGACTTACTGGCTGCA//SEQ ID NO: 4965
      BRAMY20210400//AAGATTAACCATACAACAGAAA//SEQ ID NO: 4966
      BRAMY20215230//TGAACAAGAAACACCAGT//SEQ ID NO: 4967
```

	BRAMY20218670//AGGAGGCACGGTAACAAT//SEQ ID NO: 4968	
	BRAMY20229800//GTCTTCTGTCTCATGGGG//SEQ ID NO: 4969	
5	BRAMY20229840//AAAGTTCATGAGGGGCTG//SEQ ID NO: 4970	
	BRAMY20231720//CAGCACAAAATCAGTTAAA//SEQ ID NO: 4971	
	BRAMY20247280//GGTTTAGATTTATGAGACAAGA//SEQ ID NO: 4972	
10	BRAMY20261680//GTTACTGCAGGGCTTCAG//SEQ ID NO: 4973	
	BRAMY20266850//TGCATGGAATTAAGGAGT//SEQ ID NO: 4974	
	BRAMY20267130//AATCTGTAAAATGGGAATAAG//SEQ ID NO: 4975	
	BRAMY20277140//(Reaction system A)//ATGAGATTGTGTCCA//SEQ	ΙD
15	NO: 4976	
	//(Reaction system B)//TTCCAGCATTTTCGTTTT//SEQ ID NO: 4977	
	BRAMY20280720//(Reaction system A)//TTCCCAAGTCCAGATTTT//SEQ	ΙD
20	NO: 4978	
	<pre>//(Reaction system B)//CTGAGGAGCAGTGACAAG//SEQ ID NO: 4979</pre>	
	BRAWH10000930//GGGAGAGAGAGTCCTGC//SEQ ID NO: 4980	
	BRAWH20015350//GCTATGAAGACAACCAAACT//SEQ ID NO: 4981	
25	BRAWH20017010//AGGAAGAGATGGGTCAGC//SEQ ID NO: 4982	
	BRAWH20029630//GGAGTATCACCATGTAAAGA//SEQ ID NO: 4983	
	BRAWH20100690//(Reaction system A)//AAATGAGCACTCCATTCC//SEQ I	(D
30	NO: 4984	
	//(Reaction system B)//AATGAGCACTCCATTCCC//SEQ ID NO: 4985	
	BRAWH20106180//(Reaction system A)//CATTTTATTGTCACCCAC//SEQ I	.D
35	NO: 4986	
<b>.</b>	//(Reaction system B)//CCTTTAACAGCATCTCTAGTG//SEQ ID NO: 4987	
	BRAWH20107540//GTTGAGCTATTTGCAGAG//SEQ ID NO: 4988	
	BRAWH20110660//CTTAGCAACTTTCCACAC//SEQ ID NO: 4989	
40	BRAWH20118230//GTCAGAAAACTCACACCA//SEQ ID NO: 4990	
	BRAWH20122770//AAGTTGATAGGGAAGGTTT//SEQ ID NO: 4991	
	BRAWH20126190//ACCATGTGCTCAGAATCA//SEQ ID NO: 4992	
<b>4</b> 5	BRAWH20132190//TAAGATTCACAGGGTGGA//SEQ ID NO: 4993	
	BRAWH20138650//GATGGAAAATGTAAGGCT//SEQ ID NO: 4994	
	BRAWH20139410//CCATCCTCTACACAGCAG//SEQ ID NO: 4995	
	BRAWH20155950//(Reaction system A)//CTCTCATTTTGGCTCTGC//SEQ I	ע.
50 ·	NO: 4996	
	//(Reaction system B)//CTACTCCACCTCTGCTGC//SEQ ID NO: 4997	
	BRAWH20158530//AGTTTTCTGATGGCCTTG//SEQ ID NO: 4998	

```
BRCAN20060190//AGGTAGCCCCAGAGTCAC//SEQ ID NO: 4999
     BRCAN20147880//ACTCAGCAATCAGGTCCA//SEQ ID NO: 5000
     BRCAN20273340//AATTATGAGATAGGATGTTAGCT//SEQ ID NO:5001
     BRCAN20273640//CTGCACCGATTTTATAGC//SEQ ID NO: 5002
     BRCAN20275130//CACTATCCAGACACCCT//SEQ ID NO: 5003
     BRCAN20280210//CACTGGATTTTCTTCACTT//SEQ ID NO: 5004
10
     BRCAN20280400//GGAAGGATAGCAGTTGAT//SEQ ID NO: 5005
     BRCOC20021550//TCCAAGCAGAGTTTTCAC//SEQ ID NO: 5006
     BRCOC20037400//CAAGTCTGTTCATCTGGT//SEQ ID NO: 5007
     BRCOC20105100//(Reaction system A)//ACTTGAGGTTTCTTGGCA//SEQ ID
15
     NO: 5008
     //(Reaction system B)//GATTCTTCCCCGACTCAG//SEQ ID NO:5009
     BRHIP10001740//GTACACACCTGCTCCCAC//SEQ ID NO: 5010
20
     BRHIP20001630//GGTCAGTAAGTGGTTGTG//SEQ ID NO: 5011
     BEHIP20096170//TTATTTTGGATGCCCCTG//SEQ ID NO: 5012
     BRHIF: 0103090//ACTCCAACAACCTTCATT//SEQ ID NO: 5013
     BRHIP20105710//TTTCAAGTATCCTCCCCA//SEQ ID NO: 5014
     BEHIP20110800//TAGAACTGCCTCCAACCC//SEQ ID NO: 5015
     PEHIP20111200//TACTGAACGGTGACTGGC//SEQ ID NO: 5016
     BEELP: 0118910//ACAGGAAGGGGAAAGAGT//SEQ ID NO: 5017
30
     BPHIP10129720//GAGGAGAGTGAGAAGGGG//SEQ ID NO: 5018
     BREID10143860//AGGTCAGGAGAACAAGCC//SEQ ID NO: 5019
     5PHIP?0173150//CTTTTGCAGAGTTTTCCT//SEQ ID NO: 5020
     BEHIP20175420//TCTCTAGGGCAAAACATT//SEQ ID NO: 5021
35
     EIHIF20186120//(Reaction system A)//AATTGATACGCAGGGGAG//SEQ ID
      //(Reaction system B)//AAGGTCAGTTGAAGTGCT//SEQ ID NO:5023
40
     ERHIP20194940//TAGAGAAGGTGAGGCCAG//SEQ ID NO: 5024
     BRHIP20196410//GGCATAGAAGTAATCAGAGA//SEQ ID NO: 5025
     BRHIP20207430//AAGCTGAACCCCAATAAA//SEQ ID NO: 5026
     BPHIP20218580//GATTACCAGAACACAGCC//SEQ ID NO: 5027
     BRHIP20233090//GTCCATTTACCAACGGCT//SEQ ID NO: 5028
     BRH1P202848CO//CACATCTTTACATTTATTGCTATT//SEQ ID NO: 5029
     BRHIP30004880//TCTTCTCGTAGGGCTTGA//SEQ ID NO: 5030
     BRSSN20046570//AAACACGAAATGGATGAA//SEQ ID NO: 5031
     BRSSN20142940//AGAATCAGAGAAGCCGGT//SEQ ID NO: 5032
```

```
BRSSN20152380//ATACCCATTTCAGTTCCT//SEQ ID NO: 5033
      BRSSN20176820//CAGTCCCAATACAGCTCA//SEO ID NO: 5034
      BRSSN20187310//(Reaction system A)//CAATGACTAGTTTGTGCA//SEQ ID
      //(Reaction system B)//AAAGAAGCCAGGAAGATT//SEQ ID NO: 5036
      BRTHA20046390//ACATGGAGCCTGGTTTAG//SEQ ID NO: 5037
      CD34C30004240//TGGAAGATACGGATAACTC//SEQ ID NO: 5038
      CD34C30004940//(Reaction system A)//ACCACTGTTCTCTGGTGC//SEQ ID
      NO: 5039
15
      //(Reaction system B)//CCACCACTGTTCTCTGGT//SEQ ID NO: 5040
      COLON20043180//TCGGATTGGGTTAAGGTC//SEQ ID NO: 5041
      CTONG10000620//CTCCATTCATCAGACCAC//SEQ ID NO: 5042
      CTONG20014280//TCCAAAAGACAGAACAGC//SEQ ID NO: 5043
      CTONG20095270//GTTTGTTCCCTGCTCAC//SEQ ID NO: 5044
      CTONG20095290//AACACAGCTCAACAACTC//SEQ ID NO: 5045
      CTONG20096750//TGACTAAGCATGGAGACT//SEO ID NO: 5046
25
      CTONG20100240//AGTCATAATCATCTTCCTCA//SEQ ID NO: 5047
      CTONG20103480//GGTGGAGTAATGTATATAACGTAA//SEQ ID NO: 5048
      CTONG20105660//CCATTAACACAAACCAAA//SEQ ID NO: 5049
30
      CTONG20121010//GGAAGATGGGACCTCAGT//SEQ ID NO: 5050
      CTONG20128470//TTGGGGTATCTTGGAGCT//SEQ ID NO: 5051
      CTONG20138030//GGCATAGAAGTAATCAGAGA//SEQ ID NO: 5052
      CTONG20139070//TCAAACCTCCTATCTTCTG//SEQ ID NO: 5053
35
      CTONG20146970//TTTTAATCCTCAGTACATTTTC//SEQ ID NO: 5054
      CTONG20158150//AAATAGGTTGATGTTGGC//SEQ ID NO: 5055
      CTONG20186320//TGACTTTGGCCCTTTACC//SEQ ID NO: 5056
      CTONG20265130//GGGTAGGTGCTAGAAATC//SEQ ID NO: 5057
      D3OST20006540//GGAGACCACACATAACAT//SEQ ID NO: 5058
     D3OST20037970//CACTGACGAAAGGGAAGA//SEQ ID NO: 5059
     D9OST20031370//CGACTTGCCAGACTCACT//SEQ ID NO: 5060
45
     DFNES10001850//GTGGCTCAAAGTAGGATT//SEQ ID NO: 5061
     DFNES20031920//CTTACTCCAACCCAGGCT//SEQ ID NO: 5062
     FCBBF10005060//TGCATGTTTTCTTCCTCA//SEQ ID NO: 5063
50
     FCBBF20032970//CCAGACAACAATACCA//SEQ ID NO: 5064
     FCBBF20035280//(Reaction system A)//ATACAATTTGTGCCTGTTA//SEQ ID
     NO: 5065
```

151

```
//(Reaction system B)//CGGTAAGTAGTCTTCATGTG//SEQ ID NO: 5066
     FCBBF20054280//GGTGCATCTGTACTTGAA//SEQ ID NO: 5067
     FCBBF20071860//TGGAGGAGTAGTTATCAGTTG//SEQ ID NO: 5068
     FCBBF30001840//AGTGCTCCCAATTATCCG//SEQ ID NO: 5069
     FCBBF30016320//GGCTACTCAAGGACACAG//SEQ ID NO:5070
     FCBBF30016570//AGGGATAAGATGGCAGGT//SEQ ID NO:5071
10
     FCBBF30033050//TCCTGTACTCCTTTCCAT//SEQ ID NO: 5072
     FCBBF30071520//CAGGCATAAGAGGTGGCT//SEQ ID NO: 5073
     FCBBF30083820//CCTGTGTGATACCAAATACT//SEQ ID NO: 5074
15
     FCBBF30215060//CAGCCCCAATTACTAGAA//SEQ ID NO: 5075
     FCBBF30251420//AGCATGTACTGGGAAAGC//SEQ ID NO: 5076
     FCBBF30252520//AGGGATAAAGAATGCAAA//SEQ ID NO:5077
     FCBBF30262360//GAGCTTCAGGGGCATTTA//SEQ ID NO: 5078
20
     FCBBF30266920//ATACGCAATTTTCAGACC//SEQ ID NO: 5079
     FCBBF30273630//AAAAGACAACGATGCCTG//SEQ ID NO:5080
     FCBBF30285280//AAAGCAAAGTGATATAGGAGT//SEQ ID NO: 5081
25
     FCBBF40001420//ACATTTCAGTCCATTCAC//SEQ ID NO: 5082
     FEBRA10001830//TTGTCATGGTGGTAATCC//SEQ ID NO: 5083
     FEBRA20010120//GGACCAGACTCACAAATT//SEQ ID NO: 5084
     FEBRA20017050//TATACTAAAACCCAGCCA//SEQ ID NO: 5085
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     FEBRA20034360//CGGCAGCTAGAAAACCTC//SEQ ID NO: 5086
     FEBRA20037260//CGTTGGTTTTCTGGACAC//SEQ ID NO: 5087
     FEBRA20037500//CTCGGGCAGGATTAACTC//SEQ ID NO: 5088
35
     FEBRA20082100//AGAAGATGCTAGGTTTGC//SEQ ID NO: 5089
     FEBRA20095880//AGCATGTACTGGGAAAGC//SEQ ID NO: 5090
     FEBRA20167390//GCTTATGTTGCAGTTTCA//SEQ ID NO: 5091
     FEBRA20176800//TCAGTTTCAGGGGTCAAG//SEQ ID NO: 5092
40
     FEBRA20226010//TCAGGGTATCAGCTTTCC//SEQ ID NO: 5093
     HCASM10000500//TGTGGTGACTTACTGCCT//SEQ ID NO: 5094
     HCHON20002260//CTCTCCAACAAACTGCAC//SEQ ID NO: 5095
45
     HCHON20008980//CTGCTGCCTTACACAACC//SEQ ID NO: 5096
     HCHON20009350//AGGTAATGAGGAATGCAC//SEQ ID NO: 5097
     HCHON20010990//GATTCCACCCTCAAGATT//SEQ ID NO: 5098
     HCHON20011160//CTCCTCCACGCTTGTTTT//SEQ ID NO: 5099
50
     HCHON20015230//CTTGGTCACAGTTTTCAT//SEQ ID NO: 5100
      HCHON20022470//CACACTTTCAATCCGAGG//SEQ ID NO: 5101
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HCHON20035130//GTGGAAGATGCTCGACTG//SEQ ID NO: 5102
      HCHON20043590//AGGATTAGGTATTGCTTCTC//SEQ ID NO: 5103
      HCHON20067220//TAAGGAAAACCCAACCAC//SEQ ID NO: 5104
      HCHON20076500//GAAAGACACCTGGCACAC//SEQ ID NO: 5105
      HEART20021840//GTACCCCAAAAGAAACAT//SEQ ID NO: 5106
      HEART20067870//GAACTATCTAATCACATGGG//SEQ ID NO: 5107
10
     HEART20083640//(Reaction system A)//TCTTGATGTCTCCTGCCT//SEQ ID
     NO: 5108
      //(Reaction system B)//CTCGGCTGGAAGGTAAAA//SEQ ID NO:5109
     HHDPC10000650//ACTGGTAAGATATGGGCA//SEQ ID NO: 5110
     HHDPC20034390//CTCTCCCAAACTCAGGTC//SEQ ID NO: 5111
     HHDPC20095280//TGACCCAAAGACATACTG//SEQ ID NO: 5112
     HLUNG10000550//GATTTACTTCCGGTTTCG//SEQ ID NO: 5113
20
     KIDNE20018970//AAGAGAATAAGGCTGGGC//SEQ ID NO:5114
     KIDNE20028720//AACAAAATAAGGGGCCAG//SEQ ID NO: 5115
     KIDNE20079440//AAGTTCATCTGGGTGTGG//SEQ ID NO: 5116
     KIDNE20096470//ATCACCTGGAGAGCTTTG//SEQ ID NO: 5117
     KIDNE20106740//AGGGACACTGAGAACTGG//SEQ ID NO: 5118
     KIDNE20120090//GAAGCAGGGAAGTGTGAG//SEQ ID NO: 5119
     KIDNE20127750//GCTATTACACATTCTGCATT//SEQ ID NO: 5120
30
     KIDNE20130450//CAGCTACTTGGGACAGGA//SEQ ID NO: 5121
     KIDNE20132180//(Reaction system A)//ACCAGCTCAGCAAGAACT//SEQ ID
     NO: 5122
35
     //(Reaction system B)//CTCTGACATGAACTGGTG//SEQ ID NO: 5123
     KIDNE20141190//CACATTGCCTAGAGAAAG//SEQ ID NO: 5124
     KIDNE20148900//ACAACAGCAGATGACTCG//SEQ ID NO: 5125
     KIDNE20163880//CAGTCACATCTCCCTTTA//SEQ ID NO: 5126
40
     KIDNE20182690//TCACTGTATCACCATCTG//SEQ ID NO: 5127
     LIVER10004790//TCCCTGCTAAGATGTTGA//SEQ ID NO: 5128
     LIVER20011130//GAGGTCAAGGACACAG//SEQ ID NO: 5129
     LIVER20038540//(Reaction system A)//AAGCAATGTGGCAGACTC//SEQ ID
     NO: 5130
     //(Reaction system B)//AGTGGGTTCTTTATCATTTT//SEQ ID NO: 5131
     LIVER20055440//GTTTGCCAGGGAATGTTT//SEQ ID NO: 5132
     LIVER20062510//GTAACGTGCTCTGAATGA//SEQ ID NO: 5133
     LIVER20085800//GCTCTGCTGTTTCTAATTT//SEQ ID NO: 5134
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MAMGL10000830//TCGATACGTGGAAGAATT//SEQ ID NO: 5135
     MESAN20031900//TCCCAAGGCTGTAGTTCA//SEQ ID NO: 5136
     MESAN20121130//AGCTTGTATCTAAATTCGTG//SEQ ID NO: 5137
     MESAN20127350//CAGAAGACAGGTTGCCAG//SEQ ID NO: 5138
     MESAN20130220//CCTAAGATTGGTCGTCCT//SEQ ID NO: 5139
     MESAN20154010//ATCCTGTCATCTTTTCGC//SEQ ID NO: 5140
10
     MESAN20174170//TGGCTAAGGTTCTCAGGA//SEQ ID NO: 5141
     NOVAR10001020//GGGTCAGTAAATCTAATGC//SEQ ID NO: 5142
     NT2NE20053580//CAAAACACAGAGTTATCAGAA//SEQ ID NO: 5143
15
     NT2NE20089610//TGCTGTCCTAGAAGAATAAA//SEQ ID NO: 5144
     NT2NE20089970//ACAATTATACTGGAAAAGCA//SEQ ID NO: 5145
     NT2NE20146810//GCTGAGACCTTTTGCTAG//SEQ ID NO: 5146
     NT2NE20155110//AGCCGAGGTTTTGAGTTA//SEQ ID NO: 5147
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     NT2NE20156260//ACATTTGCACTGGAACTG//SEQ ID NO: 5148
     NT2NE20158600//CTCAGAAGCCCAGCAATT//SEQ ID NO: 5149
     NT2NE20172590//ACATCATAATCAAGCAGTAAA//SEQ ID NO: 5150
25
     NT2NE20174920//AGGACAGCAACAAGAGAG//SEQ ID NO: 5151
     NT2NE20181650//AGAGCTGATTTATACGCA//SEQ ID NO: 5152
     NT2RI20005750//AAGGAGTCTACGAAGCAC//SEQ ID NO: 5153
     NT2RI20009870//AAGATGACCCCGAGTTTG//SEQ ID NO: 5154
30
     NT2RI20023160//CATGCAAATAGAGGACTG//SEQ ID NO: 5155
     NT2RI20040930//CCATACTGTTCTCTGCTG//SEQ ID NO: 5156
     NT2RI20046080//CCGTAACTTTTATATGCCTG//SEQ ID NO: 5157
35
     NT2RI20055790//GCAAGAGCTACAGACAAA//SEQ ID NO: 5158
     NT2RI20069730//AGTGTGCAGAAATCCGTG//SEQ ID NO: 5159
     NT2RI20203900//AGCAGTAGCACAGCCTTA//SEQ ID NO: 5160
     NT2RP70062230//(Reaction system A)//ACTCTAACACATTTGGCA//SEQ ID
40
     NO: 5161
     //(Reaction system B)//TATTAGTGTGAGCTGGCA//SEQ ID NO: 5162
     NT2RP70102350//(Reaction system A)//ATAGGAGGTGTCATGCCC//SEQ ID
45
     NO: 5163
     //(Reaction system B)//TCTTTTGACCTACACTGC//SEQ ID NO:5164
     NT2RP70110860//GGGGAAGGGAGTAAGGTC//SEQ ID NO: 5165
     NT2RP70111320//ACTTAGCATCCAGACCTC//SEQ ID NO: 5166
     NT2RP70130020//ATACTCTCTGCTCATGGA//SEQ ID NO: 5167
     NT2RP70143480//TTCTTGGCATCCTTCATT//SEQ ID NO: 5168
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NT2RP70150800//(Reaction system A)//GAGGCTTGTCTAGGGGAA//SEQ ID
      NO: 5169
      //(Reaction system B)//GAACAAGGGATGCAGGAT//SEQ ID NO: 5170
      NT2RP70157890//(Reaction system A)//TATGTGATGTTTTCCCCA//SEQ ID
      NO: 5171
      //(Reaction system B)//CTGCCTAAATAACACTGAAG//SEQ ID NO: 5172
      NT2RP70169110//CTGTCCTCATCTGTGCAT//SEQ ID NO: 5173
      NT2RP70175670//GGTAGAACGGGAAATCAT//SEQ ID NO:5174
      NT2RP70188020//AGGTTTGAGTAGAGGGAA//SEQ ID NO: 5175
      NT2RP70188710//ATACAGCAGGGAAGAGGC//SEQ ID NO: 5176
      NT2RP70190640//CAATGTGTCTTCAGTTTCC//SEQ ID NO: 5177
      NTONG20029480//TCTTGATGTCTCCTGCCT//SEQ ID NO: 5178
      NTONG20064840//AAAGCCATCGTACACCAT//SEQ ID NO: 5179
      NTONG20067090//AATTCTTTAGCTCTGTTGC//SEQ ID NO: 5180
      NTONG20070340//ATCCACTGCCCCTTATCA//SEQ ID NO: 5181
      NTONG20077560//CTGCTAGAATACGCCTTA//SEQ ID NO: 5182
25
      NTONG20083650//CTCATAGTTCAAGGCAGC//SEQ ID NO: 5183
      NTONG20090680//GAGTAAGGTCGTAGTCAGTG//SEQ ID NO: 5184
      OCBBF20005230//GCAAGAGCTACAGACAAA//SEQ ID NO: 5185
      OCBBF20019380//GTGGTCAGTGGAAAATGG//SEQ ID NO:5186
      OCBBF20020150//GGGACAGTATGGCAGAGA//SEQ ID NO: 5187
      OCBBF20020830//GCTTGCCATAGGTGTACT//SEQ ID NO: 5188
      OCBBF20039250//TTTCAGCAGTTAAGTGTTTT//SEQ ID NO: 5189
      OCBBF20041680//TCAGAAGGTATGCCCACT//SEQ ID NO: 5190
      OCBBF20047570//ACCCTTATGTCAAACTGC//SEQ ID NO: 5191
      OCBBF20051610//TTTTCCTACCTGCAATGG//SEQ ID NO: 5192
     OCBBF20054200//GTCAGAAGCCATACGTGC//SEQ ID NO: 5193
     OCBBF20061720//CAAAGTGGCCTAAACCCT//SEQ ID NO: 5194
     OCBBF20062140//CTGGGGAGATAAGAGCCT//SEQ ID NO: 5195
     OCBBF20071960//(Reaction system A)//CTCAGTCACGCAATAGAT//SEQ ID
45
     NO: 5196
     //(Reaction system B)//TCTCTGGAAGGGAAAATT//SEQ ID NO: 5197
     OCBBF20072320//AAGAAGGAATGGGCACAC//SEQ ID NO:5198
     OCBBF20079310//CAGTAGCAAAACCAGAGC//SEQ ID NO: 5199
50
     OCBBF20081380//GTGGAAGTGCCTGATGAG//SEQ ID NO:5200
     OCBBF20085200//TACAGGGTCAGTTGGCAG//SEQ ID NO: 5201
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155

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OCBBF20094240//ACACAATTCATCACTGCT//SEQ ID NO: 5202
     OCBBF20107920//GGTTGCTGTGAGTGCATT//SEQ ID NO: 5203
     OCBBF20127040//TAGAGGAGGCAGTAAGGG//SEQ ID NO: 5204
     OCBBF20130110//AGTGTCTATGGCTCTTCC//SEQ ID NO: 5205
     OCBBF20139260//GGGTGGTTCTGTTAGGAG//SEQ ID NO: 5206
     OCBBF20164050//TGCTGGAAATAATCGCTT//SEQ ID NO: 5207
10
     OCBBF20178990//TGAGTGTGGTGAAGATAGT//SEQ ID NO: 5208
     OCBBF20180840//AGAAACCTGAACGATGTC//SEQ ID NO: 5209
      PEBLM10000240//ATTACGATGCTTTGTTCA//SEQ ID NO: 5210
15
      PEBLM20013120//TAAAATTCTTGTGGTTGG//SEQ ID NO: 5211
      PEBLM20024550//TTGTGCCCTTAGAAAATC//SEQ ID NO: 5212
      PEBLM20052820//CCTGATAACCATGAATTG//SEQ ID NO: 5213
      PEBLM20074370//AGCATTTGGTTTTATACTGTTA//SEQ ID NO: 5214
20
      PERIC20002140//CGTTACCATCACAATTTCA//SEQ ID NO: 5215
      PERIC20004780//ACTTGAGCAGAGGAGAGC//SEQ ID NO: 5216
      PLACE60003480//ACTGGTATTTGCTGTGAA//SEQ ID NO: 5217
25
      PLACE60136720//AGGAACAGAGGCTACATC//SEQ ID NO: 5218
      PLACE60155130//GTCTAGCTGGGATGATGG//SEQ ID NO: 5219
      PLACE60169420//AAGACCCCGATAGAGAGC//SEQ ID NO: 5220
      PLACE60181070//CCTTCTTCAGTCTTGCAC//SEQ ID NO: 5221
30
      PROST10004800//AGTTTTGTTCACCCCTCC//SEQ ID NO: 5222
      PROST20120160//TAGAATGGTGGGAAGTGG//SEQ ID NO: 5223 -
      PROST20144220//TTAGTGGTCTGTTGATAGTTTT//SEQ ID NO: 5224
35
      PROST20149160//TTGGGCTTAGGTGAGTCC//SEQ ID NO: 5225
      PROST20149250//GGTACATAAGGAATCGCT//SEQ ID NO: 5226
      PROST20151240//(Reaction system A)//ACTCTCGCTTCCTGTCAC//SEQ ID
 40
      NO: 5227
      //(Reaction system B)//GACGGACCCTTGACATTA//SEQ ID NO: 5228
      PROST20153320//ACTGTGGAGAAGGAGGGA//SEQ ID NO: 5229
      PROST20161950//ATTTGACGTATCCATGCC//SEQ ID NO: 5230
 45
      PROST20189770//TGGTAAGTGGTGGAAGCT//SEQ ID NO: 5231
      PUAEN20003740//CCAAAACAATAATCCAACAT//SEQ ID NO: 5232
      PUAEN20011880//AGCCGTTGTCATCATAGA//SEQ ID NO: 5233
      PUAEN20015260//ATTGGAAGTCCCTATGAT//SEQ ID NO: 5234
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      PUAEN20025680//CTCCTCTGAAGTAGCTGC//SEQ ID NO: 5235
       PUAEN20040670//AATGGTTCTCTGGCTTGG//SEQ ID NO: 5236
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PUAEN20045250//CAAAATGGTTAAACACAAA//SEQ ID NO: 5237

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PUAFN20078980//AGAAAGGCACACAATAAA//SEQ ID NO: 5238
     PUAEN20085150//AATTTAGGGGAACTGAGTAC//SEQ ID NO: 5239
     SKMUS20018230//TTCGCTCTTATCACCCAG//SEQ ID NO: 5240
     SKMUS20023210//ACTTGCCTTGGAATTGCT//SEQ ID NO: 5241
     SKMUS20031680//CAGAAGAACAGGAGGCAC//SEQ ID NO: 5242
10
     SKMUS20046670//GCAACGTCTTACTGTGAA//SEQ ID NO: 5243
     SKNSH20062340//GACATTGACGTATTCTAACTG//SEQ ID NO: 5244
     SKNSH20080430//TACCCTCCGCTGTGTTAG//SEQ ID NO: 5245
     SMIRT20001750//CTCCTCCAGCTCTTGTCC//SEQ ID NO: 5246
     SMINT20013430//GGCACGTTTTAATATACCAC//SEQ ID NO: 5247
     SMINT20014530//CCCTCCAGACAGTTCAAA//SEO ID NO: 5248
     SMINT20033400//CGATGGGTAGGACTTAAA//SEQ ID NO: 5249
20
     SMINT20047810//(Reaction system A)//CTCCTGACATTTCCTTTT//SEQ ID
     NO: 5250
     //(Reaction system B)//TAGGAAAAGAAGCAGGGC//SEQ ID NO: 5251
25
     SMINT20051610//AGTGAGGTTAGGGAAATATC//SEQ ID NO: 5252
     SMINT2005:210//TATTCCTGTTTGATGGGG//SEQ ID NO: 5253
     SMINT20060780//TCTGTAATAGGGAGGTGTC//SEQ ID NO: 5254
     SMINT2008C540//GAGGTACTTTTCAGACAGG//SEQ ID NO: 5255
     SMINT20105000//(Reaction system A)//AAAATGAGGTTCAGTCCC//SEQ ID
     //(Reaction system B)//TCACCTCCCCATTAACTG//SEQ ID NO: 5257
     SMINT20108530//CACCCTCGTTTTCTTTAG//SEQ ID NO: 5258
     SMINT20122850//AGCTAAATCCACTGAGGT//SEQ ID NO: 5259
     SMINT20122910//GGACAGACTTGCAGAGAA//SEQ ID NO: 5260
     SMINT20153530//GGGCCTAGAGTGGAAGTG//SEQ ID NO: 5261
     SMINT20161220//AGAACCAGTCCAAGCCAT//SEQ ID NO: 5262
     SMINT20163960//TTGATAAAATAGAGCCCA//SEQ ID NO: 5263
    SMINT20154770//AGTGTGCAGAAATCCGTG//SEQ ID NO: 5264
    SMINT20168570//(Reaction system A)//TGGTCCTCATGGTACAGC//SEQ ID
    NO: 52€5
    //(Reaction system B)//ATGGCTGCTAGCTTGTCA//SEQ ID NO: 5266
    SPLEN20008320//CTGTCTGCCCTGAATCTT//SEQ ID NO: 5267
    SPLEN20011410//TTTTGGGACTGGAAGGAG//SEQ ID NO: 5268
    SPLEN20013540//TCACTCACACCAATCCTG//SEQ ID NO: 5269
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SPLEN20019450//TTCGTAAACATCTGGGCA//SEQ ID NO: 5270
      SPLEN20022230//AAGTTGCACCCAGACATC//SEQ ID NO: 5271
      SPLEN20040600//TCTTATTTCACAGTTTCCA//SEQ ID NO: 5272
      SPLEN20076530//CCCCACAGAACACTTACT//SEQ ID NO: 5273
      SPLEN20101190//AGACGTAGCAGCAACTCC//SEQ ID NO: 5274
      SPLEN20126190//TAGACCCAACCCTCACAC//SEQ ID NO: 5275
10
      SPLEN20152760//TGAGACGAATTGGTAAAA//SEQ ID NO: 5276
      SPLEN20157300//CTTGACATTTGCTCTCCA//SEQ ID NO: 5277
      SPLEN20158990//AAAACTGGGTCAAATAAAA//SEQ ID NO: 5278
15
      SPLEN20163560//TGCCCAGATAGAAAAGTG//SEQ ID NO: 5279
      SPLEN20174260//GGCCTTGTTGAATCTGAA//SEQ ID NO: 5280
      SPLEN20211570//CTCAACACACACTCCAAGC//SEQ ID NO: 5281
      SPLEN20214580//CCAAACGAATGTCAAGCT//SEQ ID NO: 5282
20
      SPLEN20245300//ATCTGCTCTTCATCCCTT//SEQ ID NO: 5283
      SPLEN20279950//CCTGTTCCTAGACCGCAT//SEQ ID NO: 5284
      SPLEN20280660//GGCCAGACAGGAAGAGTT//SEQ ID NO: 5285
25
      SPLEN20283650//AAGTTGATGCTCCTGTTG//SEQ ID NO: 5286
      SPLEN20329240//(Reaction system A)//TAACACATGGACTGCTGG//SEQ ID
      NO: 5287
      //(Reaction system B)//AAGGTAGGAAATGCCAGC//SEQ ID NO:5288
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      STOMA20010250//TTTTGACCATAAGCTCCT//SEQ ID NO: 5289
      STOMA20032890//CGAGAAATAACTAATACACCTG//SEQ ID NO: 5290
      STOMA20048520//GAGGGTGAAGCAGGTAGG//SEQ ID NO: 5291
35
      STOMA20057820//GGCATTTCCCTTGTATATT//SEQ ID NO: 5292
      STOMA20062290//CCGTGTATTCAGCTCCCT//SEQ ID NO: 5293
      STOMA20076800//TAAACGGGAATCAGGAAG//SEQ ID NO: 5294
      TESTI20001170//TTTCAGACATATCAAGTTCA//SEQ ID NO: 5295
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      TESTI20002780//ATTCCAGCCATACGGTTA//SEQ ID NO: 5296
      TESTI20004890//AAAACCACAGGAAGAAAG//SEQ ID NO: 5297
      TESTI20011200//TACAAGTTCACCTGCATT//SEQ ID NO: 5298
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      TESTI20018230//AACCACTCAGCAGAAAGA//SEQ ID NO: 5299
      TESTI20035960//TGTCCATAGAGCCAGTTA//SEQ ID NO: 5300
      TESTI20038270//GTTCTGTTGGAGGTGCTG//SEQ ID NO: 5301
      TESTI20044230//AGGTCTTTTGTGTGCTGA//SEQ ID NO: 5302
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      TESTI20046750//GTAGTTGTCCTGCATGGC//SEQ ID NO: 5303
      TESTI20060400//GGCCAGGATACTACACTT//SEQ ID NO: 5304
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TESTI20066770//AACTGGCATTGGAGACCT//SEQ ID NO: 5305
     TESTI20076850//TTGGTTTGTGATGTTAAGT//SEQ ID NO: 5306
     TESTI20083940//TTTGTCTTCCGGTAGTTA//SEQ ID NO: 5307
     TESTI20087620//TGCCACTCTTGAAAACTC//SEQ ID NO: 5308
     TESTI20098530//TCCATTACACAACAGCCT//SEQ ID NO: 5309
    TESTI20105720//GGCAGACTTGTTTGAGCT//SEQ ID NO:5310
10
     TESTI20108720//TAGTTCTGTTGAGGCCCC//SEQ ID NO:5311
     TESTI20123080//(Reaction system A)//CCTGTTTCTTCCTGAA//SEQ ID
     NO: 5312
     //(Reaction system B)//CTAAGTCCAGAAGCCTCG//SEQ ID NO:5313
     TESTI20128350//ATACCATGCTCCAACACC//SEQ ID NO: 5314
     TEST120136100//TTCACTTTTGTTCTCCAG//SEQ ID NO: 5315
     TESTI20137670//CCTCCACTCTTCCTGTTG//SEQ ID NO: 5316
20
     TESTI20143240//CTAAGAAGTCCTGGTTGG//SEQ ID NO: 5317
     TESTI20143620//(Reaction system A)//TTTTGTCTGAATTTGGAA//SEQ ID
     NO: 5318
     //(Reaction system B)//TGTAGAAAGCCTAACCCC//SEQ ID NO:5319
     TESTI20156100//ACTGGGCACATTCATAAA//SEQ ID NO:5320
     TESTI20161970//GTTCTATGCCTTGAGCCT//SEQ ID NO: 5321
     TESTI20168430//AACTCTGGGTACCAACTT//SEQ ID NO: 5322
30
     TESTI20168960//CTCCCTCTCCTTTCCTCA//SEQ ID NO: 5323
     TESTI20178160//CGTTTTCTCGATGTCCAG//SEQ ID NO: 5324
     TESTI20185810//AACATTCCTTGCAGCTCA//SEQ ID NO: 5325
35
     TESTI20199170//AGAGTGAGCTGTGCCTTG//SEQ ID NO: 5326
     TESTI20200260//CCAAGACATACCCAGGCT//SEQ ID NO: 5327
     TESTI20200710//AATTGTGACAAGCAGCAG//SEQ ID NO: 5328
     TESTI20202650//TGTTCATGTCACTGGCTG//SEQ ID NO: 5329
     TEST120220100//(Reaction system A)//CTTCATAGGGCAGACTCC//SEQ ID
     NO: 5330
     //(Reaction system B)//GCTGTGAACTAGAGGGGC//SEQ ID NO:5331
     TESTI20224620//GGAGAAACCGATGAAGAA//SEO ID NO: 5332
    TESTI20229600//(Reaction system A)//TTTAATAGTGCCCTGTGG//SEQ ID
    NO: 5333
    //(Reaction system B)//CTCTGGAATTTGCATTGA//SEQ ID NO: 5334
    TEST120230850//CAAGACTATGGAGGGGAG//SEQ ID NO:5335
    TESTI20231920//CTCCTCTTGCATTCTCCC//SEQ ID NO: 5336
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TEST120234140//CCAGTTATATCCCCAAAA//SEQ ID NO: 5337
      TEST120234270//CATAAAACCGAATAACTGAG//SEQ ID NO: 5338
      TEST120238000//AGTGTTTGTGGGCATAGA//SEQ ID NO: 5339
      TEST120238610//ACTTCAGACCTCCCTAGA//SEQ ID NO: 5340
      TESTI20239510//TTATTGAAGGAAAGCCGC//SEQ ID NO: 5341
      TEST120242990//CCCTGCCTTCCCTATAGA//SEQ ID NO: 5342
10
      TEST120265250//GGGAAATAGAGGAGTGAT//SEO ID NO: 5343
      TEST120265370//TGGTTTCAGATGTGCCTT//SEQ ID NO: 5344
      TEST120266740//TGGAAGAACGAAAGAGCC//SEQ ID NO: 5345
15
      TESTI20272390//TCCAGGGTGTCGTAGAAG//SEQ ID NO: 5346
     TESTI20275030//GCACGTTAAGGACTGTTT//SEQ ID NO: 5347
      TESTI202/5620//(Reaction system A)//TGTGCCTGACTAGGTGAG//SEQ ID
     NO: 5348
20
      //(Reaction system B)/AAGGACAGGTGAGTGTGG//SEQ ID NO: 5349
     TESTI20277360//TGGAGTACAACCTGCATC//SEQ ID NO: 5350
     TEST120282540//TGTCTGGTAGAGTTGCGG//SEQ ID NO: 5351
25
     TEST120284880//TGATTTAATGAGTGGAACC//SEQ ID NO: 5352
     TEST120235830//(Reaction system A)//CATGTGACCTTCTCTGGC//SEQ ID
     NO: 5313
     //(Reaction system B)//CAGTTCTTTAGCCAGGGA//SEQ ID NO: 5354
30
     TESTI20288110//CCTTTTGTCTGATTCGTC//SEQ ID NO: 5355
     TEST120289850//CCTTACCAAACTCATCCA//SEQ ID NO: 5356
     TESTI20307540//CGTGCATGAAAGTGAGTC//SEQ ID NO: 5357
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     TEST120308600//CTTCTCAATCATCAGGGA//SEQ ID NO: 5358
     TEST120311290//TTCTCTGCACTCCTTGAT//SEQ ID NO: 5359
     TEST120317600//GAGTGTCTGGCATGGTTA//SEQ ID NO: 5360
     TEST120319190//AAGCTGGGATGATAAGGG//SEQ ID NO: 5361
ΔO
     TESTI20332420//(Reaction system A)//CTTCTTGGTGCTGCTTTT//SEQ ID
     NO: 5362
     //(Reaction system B)//GCAGATATGTTTGTGAGAG//SEQ ID NO:5363
45
     TESTI20335200//AATAAACTACACCAGGGC//SEQ ID NO: 5364
     TESTI20342430//TCCTACGTTGAGTTGCCT//SEQ ID NO: 5365
     TEST120345060//GTCCACTAGAAGAGGGTC//SEQ ID NO: 5366
     TESTI20347300//GAAAGCTGTCGTTAAGGT//SEQ ID NO: 5367
     TESTI20357960//AATGACAGGTGAGTGGGT//SEQ ID NO: 5368
     TESTI20361140//AATTCACCAGGCTGTGTG//SEQ ID NO: 5369
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TESTI20369220//(Reaction system A)//TGGATTTGGAAGAGACCT//SEQ ID
NO: 5370
//(Reaction system B)//TTTGGGTGGAAGTAGAGA//SEQ ID NO: 5371
TESTI20369690//GCTGGTTATTCACGTGGT//SEQ ID NO: 5372
TESTI20370020//(Reaction system A)//TGGTCATACTCACTGCCC//SEQ ID
NO: 5373
//(Reaction system B)//GACCTGGTCATACTCACTG//SEQ ID NO: 5374
TESTI20371030//CTAAAGTCCAAAATGTGTAAGT//SEQ ID NO:5375
TESTI20386230//(Reaction system A)//GCTAAGGTGCTATGAAGG//SEQ ID
NO: 5376
//(Reaction system B)//ACAGTAAAAGGGCAAGTG//SEQ ID NO: 5377
TESTI20391210//AATACTCACATGCCAAGC//SEQ ID NO: 5378
TEST120392090//CTTGGTTACAGAGGACAG//SEQ ID NO: 5379
TEST120392250//ATTCCACTCTGCTCAAAG//SEQ ID NO: 5380
TEST120392270//CCTTGTTGTCCATGAGTC//SEQ ID NO: 5381
TEST120401020//CGTACACCACATAGCTGA//SEQ ID NO: 5382
TEST: 20401430 // TGGTAGAAAGAGAGTCACAT // SEQ ID NO: 5383
TEST120409440//TAGAGCACGTTTCCCTGA//SEQ ID NO: 5384
TEST:20415640//TCTGGAAAATGAGGGTTA//SEQ ID NO:5385
TEST:20424000//CCAGCTTTCTTCATCATC//SEQ ID NO:5386
TEST120424730//AGGAGTGTGGCATAGTCA//SEQ ID NO: 5387
TEST:20425070//AAAGCCATCAGACCTCAT//SEQ ID NO:5388
TESTICO433130//GTCCCATGATTTAGAACTC//SEQ ID NO: 5389
TEST:20438570//CTGCACTAGCCTTTTCCA//SEQ ID NO: 5390
TESTI20443090//GGAAGACAGGACCCAAGT//SEQ ID NO: 5391
TESTI20463520//TGTTGGACTAGAGGGGAA//SEQ ID NO: 5392
TESTI20465520//TCCAGGTCTCATTCTCTC//SEQ ID NO: 5393
TESTI20478010//TCCCTATCAGACGACCAG//SEQ ID NO: 5394
TESTI20478180//AAATCACCCTGCTTGTCA//SEQ ID NO: 5395
THYMU20029100//AGAAGCCAGGGAAGAGGT//SEQ ID NO: 5396
THYMU20061700//CTAGCTCTGAAGTGGCAT//SEQ ID NO: 5397
THYMU20095960//(Reaction system A)//TGAAGAGATTACCCAGGT//SEQ ID
NO: 5398
//(Reaction system B)//GGACTCTGTAGATGTAACTGA//SEQ ID NO: 5399
THYMU20111180//(Reaction system A)//TTCTGGGTAAGCCTGATT//SEQ ID
```

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NO: 5400

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//(Reaction system B)//CAAAGAATACCACAAATAGC//SEQ ID NO: 5401
      THYMU20118060//CCAAGGCTAAAGAGAGAG//SEO ID NO: 5402
      THYMU20130890//(Reaction system A)//AATCTCAAGGACCAGTTT//SEQ ID
      NO: 5403
      //(Reaction system B)//GACACAATGGACTCAAAA//SEQ ID NO:5404
      THYMU20142040//ACAGAAGGCCACAGTCAG//SEQ ID NO: 5405
10
      THYMU20142970//CAAGGATACTGTGATGAAA//SEQ ID NO: 5406
      THYMU20153160//GGTGGTTAGGACATTTCTC//SEQ ID NO: 5407
      THYMU20158250//AAGGAGTGGATAGATAGATAG//SEQ ID NO: 5408
     THYMU20187720//TGGTTACAAAGTCACAGG//SEQ ID NO: 5409
     THYMU20194360//TTCACTTTTGTTTCCCAG//SEQ ID NO: 5410
     THYMU20208300//ATACCACTAAGGCCCAGG//SEQ ID NO: 5411
     THYMU20226600//GACTCTTTCAGCTGCTGC//SEQ ID NO: 5412
20
     THYMU20239000//CAAATGGACAGGAACTTA//SEQ ID NO: 5413
     THYMU20253250//(Reaction system A)//AGAAAACCAGATAGGGCC//SEQ ID
     NO: 5414
25
      //(Reaction system B)//TAATGCAGGGAATGGAGT//SEQ ID NO: 5415
     THYMU20272490//CATTATACACACGACGAA//SEQ ID NO: 5416
     THYMU20284120//AAACCCACAGTGCTTCAT//SEQ ID NO: 5417
     THYMU20286290//AGTCCCTCTCATTTCCAG//SEQ ID NO: 5418
30
     TKIDN10000010//TGCCATAATTCTCCTTTT//SEQ ID NO: 5419
     TRACH20005020//GCTTTTCTCCTTCCATGA//SEQ ID NO: 5420
     TRACH20032720//CTACGCCCACTATATTCA//SEQ ID NO: 5421
35
     TRACH20041830//(Reaction system A)//AGATACTGAGAATGAGCCT//SEQ ID
     NO: 5422
     //(Reaction system B)//TTTCCATGCCTACCCTTT//SEQ ID NO: 5423
     TRACH20060150//(Reaction system A)//AGTCTCCTGCTGGCTAAG//SEQ ID
40
     NO: 5424
     //(Reaction system B)//GTCCCTTCTGTCTCCTGA//SEQ ID NO: 5425
     TRACH20076760//GTGGAAGTGCCTGATGAG//SEQ ID NO: 5426
45
     TRACH20082780//CTTTCACCTGGGATGGAT//SEQ ID NO: 5427
     TRACH20091230//AACATAGTCATTTCGTTCA//SEQ ID NO: 5428
     TRACH20099340//GAGCACTGTAAGAGCCAT//SEQ ID NO: 5429
     TRACH20109650//AAACATACCACGGAGAGA//SEQ ID NO: 5430
50
     TRACH20115740//TATGAGCACACGAGGTCC//SEQ ID NO: 5431
     TRACH20134950//AAGAGGGAACATCAGGCT//SEQ ID NO: 5432
```

TRACH20135520//TTCTTGGGCTTTATGTGG//SEQ ID NO: 5433 TRACH20153810//(Reaction system A)//GCAGTGAGTCGTAGATGA//SEQ ID NO: 5434 //(Reaction system B)//CTGCCTAGCCCTCTCACT//SEQ ID NO: 5435 TRACH20184490//ACTGTGAAGAGCCTGTTG//SEQ ID NO: 5436 TSTOM20001390//GGAATAGTAAGGACATAATGACA//SEQ ID NO: 5437 TSTOM20005690//GGAACCTTTTGTAACCCT//SEQ ID NO: 5438 UMVEN10001560//GCCACAACATCATTTTACTT//SEQ ID NO: 5439 UMVEN20003540//AAGTAAAAGACATCGGCA//SEQ ID NO: 5440 UTERU20004240//TACCTCCAGACTTTTGTG//SEQ ID NO: 5441 UTERU20046980//AGGATGGGAAGAAGGTTT//SEQ ID NO: 5442 UTERU20055930//GGATGAGTTGTGTGAAAA//SEQ ID NO: 5443 UTERU20068990//CCAAGGCTAAAGAGAGAG//SEQ ID NO: 5444 UTERU20070810//AAGTAGAGAATCCCAGCT//SEQ ID NO: 5445 UTERU20115740//TTTATGATTGAGGGGACC//SEQ ID NO: 5446 UTERU20119060//ACAGCATCCAATCAAAGA//SEQ ID NO: 5447 UTERU20124070//ACATCTGGTGGAAGCATC//SEQ ID NO: 5448 UTERU20126880//ACCTTAACCCCTCTTCCC//SEQ ID NO: 5449 UTERU20134910//AAGGAAGCCAACTCATGC//SEQ ID NO: 5450 UTERU20146680//ACCTTAACCCCTCTTCCC//SEQ ID NO: 5451 UTERU20176130//TAGAAAGGGGTGGTGAGA//SEQ ID NO: 5452 UTERU20185230//CGTTGAGAGCTTTTACAG//SEQ ID NO: 5453 UTERU20186740//CCACTTTGAGAGAACCCT//SEQ ID NO: 5454

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[0314] The result of expression frequency analysis is shown in Table 52. The clones not shown in the table contain clones whose expression levels could not be measured because the levels were too low or the sizes of the PCR products were different from the expected. It was confirmed that the expression levels of IL-8 genes used as positive control genes were elevated.

[0315] The result obtained by the search for the genes whose expression levels were altered depending on the presence of TNF-α in culturing THP-1 cell, which is a human monocyte cell line, showed that the clones whose expression levels were elevated by twofold or more one or three hours after the stimulation (the clones whose expression levels were 0.1 or lower both before and after the stimulation were excluded), were ASTRO20152140, BRACE20057620, BRACE20060720, BRACE20090440, BRACE20152870, BRACE20229280, BRAMY20002770, BRAMY20266850, BRAMY20280720, BRAWH20106180, BRAWH20122770, BRHIP20096170, BRHIP20111200, BRHIP20186120, BRHIP20194940, BRHIP20207430, BRSSN20152380, CTONG20095270, CTONG20100240, CTONG20158150,

CTONG20265130, D3OST20006540, D9OST20031370, FCBBF20071860, FCBBF30251420, FCBBF30252520, FCBBF40001420, FEBRA20017050, FEBRA20082100, HCHON20011160, KIDNE20141190, KIDNE20163880, KIDNE20182690, LIVER10004790, LIVER20038540, LIVER20085800, MESAN20130220, MESAN20174170, NT2NE20158600, NT2RI20005750, NT2RP70110860, NT2RP70169110, NT2RP70175670, NT2RP70188710, PERIC20002140, PLACE60155130, PROST20120160, PROST20149250, PROST20161950, PUAEN20015260, SKNSH20080430, SMINT20051610, SMINT20060780, SMINT20161220, SMINT20163960, SPLEN20101190, SPLEN20157300, TESTI20108720, TESTI20220100, TESTI20239510, TESTI20266740, TESTI20342430, TESTI20370020, TESTI20391210, TESTI20401020, TESTI20415640, THYMU20130890, THYMU20286290, TRACH20060150, TRACH20099340, UTERU20004240, UTERU20068990, UTERU20119060.

[0316] On the other hand, in particular cases where the expression levels were relatively high in the unstimulated cells (the relative value was 1 or higher), the clones whose expression levels were decreased by twofold or more by the TNF- $\alpha$  stimulation (the clones whose expression levels were increased 1 or 3 hours after the stimulation were excluded) were

ASTRO20032120, ASTRO20084250, ASTRO20181690, BRACE20062640, BRACE20067430. BRACE20235400, BRALZ20018340, BRALZ20069760, BRALZ20075450, BRAMY20163270, BRAMY20204450, BRAMY20218670, BRAMY20229800, BRAWH10000930, BRAWH20107540, BRAWH20132190, BRAWH20158530, BRCAN20273340, BRHIP20105710, BRHIP20186120, BRSSN20176820, CTONG20095290, DFNES20031920, FCBBF30033050, FCBBF30071520, FCBBF30083820, HCHON20008980, HCHON20022470, HHDPC20034390, KIDNE20028720, KIDNE20079440, KIDNE20127750, KIDNE20148900, LIVER20011130, MAMGL10000830, MESAN20127350, NT2NE20181650, NT2RI20023160, NT2RP70102350, NT2RP70157890, NTONG20029480, OCBBF20020830, OCBBF20041680, OCBBF20061720, OCBBF20127040, OCBBF20139260, OCBBF20178990, PEBLM20013120, PLACE60003480, PLACE60181070, PROST20151240. PUAEN20003740, PUAEN20011880, PUAEN20078980, PUAEN20085150, SKNSH20080430, SMINT20001760, SMINT20047810, SMINT20108530, SPLEN20158990, SPLEN20283650, TESTI20386230, TESTI20392250, TESTI20409440, TESTI20424730, THYMU2095960, THYMU20111180, THYMU20226600, THYMU20253250, THYMU20272490, TRACH20153810, UTERU20176130, UTERU20186740.

[0317] These clones were thus revealed to be involved in the inflammation reaction induced by TNF- $\alpha$ .

[0318] The result obtained by the search for the genes whose expression levels were altered depending on coculturing gastric cancer cell line MKN45 with cag PAI positive Helicobacter pylori (TN2), showed that the clones whose
express on levels were elevated by twofold or more (the clones whose expression levels were 0.1 or lower both before
and after the stimulation were excluded), were ADRGL20067670, BLADE20004630, BRACE20039040,
BRACE20151320. BRACE20229280, BRACE20235400, BRALZ20058880, BRAMY20060920, BRAMY20184670,
BRAMY20218670. BRAMY20229800, BRCAN20147880, BRHIP20196410, BRHIP30004880, BRSSN20187310,
CD34C30004940. CTONG20265130, DFNES20031920, FCBBF30278630, FCBBF40001420,

HHDPC20095280. KIDNE20130450, LIVER20011130, LIVER20038540, NT2NE20172590, NT2RP70169110, OCBRF20085200 OCBBF20180840, PEBLM10000240, PLACE60003480, PROST20120160, PROST20151240, PUAFN20C11880 SKMUS20031680, SKNSH20080430, SMINT20056210, SMINT20105000, SPLEN20019450, SPLEN20211570. STOMA20048520, TESTI20004890, TESTI20083940, TESTI20168480, TESTI20239510, TESTI20308600. TESTI20478010, UTERU20126880.

[0319] Of these clones, the expression levels of ADRGL20067670, BLADE20004630, BRACE20151320, BRACE20229280, BRACE20235400, BRALZ20058880, BRAMY20218670, BRAMY20229800, BRHIP20196410, BRHIP30004880, CD34C30004940, DFNES20031920, FCBBF30278630, FCBBF40001420, HHDPC20095280, KIDNE20130450, LIVER20011130, LIVER20038540, NT2NE20172590, NT2RP70169110,

PEBLM 0000240. PROST20151240, PUAEN20011880, SKMUS20031680, SKNSH20080430, SMINT20056210, SMINT20105000 SPLEN20019450, SPLEN20211570, STOMA20048520, TESTI20168480, TESTI20308600, TESTI20478010. UTERU20126880 were not increased by the co-culture with the cagE mutant (TN2ΔcagE). There may be the possibility that the expression levels of the 34 clones are altered *via* the NF-κB pathway. Among them, the express on levels of BRACE20229280, FCBBF40001420, LIVER20038540, NT2RP70169110. SKNSH20080430, STOMA20048520 were also increased when human monocyte cell line THP-1 was stimulated with TNF-α.

[0320] On the other hand, in particular cases where the expression levels were relatively high in the unstimulated cclls (the relative value was 1 or higher), the clones whose expression levels were decreased by twofold or more in the presence of *Helicobacter pylori* were ASTRO20032120, BRACE20090440, BRACE20114780, BRALZ20064740, BRAMY20002770. BRAMY20210400, BRAMY20215230, BRAMY20247280, BRAMY20267130, BRAWH2019630, BRAWH20118230, BRCOC20105100, BRHIP20218580, BRSSN20046570, CTONG20138030, CTONG20146970. CTONG20158150, D3OST20037970 FCBBF30001840,

FCBBF30033050. FEBRA20082100, HCHON20035130, HCHON20043590, HCHON20067220, NT2NE20174920, NT2RI200C9870. NT2RI20023160, NT2RP70062230, NT2RP70130020, NT0NG20070340, OCBBF20020150, OCBBF20094240. OCBBF20107920, PROST20144220, PROST20149160, PROST20153320, PUAEN2003740, PUAEN20025680. PUAEN20040670, SMINT20014580, SPLEN20101190, STOMA20076800, TESTI20087620, TESTI20098530. TESTI20123080, TESTI20161970, TESTI20234140, TESTI20288110, TESTI20357960, TESTI20391210, TESTI20424730, THYMU20158250, THYMU20226600, TRACH2005020, TRACH20134950, TRACH20184490, TSTOM20001390, UTERU20119060, UTERU20134910, UTERU20176130.

[0321] These clones are involved in gastritis or gastroduodenal ulcer.

Table 3

ClonelD .	CD34C	D3OST	D6OST	D9OST
ASTRO20001410	0	17.731	0	20.479
D3OST10001090	0	62.515	0	24.068
D3OST20036070 ·	0	46.404	0	53.596
THYMU20039810	0	18.291	o	21.126
KIDNE20028720	0	.0	38.385	46.259
BRAWH10000930	0	0	0	6.219
BRHIP20005340	o	0	0	4.615
CTONG20141650	0	0	0	64.925
D9OST20000310	0	0	0	63.705
D9OST20002780	0	0	0	100
D9OST20023970	0	0	0	37.837
D9OST20025970	0	0	0	19.695
1	0	0	0	19.093
D9OST20031370	-	_		
D9OST20033970	0	0	0	38.536 93.047
D9OST20035800	_ i		-	
D9OST20035940	0	0	0	100
D9OST20040180	0	_	. 0	100
FCBBF30018550	0	0	0	37.763
FCBBF30233680	0	0	0	33.084
KIDNE20102650	0	0	0	63.715
NT2RI20023160	0	0	0	10.811
PROST20107820	0	0	0	3.279
SKNSH20089400	0	0	0	25.857
SMINT20033400	0	0	0	39.619
CTONG20108210	0	0	47.973	0
D6OST20003580	0	0	95.4	0
D6OST20005070	0	0	100	0
ASTRO20155290	0	21.631	0	0
D3OST10002670	0	50.415	0	0
D3OST10002700	0	30.165	0	0
D3OST20006180	0	100	0	0
D3OST20006540	0	100	0	0
D3OST20007340	0	93.334	0	0
D3OST20013280	0	100	0	0
D3OST20024170	0	100	0	0
D3OST20024360	0	100	0	0
D3OST20037970	0	100	0	0
D3OST30002580	0	72.574	0	0
D3OST30002910	0	93.334	0	0
FCBBF10004120	0	22.594	0	0
NT2RI20001330	0	29.915	0	0
NT0NG20009770	0	11.477	0	0
SPLEN20084600	0	30.589	0	0
SPLEN20140800	0	55.315	0	0
THYMU20169680	0	86.295	0	0
TRACH20141240	0	12.051	0	0
CD34C30001250	97.628	0	0	0
CD34C30003140	100	0	0	0
CD34C30004240	96.167	0	0	0

Table 3 (continued)

ClonelD	CD34C	D3OST	D6OST	D9OST
CD34C30004940	100	0	0	0
DFNES10001850	55.393	0	0	0
HHDPC20034390	21.364	0	0	0
NT2RI20091730 `	46.845	0	0	0
SKMUS20003610	44.913	0	0	0
SPLEN20225220	59.537	0	0	0
BRCOC20101230	46.01	0	0	14.772

Table 4

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
CTONG20027090	62.349	0	0	0
CTONG20160560	57.22	0	0	0
NT2RP70032610	39.095	3.274	0	0
OCBBF20188730	39.876	0	0	0
SPLEN20162680	12.432	0	2.355	6.263
BRCOC20101230	0	2.64	. 3.981	3.97
BRHIP20005340	0	0.825	1.244	1.24
BRHIP20238880	0	2.66	7.355	2.667
FCBBF30016320	- 0	7.441	2.805	5.595
FEBRA20080810	0	6.827	5.147	2.566
FEBRA20225040	0	3.958	2.985	5.952
HCHON20008320	0	17.053	19.287	12.822
HHDPC20034390	0	0.613	1.387	0.922
HLUNG10000550	0	2.609	0.984	1.962
NT2RI20028470	0	9.076	6.843	4.549
NT2RI20054050	0	2.03	1.02	4.069
NT2RI20091730	0	2.688	2.027	4.042
NT2RP70078420	0	4.623	3.485	13.902
PUAEN20003740	0	2.314	0.582	1.16
THYMU20271250	0	0.431	0.651	1.297
BRACE20003070	0	8.516	4.281	0
BRACE20039040	0	6.248	4.711	0
BRAWH20004600	0	1.471	5.545	0
BRAWH20011710	0	8.931	2.245	0
BRCOC20121720	0	13.559	5.112	0
BRHIP20005530	0	12.387	9.34	0
D3OST10002700	0	6.227	4.695	0
HCHON20007380	0	7.176	5.411	0
HEART20072310	0	11.675	17.605	0
KIDNE20121880	0	21.519	16.225	0
MESAN20121130	0	14.219	10.721	0
NT2RI20022600	0	57.012	42.988	0
NT2RI20023160	0	1.932	1.457	0
NT2RI20086220	0	7.606	5.735	0
NT2RI20216250	0	45.928	34.63	0
NT2RP60000850	0	11.147	16.809	0
NT2RP70036880	0	1.78	5.367	0
NT2RP70043480	0	10.893	4.107	0

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Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
NT2RP70062230	0	10.183	7.678	0
NT2RP70081610	0	15.131	22.818	0
NT2RP70102350	0	84.14	15.86	0
NT2RP70130020 ·	0	57.012	42.988	0
NT2RP70190640	0	30.952	23.338	o
OCBBF10001850	0	20.293	7.65	0
OCBBF20097720	0	5.676	4.28	0
OCBBF20173980	0	3.1	2.338	o
PEBLM20044520	0	3.253	2.453	o
SPLEN20173510	0	7.249	10.932	0
TRACH20007020	0	9.462	7.134	0
UTERU20065930	0	10.676	8.05	0
HCHON20022470	0	6.766	0	10.174
NT2NE20010490	0	21.179	0	31.847
NT2NE20010490 NT2NE20174800	0	39.941	0	60.059
NT2NE20174800 NT2NE20177520	0	28.292	0	42.542
PROST20087700	0	1.88	0	14.135
PROST20087700 PROST20107820	0	0.586	. 0	2.644
SMINT20028820	0	6.998	0	10.523
1	0	9.768	0	14.689
TESTI20063830		9.766	2.686	5.357
ASTRO20125520	.0			3.71
BRHIP30001110	0	0	1.86	
HCHON20002260	0	0	0.733	1.461
HCHON20008150	0	0	5.075	20.242
KIDNE20002520	0	0	1.553	6.195
NT2NE20130190	0	0	33.397	66.603
NT2NE20158600	0	0	33.397	66.603
NT2RI20001330	0	0	4.656	9.286
NT2RI20025400	. 0	0	3.141	6.265
NT2RI20036670	0	0	33.397	66.603
NT2RI20048840	0	0	1.404	5.6
SKMUS20020840	0	0	11.346	22.628
BRACE20057190	0	0	0	10.763
BRACE20060550	0	0	0	14.499
BRACE20267250	0	0	0	66.449
BRAWH20107540	0	0	0	40.54
BRAWH20118230	0	0	0	78.374
CTONG20075860	0	0	0	21.782
CTONG20095290	0	0	0	22.915
FEBRA20086620	0	0	0	11.505
FEBRA20144170	0	0	0	1.957
FEBRA20196370	0	0	0	59.247
HLUNG20023340	0	0	0	33.313
NT2NE20003740	0	0	0	100
NT2NE20010050	0	0	0	84.719
NT2NE20010210	0	0	0	100
NT2NE20010400	0	0	0	56.184
NT2NE20015240	0	0	0	100
NT2NE20021620	0	0	0	44.305
NT2NE20043780	0	0	0	100

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Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
NT2NE20053580	0	0	0	75.239
	0	0	0	100
NT2NE20068130	0	0	0	100
NT2NE20072200	· I		0	100
NT2NE20074250 `	0	0	_	1
NT2NE20080170	0	0	0	100
NT2NE20089610	0	0	0	100
NT2NE20089970	0	0	0	100
NT2NE20108540	0	0	0	84.719
NT2NE20110360	0	0	0	100
NT2NE20118960	0	0	0	100
NT2NE20122430	0	0	0	76.57
NT2NE20124480	0	0	0	100
NT2NE20125050	0	0	0	66.449
NT2NE20131890	0	0	0	100
NT2NE20132170	0	0	0	100
NT2NE20142210	0	0	0	100
NT2NE20146810	0	0	0	100
NT2NE20152750	0	0	0	100
NT2NE20155110	0	. 0	0	100
NT2NE20156260	0	0	0	100
NT2NE20157470	0	0	0	100
NT2NE20159740	0	0	0	27.684
NT2NE20172590	0	0	0	100
NT2NE20174920	0	0	0	61.159
NT2NE20181650	0	0	0	100
NT2NE20183760	0	0	0	100
NT2NE20184900	0	0	0	84.719
NT2NE20187390	0	0	0	100
OCBBF20108430	0	1 0	1 0	53.98
RECTM20005100	0	0	1 0	10.923
SMINT20001760	0	1 0	0	50.667
SPLEN20169720	0	0	0	7.349
TESTI20265250	0	0	0	
ASTRO10001650	0	0	8.055	
ASTRO20033160	0		1	0
BRACE20011070	0			
BRACE20011070 BRACE20039440	0	0		0
	0			_
BRACE20151320				i
BRAMY20104640				1
BRAMY20137560	1	1	i	1
BRAMY20167060	0	1	1	1
BRAWH20028110	0	-	1	·
BRCAN20280360	0	1 .	i i	1
BRCOC20004870	0	1	<b>I</b>	
BRHIP20207990	0	Į.		
BRHIP20217620	0	1	1	
BRHIP20249110	0		67.372	1
BRSTN10000830	0		3.48	1
CTONG10000940		1	1.41	1
CTONG20004690	C	) ](	5.30	7 0

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Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
		0	12.439	
CTONG20050280	0	_		0
CTONG20105660	0	0	24.642	0
CTONG20125640	0	0	7.18	0
CTONG20133520	0	0	49.384	0
CTONG20186320	0	0	29.069	0
FCBBF10000770	0	. 0	1.472	0
FCBBF10002800	0	0	10.265	0
FCBBF10003770	0	0	19.652	0
FCBBF30018550	0	0	5.089	0
FCBBF30123470	0	0	3.989	0
FCBBF30246230	0	0	5.091	0
FEBRA20018280	0	0	9.887	0
FEBRA20095140	0	0	6.019	0
FEBRA20192420	0	0	58.974	0
HCHON20064590	0	0	19.614	0
HHDPC10000830	0	0	1.779	0
HLUNG20016770	0	0	6.385	0
HLUNG20033780	0	0	· 16.824	0
IMR3220002430	0	0	3.118	0
KIDNE20104300	0	0	17.33	0
MESAN20004570	٠٥	0	7.197	0
MESAN20089360	0	0	14.459	. 0
NOVAR10000910	0	0	3.519	0
NT2RI20003480	0	0	32.207	0
NT2RI20005750	0	0	100	0
NT2RI20009870	0	0	100	0
NT2RI20023590	0	0	29.911	0
NT2RI20023910	0	0	11.79	0
NT2RI20025640	0	0	100	0
NT2RI20040930	0	0	100	0
NT2RI20041880	0	o	10.436	0
NT2RI20046080	0	0	6.723	0
NT2RI20050960	o	Ö	73.545	0
NT2RI20055790	0	0	17.054	0
NT2RI20056700	0	0	100	0
NT2RI20069730	o	0	100	0
NT2RI20076290	o	0	14.653	0
NT2RI20091940	0	o	5.358	o
NT2RI20198260	0	o	100	0
NT2RI20203900	0	0	100	o
NT2RI20203900	0	0	100	0
NT2RI20240080	0	0	61.866	o
	0	0	100	0
NT2RI20244600 NT2RI20244960	0	0	100	0
	_	0	30.809	0
NT2RI20250750	0		t	i
NT2RI20252550	0	0	62.102	0
NT2RI20273230	0	0	60.375	0
NTONG20067090	0	0	16.469	0
OCBBF10001750	0	0	13.09	0
OCBBF20047570	0		4.504	0

Table 4 (continued)

Clana ID	NT2RM	NT2RP	NT2RI	NT2NE
Clone ID	0	0	8.495	0
OCBBF20054760	_	- 1	10.318	0
OCBBF20059560	0	0	1	0
OCBBF20073540	0	0	3.651	
OCBBF20125530	0	0	2.131	0
OCBBF20126780	0	0	12.535	0
OCBBF20127040	0	0	37.942	0
OCBBF20140890	0	0	35.863	0
SKMUS20003610	0	0	1.943	0
SKNSH20008190	0	0	4.523	0
SKNSH20080430	0	0	18.4	0
SMINT20144800	0	0	2.887	0
SPLEN20027440	0	0	4.053	0
SPLEN20095550	0	0	15.436	0
SPLEN20140800	0	0	8.61	0
TESTI20094020	0	0	16.66	0
TESTI20369690	0	0	6.529	0
TESTI20391770	0	0	7.531	0
TESTI20442760	0	0	17.235	0
TRACH20084720	0	. 0	5.703	0
TRACH20107710	0	0	61.866	0
TRACH20118940	0	0	16.16	0
UTERU20022940	0	0	9.896	0
ASTRO20108190	0	1.622	0	0
BGGI120006160	0	2.155	0	. 0
BRAMY20136210	0	70.518	0	0
BRAWH20016620	0	22.162	0	0
BRAWH20164460	0	20.968	0	0
BRCQC20144000	0	40.488	1 0	0
BRHIP20132860	0	82.532	0	0
BRSSN20146100		17.209	0	0
CTONG10000100	0	15.625	0	0
CTONG20103480	0	4.268	٥	0
CTONG20103480	0	1.722	0	0
	0	10.392	0	0
CTONG20139070	1	10.583	0	0
FCBBF10000240	0	14.415	0	0
FCBBF10000630		30.502	0	1 _
FCBBF20067810	0	1		
FCBBF30010810	0	6.328	0	
FCBBF30012810	0	49.073	0	_
FCBBF30013770	0	24.817	0	0
FCBBF30039020	0	56.608	0	0
FCBBF40001420	0	8.811	0	
FEBRA10001880	0	5.044	0	1
FEBRA20082010	0	17.339	0	_
HHDPC20001040	0	4.459	0	l .
KIDNE20021910	0	34.358	0	1
NT2RP6000077	0	15.492	0	
NT2RP70010740	0	100	0	0
NT2RP70027380	0	27.748	0	0
NT2RP70037240	0	22.256	0	0

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Classific		NT200	NITODI	NITONE
Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
NT2RP70044280	0	16.256	0	0
NT2RP70045590	0	20.543	0	0
NT2RP70056750	0	7.009	0	0
NT2RP70063950 `	0	82.532	0	0
NT2RP70072690	0	56.608	0	0
NT2RP70077660	0	74.295	0	0
NT2RP70085440	0	100	0	0
NT2RP70105210	0	100	0	0
NT2RP70110860	0	100	0	0
NT2RP70111320	0	100	0	0
NT2RP70122910	0	100	0	0
NT2RP70125160	0	100	0	0
NT2RP70133740	0	100	0	0
NT2RP70134990	0	100	0	0
NT2RP70137290	0	100	0	0
NT2RP70137640	0	54.725	0	0
NT2RP70143480	0	100	0	0
NT2RP70147210	0	100	. 0	0
NT2RP70150800	0	100	0	0
NT2RP70157890	0	100	0	0
NT2RP70159960	, 0	100	0	0
NT2RP70169110	0	100	0	0
NT2RP70175670	o	100	0	0
NT2RP70179710	0	100	0	0
NT2RP70181970	0	100	0	0
NT2RP70188020	0	100	0	0
NT2RP70188710	0	100	0	0
NT2RP70192730	0	100	0	0
NT2RP70194450	0	100	0	o
NT2RP70195430	0	50.987	0	0
NT2RP70198350	0	2.512	0	0
NT2RP70203790	0	100	0	o
OCBBF20039250	0	4.016	o	0
OCBBF20039230	0	5.038	o	0
OCBBF20080410	0	30.231	0	
OCBBF20108190	0	16.054		0
OCBBF20108580 OCBBF20122620	0	34.956		0
OCBBF20122620 OCBBF20130110	0	18.197	0	0
	0	43.004	0	0
OCBBF20151150	0	43.004		0
OCBBF20189560	1	I	0	
PROST10003220	0	57.613 20.618	0	
TESTI20001720	0	1	ļ .	
TEST120121550	0	15.444	0	
TESTI20152460	0	28.533	ł	0
TESTI20211240	0	13.774	0	0
TESTI20234140	0	39.241	0	1
UMVEN20003540	0	1.985	0	0
UTERU20006960	0	6.858	0	0
UTERU20094350	0	12.888	0	0
UTERU20164260	0	30.63	0	0

Table 5

CloneID	BEAST	TBAES
BRACE20039040	0	18.237
BRAMY20163250	0	26.506
BRCOG20031250	. 0	39.975
BRHIP20005340	0	2.408
BRHIP20217620	. 0	19.598
BRHIP30001110	0	7.202
FCBBF10000770	0	5.697
FCBBF30010810	0	18.471
FEBRA20080810	0	9.963
FEBRA20144170	0	3.798
FEBRA20196630	0	61.269
FEBRA20197110	0	14.875
HCHON20002260	0	11.347
HCHON20040020	0	5.523
HHDPC20034390	0	1.789
HLUNG10000550	0	3.808
NOVAR10000910	0	27.245
NT2RI20023160	0	11.28
NT2RI20054050	0	1.975
NT2RI20091730	0	7.846
OCBBF20188730	0	9.748
SMINT20144800	0	22.352
SPLEN20128000	0	2.403
SPLEN20171210	0	54.539
SPLEN20264110	0	80.173
TBAES20000590	0	84.801
TBAES20002550	0	100
TBAES20003150	0	100
TESTI20334410	0	15.439
TESTI20432750	0	62.244
TRACH20003590	0	20.978
TRACH20084720	0	11.037
UTERU20046640	0	11.937
BEAST20004540	100	0
SPLEN20008740	10.632	0

Table 6

CloneID	CERVX	TCERX
BGGI120006160	0	18.869
BRAMY20063970	0	59.264
BRHIP20218580	0	70.621
FEBRA20002100	0	14.918
SPLEN20162680	0	9.118
TEST 20214250	0	36.333
CTONG20105080	84.727	0
HCHON20015980	50.212	0
PROST20175290	52.453	0

Table 6 (continued)

ClonelD	CERVX	TCERX
TEST 20254220	51.293	0
THYMU20279750	82.6	0

Table 7

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CloneID	COLÓN	TCOLN
ASTRO20001410	0	32.199
BRAWH20162690	0	27.951
CTONG20132220	0	79.674
HCHON20002260	0	17.098
NT2RI20001330	0	54.324
TCOLN20001390	0	100
3NB6910001910	42.978	0
BRAMY20120910	41.689	0
BRAWH20004600	4.285	0
BRCOC20031250	39.895	0
BRCOC20031870	11.042	. 0
COLON10001350	100	0
COLON20043180	100	0
COLON20093370	100	0
FEBRA20002100	4.963	0
FEBRA20082010	16.836	0
FEBRA20197110	29.691	0
KIDNE20007770	53.588	0
KIDNE20013730	50.02	0
NT2RP70045590	59.84	0
OCBBF20078920	29.908	0
PROST20083600	12.636	0
SPLEN20011410	6.63	0
TRACH20084720	11.015	0
THYMU20271250	1.257	15.18

Table 8

CloneID	NESOP	TESOP
ASTRO20033160	0	20.183
ASTRO20125520	0	10.113
BRAMY20266850	0	16.957
BRAWH20164460	0	59.524
BRHIP20005340	0	9.367
BRHIP20191490	0	75.561
CTONG20095290	0	43.261
CTONG20143690	0	28.473
CTONG20161850	0	17.787
DFNES20001530	0	21.906
DFNES20071130	0	45.721
FCBBF30123470	0	15.017
FCBBF30175310	0	10.97
FEBRA20095140	0	45.326

Table 8 (continued)

CloneID	NESOP	TESOP
HCHON20016650	0	10.558
MESAN20025190	0	31.731
NT2RI20028470	0	8.588
NT2RI20054050	. 0	1.921
NT2RP70036880	0	5.052
NTONG20009770	. 0	6.726
NTONG20064840	0	29.574
NTONG20076930	0	48.142
SMINT20042990	0	61.748
SPLEN20008820	0	12.019
SPLEN20128000	o	2.337
SPLEN20149110	0	7.218
STOMA20013890	0	39.515
TESOP20000900	0	100
TESOP20003120	0	66.097
TESOP20004000	0	100
TESOP20005270	0	70.604
TESOP20005690	0	100
TESTI20334410	0	7.508
THYMU20271250	0	2.449
TRACH20141240	0	7.062
UTERU20022940	0	12.42
NESOP10001080	100	0
NT2RI20023160	17.058	0
NTONG20013620	74.273	0
TRACH20077540	31.967	0
NTONG20015870	69.673	12.221

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Table 9

CloneID	KIDNE	TKIDN
ASTRO20008010	0	3.776
ASTRO20181690	0	3.496
BRACE20111830	0	23.795
BRACE20152870	0	8.501
BRACE20237270	0	73.082
BRAMY20147540	0	5.185
BRAMY20286820	0	78.604
BRAWH20015350	0	12.794
BRAWH20096780	0	78.731
BRAWH20132190	0	35.86
BRAWH20182060	0	40.908
BRCAN20060190	0	13.906
BRCOC20004870	0	1.072
BRCOC20176520	0	51.098
BRHIP20000870	0	24.363
BRHIP20198190	0	32.096
BRHIP20233090	0	43.183
BRHIP30001110	0	3.79

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Table 9 (continued)

Table 9	(continued)	
CloneID	KIDNE	TKIDN
BRSSN20015790	0	49.863
BRSTN20000580	0	8.929
CTONG10000940	0	1.442
CTONG20098440	0	66.526
CTONG20150910	0	6.012
CTONG20165050	.0	66.526
DFNES20014040	0	38.579
DFNES20037420	0	38.579
FCBBF10000770	0	2.998
FCBBF30083820	0	39.87
FCBBF30247930	0	59.143
FEBRA20037500	0	6.758
FEBRA20072120	0	14.531
FEBRA20080810	0	2.621
FEBRA20086620	o	17.626
FEBRA20140100	0	59.757
FEBRA20144170	0	1.999
FEBRA20176800	0	35.198
HCHON20008320	0	13.096
HCHON20059870	0	36.909
HLUNG10000550	0	2.004
MESAN20106640	0	32.125
NT2RI20025400	0	6.399
NT2RI20076290	0	7.462
NT2RI20091940	0	3.638
OCBBF20019830	0	26.741
OCBBF20022900	0	37.332
OCBBF20039250	0	3.084
OCBBF20080050	0	11.755
OCBBF20097720	0	8.718
OCBBF20125530	0	4.341
OCBBF20130110	0	27.949
OCBBF20140640	0	5.056
OCBBF20173980	0	9.523
PANCR10000910	0	1.114
PROST20087700	0	2.887
PUAEN20044000	0	26.668
SPLEN20144520	0	68.029
SPLEN20160980	0	68.029
TKIDN10000010	0	41.198
TKIDN20004640	0	68.029
TKIDN20005210	0	55.069
TKIDN20030590	0	78.393
TKIDN20030620	0	100
TKIDN20047480	0	35.796
TRACH20003590	0	11.039
TRACH20028030	0	7.714
TRACH20183170	0	10.844
TRACH20184490	0	56.123
UMVEN20003540	0	3.049

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Table 9	(continued)	
CloneiD	KIDNE	TKIDN
UTERU20004240	0	3.144
UTERU20055930	0	12.464
ASTRO10001650	7.727	0
ASTRO20108190	2.346	0
BGGI120006160	3.117	0
BRACE20039040	9.038	0
BRAMY20102080	63.37	0
BRAWH20004600	2.128	0
BRAWH20125380	35.37	0
BRAWH20162690	4.596	0
BRHIP20115760	66.835	0
BRHIP20205090	65.282	0
CTONG20052650	65.178	0
CTONG20108210	2.491	0
CTONG20128470	6.004	0
CTONG20133480	19.179	0
CTONG20139070	7.516	0
D9OST20000310	16.47	. o
DFNES20001530	11.162	0
FCBBF10001820	59.128	o
FEBRA20002100	4.929	0
HCHON20008980	35.524	0
HCHON20016650	5.38	0
HLUNG20033780	32.277	0
KIDNE20002520	2.979	0
KIDNE20003940	100	0
KIDNE20006780	100	0
KIDNE20007210	73.728	0
KIDNE20007770	19.958	0
KIDNE20008010	100	0
KIDNE20009470	8.811	О
KIDNE20011170	77.71	0
KIDNE20011400	100	0
KIDNE20013730	24.839	0
KIDNE20017130	54.019	o l
KIDNE20018730	100	ō
KIDNE20018970	100	0
KIDNE20020150	100	0
KIDNE20021680	100	0
KIDNE20021910	24.85	0
KIDNE20021980	100	0
KIDNE20022620	100	o
KIDNE20024830	100	0
KIDNE20027250	35.87	0
KIDNE20027950	100	0
KIDNE20028390	25.593	o l
KIDNE20028720	1.993	o
KIDNE20028830	7.907	ő
KIDNE20029800	10.988	ő
KIDNE20067330	100	ő
	100	U

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Table 9 (continued)

	(continued)	
CloneID	KIDNE	TKIDN
KIDNE20079440	35.045	0
KIDNE20096280	100	0
KIDNE20096470	100	0
KIDNE20100070	- 100	0
KIDNE20100840	100	0
KIDNE20101370	100	0
KIDNE20101510	100	0
KIDNE20102650	8.237	0
KIDNE20102710	100	0
KIDNE20104300	33.246	0
KIDNE20106740	100	0
KIDNE20107390	100	o
KIDNE20107500	74.264	0
KIDNE20107620	100	0
KIDNE20109730	100	0
KIDNE20109890	100	ا ہ
KIDNE20112000	100	0
KIDNE20115080	65.178	. 0
KIDNE20118580	100	0
KIDNE20120090	33.186	0
KIDNE20121880	62.256	0
KIDNE20121880	83.085	0
	6.171	!
KIDNE20124400		0
KIDNE20125630	100	0
KIDNE20126010	100	0
KIDNE20126130	100	0
KIDNE20127100	33.012	0
KIDNE20127450	100	0
KIDNE20127750	100	0
KIDNE20130450	100	0
KIDNE20131580	63.24	0
KIDNE20132180	100	0
KIDNE20137340	100	0
KIDNE20138010	100	0
KIDNE20141190	49.697	0
KIDNE20144890	100	0
KIDNE20148900	100	0
KIDNE20163880	100	0
KIDNE20180710	49.105	0
KIDNE20181660	100	0
KIDNE20182690	100	0
KIDNE20186780	100	0
KIDNE20190740	100	0
LIVER20035110	28.683	0
MESAN20025190	16.169	0
NT2RP70043480	7.879	О
PROST20107820	1.696	o
PROST20123530	32.771	0
PROST20161950	20.387	0
PUAEN20030180	46.744	0

Table 9 (continued)

CloneID	KIDNE	TKIDN
SKMUS20003610	3.728	0
SMINT20033400	10.243	0
TBAES20000590	5.253	0
TESTI20044310	29.162	0
TESTI20082330	45.847	0
TRACH20032720	12.917	0
UTERU20099720	12.351	0

Table 10

CloneID	LIVER	TLIVE
BRAWH20166790	83.525	0
CTONG20103480	15.35	o
HEART20005410	11.598	o
LIVER10001260	66.455	0
LIVER10004790	100	0
LIVER20002160	100	. 0
LIVER20011130	92.988	0
LIVER20011910	100	0
LIVER20028420	16.548	o
LIVER20035110	71.317	0
LIVER20035680	100	0
LIVER20038540	100	0
LIVER20045650	100	0
LIVER20055200	100	0
LIVER20055440	100	0
LIVER20059810	24.82	0
LIVER20062510	100	0
LIVER20064100	88.658	0
LIVER20064690	100	0
LIVER20075680	100	0
LIVER20080530	100	0
LIVER20084730	100	0
LIVER20085800	100	0
LIVER20087510	75.266	0
LIVER20091180	100	0
NTONG20063010	47.641	0
PROST20087700	6.762	0
PROST20107820	2.108	0
TRACH20005400	12.349	0
ASTRO20001410	0	10.441
ASTRO20125520	0	10.162
BRACE20152870	0	15.788
BRAMY20167060	0	34.076
BRAMY20181220	0	87.217
BRAMY20285160	0	81.346
BRCOC20001860	0	20.45
FEBRA20144170	0	3.712
HLUNG10000550	0	3.721

Table 10 (continued)

CloneID	LIVER	TLIVE
OCBBF20073540	0	6.907
OCBBF20088220	0	16.388
PLACE60169420	0	26.895
SMINT20152940	. 0	54.735
SPLEN20242320	0	45.601
THYMU20000570	. 0	18.649
TRACH20077540	0	30.987
UTERU20055930	0	15.433
UTERU20065930	0	10.151

Table 11

ClonelD	HLUNG	TLUNG
BRACE20096200	70.38	0
BRAWH20004600	2.238	ő
BRAWH20030250	11.121	0
BRCAN20006390	61.519	o
BRCAN20280360	8.855	o
BRHIP20238880	1.35	0
CTONG10000940	1.428	0
CTONG20103480	6.495	0
CTONG20129960	10.709	0
CTONG20155180	48.707	0
FCBBF10001210	36.439	0
FEBRA20144170	1.98	0
FEBRA20197110	7.756	0
HCHON20002260	2.958	0
HHDPC20034390	0.933	0
HLUNG10000550	3.971	0
HLUNG20016330	29.367	0
HLUNG20016770	12.888	0
HLUNG20017120	12.093	0
HLUNG20023340	33.714	0
HLUNG20033780	33.957	0
HLUNG20084390	100	0
IMR3220002430	3.147	0
LIVER20028420	14.004	0
NOVAR20000380	2.278	0
NT2RI20023910	8.923	0
NT2RI20054050	2.059	0
NT2RI20091730	4.091	0
NT2RP70044280	12.369	0
OCBBF20020830	40.304	0
OCBBF20125530	4.302	0
PLACE60004630	28.618	0
PROST20057930	14.383	0
PROST2010782	0.892	0
PROST20185830	33.898	0
PUAEN20030180	12.294	0

Table 11 (continued)

CloneID	HLUNG	TLUNG
SMINT20121220	12.822	O
SPLEN20002220	44.799	0
SPLEN20008740	1.788	0
SPLEN20054290	26.875	0
SPLEN20128000	1.253	0
SPLEN20157300	51.319	0
SPLEN20176200	18.8	0
SPLEN20179180	3.344	0
SPLEN20211940	12.373	0
STOMA20013890	21.183	0
TBAES20000590	5.527	0
TESTI20094230	59.311	0
TESTI20184620	10.365	0
TESTI20334410	8.049	0
THYMU20000570	4.974	0
THYMU20039810	1.915	0
TRACH20007020	14.4	0
TRACH20141240	3.786	0
TRACH20183170	10.745	0
ASTRO20108190	0	13.924
ASTRO20155290	0	38.341
BRHIP20096850	0	73.716
FEBRA20080810	0	14.654
MESAN20014500	0	59.68
SMINT20028820	0	60.089
SPLEN20162680	0	8.941

Table 12

CloneID	NOVAR	TOVAR
BGGI120006160	21.31	0
BRHIP20005340	8.158	0
BRHIP20191860	47.038	0
HHDPC20001040	44.094	0
NOVAR10000150	72.374	0
NOVAR10000910	46.155	0
NOVAR10001020	99.094	0
NOVAR20000380	14.805	0
NOVAR20003520	100	0
THYMU20271250	4.266	0
ASTRO20141350	0	75.66
BRAMY20157820	0	85.296
BRCOC20001860	0	64.79
HLUNG20016770	0	76.536
NT2RI20054050	0	12.229
NTONG20090600	0	60.694
PROST20087700	0	16.991
PUAEN20015860	0	62.197
SPLEN20029310	0	88.828

Table 12 (continued)

CloneID	NOVAR	TOVAR
TOVAR20004760	0	49.428
TOVAR20005750	0	96.313
TRACH20079690	0	55.276
UTERU20004240	. 0	18.499

Table 13

Iai	Table 13		
CloneID	STOMA	TSTOM	
BRACE20060840	0	65.917	
FEBRA20052910	0	77.883	
HCHON20002260	0	8.66	
HLUNG10000550	0	11.625	
NTONG20009770	0	21.112	
PROST20107820	0	5.223	
THYMU20039810	0	11.216	
TSTOM10001860	0	100	
TSTOM20001390	0	89.823	
TSTOM20003150	0	48.943	
TSTOM20005690	· 0	100	
ASTRO20125520	10.059	0	
BRACE20039040	17.642	0	
BRAMY20124260	42.064	0	
BRCOC20031870	10.704	0	
BRHIP20191860	13.43	0	
CTONG20128470	11.719	0	
FEBRA20037500	12.423	0	
HCHON20040020	5.343	0	
HHDPC10000830	6.661	0	
IMR3220002430	5.838	0	
KIDNE20007770	12.986	0	
NOVAR20000380	4.227	0	
NT2RI20054050	1.91	0	
NT2RI20091730	7.59	0	
PROST20130530	20.156	0	
SPLEN20149110	7.179	0	
SPLEN20157880	32.942	0	
STOMA20001830	100	0	
STOMA20005390	100	0	
STOMA20005670	100	0	
STOMA20006400	100	0	
STOMA20006780	100	0	
STOMA20006860	100	0	
STOMA20008880	100	0	
STOMA20010250	100	0	
STOMA20013890	39.303	0	
STOMA20026880	100	0	
STOMA20032890	100	0	
STOMA20034770	100	0	
STOMA20036460	100	0	

Table 13 (continued)

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	(Gontingea)	
CloneID	STOMA	TSTOM
STOMA20046680	100	0
STOMA20048520	100	0
STOMA20048840	100	0
STOMA20051200	85.988	0
STOMA20056640	100	0
STOMA20056670	100	0
STOMA20057820	91.236	0
STOMA20062130	100	0
STOMA20062290	40.913	0
STOMA20063250	100	0
STOMA20063980	100	0
STOMA20064470	100	0
STOMA20067800	59.113	0
STOMA20069040	100	0
STOMA20072690	100	0
STOMA20076800	100	0
STOMA20077450	100	. 0
STOMA20080500	100	- 0
STOMA20083610	. 100	0
STOMA20086	100	0
STOMA20088380	100	0
STOMA20092530	100	0
STOMA20092560	100	0
STOMA20092890	39.042	0
TESTI20184620	19.231	0
TRACH20003590	40.588	0
TRACH20183170	19.936	0
PROST20083600	12.248	38.653
TRACH20068660	6.753	21.311

Table 14

CloneID	UTERU	TUTER
DFNES10001850	0	29.393
NT2RI20023910	0	18.073
SMINT20144800	0	35.406
SPLEN20162680	0	9.628
TOVAR20004760	0	50.572
TUTER20002830	0	100
ASTRO20008010	1.217	0
ASTRO20033160	10.555	0
ASTRO20058630	4.534	0
ASTRO20105820	20.644	0
ASTRO20108190	3.21	0
BRACE20039040	3.092	0
BRACE20057190	3.542	0
BRACE20060840	3.661	0
BRACE20111830	7.667	0
BRACE20223330	10.589	0

Table 14 (continued)

	<u> </u>	
CloneID	UTERU	TUTER
BRAMY20266850	2.956	0
BRAWH20113430	8.367	0
BRAWH20126980	22.868	0
BRCOC20031870	. 0.938	0
BRCOC20107300	12.892	0
BRCOC20121720	6.71	0
BRCOC20155970	25.187	0
BRHIP20105710	18.366	0
BRHIP20191490	13.172	0
BRHIP20207990	12.072	0
BRHIP20217620	6.646	0
BRHIP20222280	10.898	o
BRHIP20238880	0.439	o
BRHIP20249110	11.054	О
BRSSN20018690	3.6	o
BRTHA20000570	51.819	o
CTONG10000940	0.464	0
CTONG10002770	24.668	- 0
CTONG20095290	7.541	o
CTONG20099380	23.863	0
CTONG20103480	6.336	0
CTONG20108210	2.557	0
CTONG20108210	10.239	0
1	3.482	0
CTONG20129960		0
CTONG20131560	24.668	l :
CTONG20139070	2.571	0
CTONG20139340	8.273	0
CTONG20143690	4.963	0
CTONG20160560	2.372	0
D3OST30002580	22.242	0
FCBBF10000240	5.237	0
FCBBF10001820	10.114	0
FCBBF10003670	1.812	0
FCBBF10004120	2.308	0
FCBBF10005740	4.952	0
FCBBF30175310	1.912	0
FCBBF30240020	6.769	0
FCBBF30246230	6.682	0
FCBBF40001420	4.36	0
FEBRA20002100	0.843	0
FEBRA20004620	6.733	0
FEBRA20018280	6.489	0
FEBRA20025270	3.416	0
FEBRA20034360	6.63	0
FEBRA20037500	19.596	0
FEBRA20080810	0.845	0
FEBRA20082100	15.999	0
FEBRA20144170	1.288	0
FEBRA20225040	1.959	0
HCHON20002260	0.962	0

Table 14 (continued)

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ClaralD	(Continued)	TUTES
CloneID	UTERU	TUTER
HCHON20007380	3.551	0
HCHON20015980	5.796	0
HCHON20016650	1.84	0
HCHON20022470	3.348	0
HCHON20040020	0.936	0
HCHON20076500	7.263	0
HEART20072310	11.555	0
HHDPC20034390	1.517	0
HLUNG10000550	1.937	0
HLUNG20016770	4.191	0
KIDNE20131580	21.635	0
LIVER20028420	9.107	0
MAMGL10000830	0.346	0
MESAN20171520	24.337	0
NOVAR10000150	3.622	0
NOVAR10000910	2.31	0
NT2NE20053580	24.761	0
NT2NE20159740	9.111	- 0
NT2NE20174920	20.127	0
NT2RI20023160	0.956	o
NT2RI20041880	3.425	0
NT2RI20054050	1.004	0
NT2RI20076290	2.404	0
NT2RI20273230	39.625	0
NT2RP60000770	30.666	o
NT2RP60000850	11.032	0
NT2RP70036880	0.881	0
NT2RP70043480	2.695	o
NT2RP70045590	10.166	o
NT2RP70056750	10.406	0
NT2RP70062230	5.039	o
NT2RP70081610	7.488	o
OCBBF10001750	8.591	0
OCBBF20006770	19.428	0
OCBBF20032460	11.672	0
OCBBF20039250	0.994	o
OCBBP20047570	2.956	0
OCBBF20054760	16.727	o
OCBBF20059560	3.386	o
OCBBF20068490	2.41	0
OCBBF20080050	3.787	0
OCBBF20094240	8.655	0
OCBBF20097720	1.404	0
OCBBF20103130	16.359	0
OCBBF20105570	43.708	0
OCBBF20140640	3.258	0
OCBBF20140840	3.068	0
OCBBF20173980	10.043	0
OCBBF20180120	6.611	
OCBBF20188730	2.019	0
OC00F20169560	2.019	<u> </u>

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Table 14 (continued)

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Table 14	(continued)	
CloneID	UTERU	TUTER
PEBLM20044520	6.439	0
PLACE60060420	6.493	0
PROST20087700	0.93	0
PROST20107820	0.29	0
PROST20149160	4.345	0
PROST20159240	8.082	0
PROST20176170	25.167	0
PROST20189770	15.499	0
PUAEN20003740	1.145	0
PUAEN20015860	3.406	0
SKMUS20003610	1.275	0
SKNSH20008190	5.937	0
SKNSH20080430	12.076	0
SMINT20026890	51.875	0
SMINT20029760	6.221	0
SMINT20068010	19.209	0
SMINT20110330	25.261	0
SMINT20121220	4.169	- 0
SPLEN20008390	10.886	0
SPLEN20011410	2.253	0
SPLEN20054290	17.478	o
SPLEN20128000	0.407	0
SPLEN20140800	5.651	0
SPLEN20145720	7.423	0
SPLEN20169720	4.837	0
SPLEN20179180	3.262	o
SPLEN20193110	57.827	0
SPLEN20194050	3.416	ō
SPLEN20211940	8.047	o
SPLEN20212730	17.589	0
SPLEN20225220	1.691	0
TBAES20000590	1.797	0
TESTI20061110	24.59	o
TESTI20116830	38.615	o
TESTI20184620	3.37	0
TESTI20208710	64.596	Ö
TEST120211240	6.816	o
TESTI20213580	40.357	0
TESTI20213360	4.107	0
TESTI20334410	2.618	0
TESTI20369130	24.204	0
		0
TESTI20369690 TESTI20391770	4.285 4.943	0
THYMU20039810	2.491	
1	58.853	·
THYMU20216840	1	0
THYMU20240710	39.309	0
TRACH20003590	3.557	0
TRACH20032720	4.419	0
TRACH20033230	2.123	0
TRACH20141240	3.693	0

Table 14 (continued)

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Table 14	(continued)	
CloneID	UTERU	TUTER
TRACH20149970	25.316	0
UMVEN10001860	0.63	0
UTERU20000740	62.692	0
UTERU20004240	1.013	0
UTERU20006290	100	0
UTERU20020010	40.126	0
UTERU20022940	2.165	0
UTERU20030570	3.085	0
UTERU20040610	100	0
UTERU20046640	4.048	0
UTERU20046980	100	0
UTERU20050690	64.596	0
UTERU20054460	24.816	0
UTERU20055330	100	0
UTERU20055930	4.016	0
UTERU20056010	3.04	0
UTERU20059050	100	0
UTERU20061030	100	- 0
UTERU20064000	15.228	0
UTERU20064860	51.819	0
UTERU20065930	3.522	0
UTERU20067050	100	0
UTERU20068990	100	0
UTERU20070040	24.856	0
UTERU20070810	17.449	0
UTERU20076390	100	0
UTERU20081300	53.896	0
UTERU20084260	26.26	0
UTERU20094350	12.756	0
UTERU20095380	40.674	0
UTERU20095400	100	0
UTERU20097760	10	0
UTERU20099720	16.901	0
UTERU20101240	100	0
UTERU20114100	100	0
UTERU20115740	100	0
UTERU20116570	100	0
UTERU20118110	100	0
UTERU20118970	100	0
UTERU20119060	16.267	0
UTERU20119680	100	0
UTERU20120310	53.896	0
UTERU20124070	29.356	0
UTERU20126880	51.568	0
UTERU20134910	13.929	
UTERU20135860	7.858	0
UTERU20143980	100	
UTERU20144640	16.101	
UTERU20145480	39.231	0
UTERU20146310	100	0
3 (2.1020140010		<u> </u>

Table 14 (continued)

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CloneID	UTERU	TUTER
UTERU20146680	39.231	0
UTERU20150870	100	0
UTERU20151980	100	0
UTERU20158300	58.853	0
UTERU20158800	100	0
UTERU20161570	100	0
UTERU20164260	15.158	0
UTERU20168220	19.178	0
UTERU20176130	12.264	0
UTERU20176320	64.596	0
UTERU20178100	100	0
UTERU20179880	100	0
UTERU20183640	53.896	0
UTERU20185230	40.126	0
UTERU20186740	100	0
UTERU20188110	100	0
UTERU20188810	100	0
BRAWH10000930	2.2	10.279
CTONG20128470	2.054	38.378
UTERU20006960	3.394	63.416

Table 15

CloneID	NTONG	CTONG
ADRGL20018300	0	22.262
ASTRO20058630	0	14.161
ASTRO20072210	0	34.963
ASTRO20108190	0	5.013
BRACE20003070	0	2.194
BRACE20039040	0	4.829
BRACE20060720	0	36.712
BRACE20061050	0	39.515
BRACE20210140	0	11.034
BRACE20276430	0	26.828
BRAMY20152110	0	24.194
BRAMY20266850	0	4.616
BRAMY20271400	о	48.032
BRAWH10000930	0	3.436
BRAWH20004600	0	1.137
BRCAN20280360	0	4.497
BRCOC20004870	0	0.54
BRHIP20005340	0	5.1
BRHIP20005530	0	4.786
BRHIP20238880	0	2.741
BRSSN20146100	0	6.65
CTONG10000100	0	12.075
CTONG10000220	0	100
CTONG10000620	0	100
CTONG10000930	0	74.021

Table 15 (continued)

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ClanalD	NTONG	CTONG
CloneID		i I
CTONG10000940	0	0.725
CTONG10001650	0	100
CTONG10002770	0	38.523
CTONG20002180	0	100
CTONG20004690	0	5.439
CTONG20009770	0	100
CTONG20014280	0	62.446
CTONG20027090	0	4.036
CTONG20028410	0	19.729
CTONG20038890	0	100
CTONG20049410	0	100
CTONG20050280	0	25.499
CTONG20052650	0	34.822
CTONG20052900	0	42.764
CTONG20075860	0	11.194
CTONG20076130	0	16.303
CTONG20077790	0	62.68
CTONG20082690	0	12.672
CTONG20085950	. 0	100
CTONG20091080	0	44.201
CTONG20091320	0	100
CTONG20092570	0	100
CTONG20092580	0	100
CTONG20092680	0	100
CTONG20092700	0	100
CTONG20093950	0	100
CTONG20095270	0	100
CTONG20095290	0	11.777
CTONG20095340	0	14.323
CTONG20096430	0	100
CTONG20096750	0	100
CTONG20097660	0	100
CTONG20097660 CTONG20098440		33.474
CTONG20098440		37.266
		1
CTONG20099550 CTONG20099630	0	100 38.502
CTONG20100240	0 0	100
CTONG20101480	1	
CTONG20103480	0	13.193
CTONG20105080	0	15.273
CTONG20105660	0	25.256
CTONG20106230	0	100
CTONG20106520	0	29.937
CTONG20108210	0	2.662
CTONG20114290	0	100
CTONG20114740	0	100
CTONG20118150	0	100
CTONG20118250	0	15.991
CTONG20119200	0	100
CTONG20120770	0	100

Table 15 (continued)

lable 15	(continued)	
CloneID	NTONG	CTONG
CTONG20121010	0	29.404
CTONG20121580	0	33.983
CTONG20124010	0	7.835
CTONG20124220	0	69.076
CTONG20124470	0	100
CTONG20124730	.0	100
CTONG20125540	0	100
CTONG20125640	0	7.359
CTONG20126070	0	3.221
CTONG20127450	0	10.331
CTONG20128470	0	9.622
CTONG20129960	0	32.63
CTONG20131490	0	24.817
CTONG20131560	0	38.523
CTONG20132220	0	6.999
CTONG20133390	0	100
CTONG20133480	0	10.246
CTONG20133520	0	50.616
CTONG20136300	0	100
CTONG20138030	0	100
CTONG20139070	o	8.031
CTONG20139340	0	12.919
CTONG20139860	0	100
CTONG20140320	0	100
CTONG20140580	0	100
CTONG20140500	0	8.968
CTONG201476300	0	100
CTONG20147050	0	34.963
CTONG20149460	0	100
CTONG20149400 CTONG20149950	0	100
CTONG20143930	0	52.97
CTONG20153580	0	74.021
CTONG20155180	0	24.734
CTONG20155400	0	100
CTONG20156780	0	62.446
		100
CTONG20158040	0	1
CTONG20158150	0	16.385 100
CTONG20158660	1	1
CTONG20159530	0	100 3.704
CTONG20160560	0	
CTONG20161850	0	19.368
CTONG20162170	0	100
CTONG20163550	0	100
CTONG20164990	0	65.066
CTONG20165050	0	33.474
CTONG20186320	0	14.897
CTONG20200310	0	100
CTONG20265130	0	100
CTONG20267700	0	100
CTONG20273610	0	100

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Table 15 (continued)

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Table 15	(continued)	
CloneID	NTONG	CTONG
FCBBF10000240	0	12.268
FCBBF10005740	0	3.866
FCBBF30123470	0	4.088
FCBBF30233680	0	9.14
FEBRA20025270	0	5.334
FEBRA20037500	- 0	6.8
HCHON20002260	0	1.502
HCHON20007380	0	5.546
HCHON20007510	0	6.65
HCHON20015350	0	17.176
HCHON20040020	0	1.462
HHDPC20034390	0	0.474
HLUNG10000550	0	2.016
KIDNE20002520	0	3.184
KIDNE20009470	0	9.415
KIDNE20115080	0	34.822
KIDNE20127100	0	35.274
LIVER20028420	0	3.556
MESAN20029400	0	5.924
NT2RI20023160	0	1.493
NT2RI20023910	0	1.51
NT2RI20091730	0	4.155
NT2RP70043480	o	4.209
NT2RP70078420	0	3.572
NT2RP70081610	0	11.694
OCBBF20006770	0	30.34
OCBBF20059560	0	5.287
OCBBF20073540	0	1.871
OCBBF20094240	0	13.516
OCBBF20108580	0	12.407
PEBLM20044520	0	15.083
PEBLM20071880	0	16.259
PROST20107820	0	0.453
PUAEN20030180	l 0	6.243
SKNSH20008190	١٠٠	4.636
SMINT20023280	Ó	34.547
SMINT20089170	1 0	20.839
SPLEN20179180	0	5.094
TESTI20094020	0	17.075
TESTI20094230	1 0	30.119
TESTI20152460	0	22.051
TESTI20184620	0	5.263
TESTI20211240	0	10.645
TESTI20442760	0	8.832
THYMU20039810	0	0.973
TRACH20028030	0	11.644
TRACH20141240	ő	1.923
TSTOM20003150	0	4.245
UTERU20004240	0	1.582
UTERU20055930		2.091
0121020033930	<u> </u>	4.031

Table 15 (continued)

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	(continued)	
CloneID	NTONG	CTONG
UTERU20065930	0	2.75
UTERU20119060	0	12.702
UTERU20124070	0	45.844
BRACE20039440	34.336	0
BRACE20068590	74.88	0
FCBBF30018550	20.639	0
IMR3220002430	6.323	0
KIDNE20028830	16.715	0
NT2RI20028470	9.251	0
NT2RI20054050	2.069	0
NT2RI20086220	23.258	o
NTONG20009770	7.245	o
NTONG20013620	25.727	o
NTONG20028070	86.921	0
NTONG20029480	32.729	o
NTONG20029700	100	o
NTONG20046140	43.643	ō
NTONG20048060	51.123	. 0
NTONG20049910	.100	0
NTONG20050620	100	ا ه ا
NTONG20050860	100	0
NTONG20051530	58.314	0
NTONG20052650	100	
NTONG20052650	100	0
NTONG20061870	100	0
NTONG20063010	40.505	0
	100	0
NTONG20064400	31.857	0
NTONG20064840		
NTONG20065010	100	0
NTONG20066460	100	0
NTONG20067090	66.789	0
NTONG20067830	20.865	0
NTONG20070200	100	0
NTONG20070340	52.247	0
NTONG20075220	100	0
NTONG20076930	51.858	0
NTONG20077560	49.744	0
NTONG20083650	100	0
NTONG20088620	100	0
NTONG20090600	20.536	0
NTONG20090680	100	0
NTONG20092290	100	0
NTONG20092330	100	0
OCBBF20068490	14.895	0
SKMUS20001980	23.281	0
SMINT20138900	67.622	0
SPLEN20008390	67.269	0
SPLEN20162680	3.184	0
UTERU20134910	86.071	0
ASTRO20155290	13.655	3.451

Table 15 (continued)

	<del></del>	
CloneID	NTONG	CTONG
FEBRA20080810	10.438	1.319
NT2RP70032610	10.013	27.835
NT2RP70036880	5.442	16.504
NTONG20015870	17.552	0.554
OCBBF20188730	10.213	2.581
SMINT20122910	33.985	8.589
SPLEN20099700	37.585	9.499

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Table 16

	0	ि	0	0	0	519	0	0	0	0	5	0	0	0	0	0	394	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-	0
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BRSTN	0	0	0	0	0	0	0	0	0	0	3, 224	0	0	0	0	0	0	0	0	0	1.867	0	0	0	٥	0	0	0	0	0	0	0	0	0	0	0
BRSSN	0	0	0	0	0	0	0	0	42.066	0	0	0	0	0	0	0	0	0	0	0	1.927	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9RH1P	6. 246		0	0	0	0	0	0	0	1.927	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	21.084	0
энсос	0	0	0	0	0	0	0	12, 305	0	0	0	0	0	0	0	0	0		0	0	1.834	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRCAN	0	0	0	0	0	0	39, 838	0	0	2.167	2.051	0	0	0	0	0	0	0	0	0	1.188	0	0	0	0		0	0	0	0	0	0	0	0	0	0
BRAMH	6.122	0	0	2.95	7. 603	0	0	0	0	0	0	0	0	0	0	0	0	0	Ŋ	0	0.518	0	0	0	0	0	0	0	0	0	0	0	0	0	41, 331	0
BRAMY	0	0	3 06	U	0	7, 505	0	0	11, 388	0.952	0.901	0	0	0	0	0	0	0	0	0	2.086	0	O	0	0	0	0	0	0	0	0	0	0	0	0	0
BRALZ		0	C	0	0	0	0	0	0	0	0	0	53, 184	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRACE	0	8. 483	0	2.094	0	0	0	0	0	0	1, 269	100	10.447	100	100	100	38, 906		38. 787	100	0.367	16.746	52.057	100	100	8	100	100	10,086	100	100	5	18	100	14.668	100
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FEBRA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9			0
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Table 17

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		ACE20061740	3ACE20061740	RACE20061740 RACE20062400 RACE20062740	RACE20061740 RACE20062400 RACE20062740 RACE20063630	3RACE20061740 3RACE20062400 3RACE20062740 3RACE20063630 3RACE200633780	9RACE20061740 9RACE20062400 9RACE20062740 9RACE20063380 9RACE20063380	3RACE20061740 3RACE20062400 8RACE20062740 BRACE20063380 BRACE20063380 BRACE20063930	BRACE20061740 BRACE20062400 BRACE20062740 BRACE20063330 BRACE200633800 BRACE20063330	BRACE20061740 BRACE20062400 BRACE20062740 BRACE20063330 BRACE20063330 BRACE20063330 BRACE20063330 BRACE20063930 BRACE2006880	BRACE20061740 BRACE20062400 BRACE20062740 BRACE20063330 BRACE20063330 BRACE20063330 BRACE20063930 BRACE2006390	3RACE20061740 3RACE20062400 3RACE20062740 3RACE20063330 3RACE20063330 3RACE20063330 3RACE20063330 3RACE20063330 3RACE20063330 3RACE20063330 3RACE20063330	3RACE2006 1740 3RACE2006 2400 BRACE2006 2 400 BRACE2006 3 800 BRACE2006 3 800 BRACE2006 3 800 BRACE2006 8 800	3RACE2006 1740 3RACE2006 2400 3RACE2006 2400 3RACE2006 350 BRACE2006 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Table 18

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Table 20

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0	0	78, 159		0	0	0	0	0	0	0	0										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	10, 452	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10.427	0	0	0	0	0	0	0	0	0	0	0	0	51.427	0	0	0
0	ō	0	11. 626	0	2.865	0	0	0	0	0	0	0	0	0	0	0	0	o	50.312		0	0	0	0	0	3.844	0	0	0	44, 442	0	0	14, 097	0	0	0
0	0	0	40.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9.924	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	6.443	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12, 854	0	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	0
0	0	0	0	0	0	0	0	11.017	0	0	0	0	0	0	0	0	o	0	0	5. 603	0		0		00	11.304	0	0	0	14. 52	0	0	0	0	0	0
8	8	21.841	22. 964	100	2.83	100	36.63	33, 302	100	100	100	100	100	6. 228	100	43.537	29. 482	19, 026	49.688	4. 234	19.441	13.088	100	7.891	100	3. 796	100	4.994	100	14. 63	100	100	13.922	12, 783	100	100
0	0	Э	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.061	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ō	0	0	8.088	0	0	0	0	15. 639	0	0	0	0	0	0	0	0	0	0	0	5, 965	0	0	0	0	0	0	0	0	0	10.306	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RANY 2002 5840	BRAWY20039260	BRANY20045240	RAMY20054880	RAWY20060920	BRAMY20063970	BRAMY20071850	BRAMY20102080	BRANY20104640	BRAMY20110640	BRAMY20111960	3RAMY20116790	BRAMY20121190	BRANY20121620	BRAMY20124260	BRANY20134140	BRAMY20135900	BRAMY20136210	BRAMY20137560	RANY20144620	RAMY20147540	RAMY20148130	BRAMY20152110	BRAMY20153110	RANY20157820	RAMY20160700	BRAMY20163250	RAMY20163270	RAMY20167060	RAMY20167710	RAMY20168920	RAMY20170140	RAMY20174550	BRAMY20178640		RANY20182730	IRAMY20183080
0	80	(حم		œ	8	Œ	8	Ö		8	8	8	<u> </u>	œ	8	Œ	ã	اقه	8	8	2	8	20	8	8	8	∞]	8	8	8	8	8	8	20)	8	æ

Table 21

0	0	٥	0	0	a	0	0	0	0		39, 237	9	0			3.067	٥	0	0	0	0	0	0	52, 395		35, 583	0	0	0	0	0	0	0	50, 221		
0	0	0	0	0	0	0	0	0	0	0	٥	0	0	9	0	٥	0	44, 21	0	0	0	0	0	0	0	0	0	0	0	0	٥		0	0		0
0	0	0	0	0	0	0	0	0	٥	٥	0	0	9	0	0	0	0	٥	0	0	0	0	0	0	0	9		0	0	0			0		0	9
0	0	0	0	0		0			0	33.61			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12, 601	0	3
0	0	0	0	0	0	0	0	0	0	0		54.084	0	0	0	9. 799	0	43. 436	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	0
0	0	0				0				0		1	0	0	0	6, 346	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	30, 533	0	0	0	0	0	0	0	0	0	0	0	0	0	32, 087	0	0	0	0	0	0	0	20, 585	0	0
100	100	100	001	001	25. 787	26.981	12, 518	21, 367	100	66. 389	35.65	15, 383	100	100	100	2. 787	100	12, 354	100	100	8	5	8	47.605	100	32. 33	2, 497	100	100	100	51.968	100	100	16, 593	100	36. 15
0	0	0	0	0	0	0	0	0	0	0	0	0	0	O	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	38.011		0	0	0	25, 113	0	0	0	0	1.963	0							0				0				0			0	0
10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	٥	0	0	0	0
0	0	0	0	0	0	0	0	0	0															0						0				0		0
C	0	0	0	0	0	0	Te	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RRANY20184870	V201	Y202		BRANY20210400	BRAWY20211390	BRAWY20211420	RRAMY20213100	BRAWY20215230	BRAMY20217460	BRAMY20218250	BRAMY20218670	BRANY20229800	BRAMY20229840	BRAWY20230600	BRANY20231720	BRANY20240040	BRAINY20245300	BRAWY20247110	BRAMY20247280	BRANY 20248490	BRAWY20250240	BRAWY20250320	RRAMY20252180	BRAWY20252720	BRAMY20260910	BRAMY20261680	BRAMY20266850	BRAMY20267130	BRANY20268990	BRANY20270730	BRAWY20271400	BRAWY20273960	RRAMY20277140	BRAMY20277170	BRAHY20280720	BRAMY20284910

Table 22

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6	0	0	0	8.091	0	10.951	0	0	0	0	0	9.564	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2. 96
0	0	0	0	0	0	14, 243	0	0	0	0	0	0	0	0	0	ō	0	0	0	0	0	40.334	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14.68	0	ō	0	27, 156	0	16. 539	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.822	0	0	0	0	0	0	0	0	18.88	0	0	0	9.934
0	0	0	0	o	0	10.075	0	0	0	0	0	17, 598	0	13.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2, 723
0	0	0	0	0	0	5.247	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9.455
0	0	0	0	0	0	15, 859		0	0	0	0	0	0	0	0	0	0	0	0	69, 644	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6. 123
0	0	0	100	7. 296	100	1.975	100	100	9	100	100	8.624	11. 932	12.977	100	21. 269	100	26. 404	100	30, 356	100	11, 186	21. 178	100	54. 53	100	5	100	100	21. 626	100	10. 145	100	1		2. 669
3.974	100	21.396	0	0	0	6.965	0	0	0	0	0	17. 379	0	0	0	0	0	26. 605	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.958		8.068
0	0	0	0	0	0	5. 352	0	0	0	0	0	31, 162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		35.004	0
0	0	0	0	0	0	0	0	0	0	0	0	0	8. 469	0	0	0	0	0	0	0	0	7.94	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	0	0	0	0	0	0	٥	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	٥	٥	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	٥	0	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	0	0	٥	٥	0	0	9	0	0	0	0	0	0	0	0	0	0
BRAMY20285160	BRA#Y20285930	BRAMY20286820	BRAWH20002320	BRAWH20012390	BRAMH20014920	BRAMH20015350	BRANH20015890	BRANH20016660	BRAWH20016860	BRAWH20017010	BRANH20018730	BRAWH20028110	BRAMH20029630	BRAMH20064050	BRAMH20075700	BRAMH20096780	BRAWH20100690	BRAWH20101360	BRAMH20103180	BRAWH20105840	BRANH20106180	BRAMH20107540	BRAWH20110660	BRAWH20110790	BRAWH20110960	BRAWH20111550	BRAM120112940	BRAWH20114000	BRAWH20117950	BRAWH20118230	BRAWH20122580	BRAWH20125380	BRAIN 20126190	1269	BRAMH20132190	BRAMH20137480

Table 23

0	0	0	0	0	0	0	0	0	0	9	0	766	9	0	0	0	0	0	0	. 142	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0 36.	0	0	. 0	0	0	0	9	0 25.	115	0	0	0	0	0	9	0	0	0	0		9	0	9	0
																			13, 546		61.11		,													į
0	0	0	0	0	0	0	0	4, 907	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0		11.275					0		က	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	٥	0	0	0	4.67	0	0	0	0	0	0	0	0	0	0	26. 617	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	3, 025	0	0	0	0	0.	56.874	100	100	38. 481	100	25.857	52.014	38.885		69. 484	100	100	100	100	100	100	100	34.67	100	69.484	100	100	100
100	200	100	100	35.975	100	100	49.811	1.318	9. 636	100	100	11.051	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	50, 189	1.328	0	0	0	0	0	0	0	0	0	0	0	22. 844	0	0	30, 516	0	0	0	0	0	0	0	0	0	30, 516	0		0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13. 575	0	0	0	0	0	0	0	0	0	0	0	54.604	0	0	0	0	0
0	0	0	0	0	0	0	0	0.936	6. 839	0	0	0	0	0	0	0	0	0	2. 666	0	0	0	0	0	0	0	0	0	0	0	10, 726	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	ō	0	0	0	0	0	0	0	0	0	0	0	0	0	ō
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRAM120138660	BRAWH20139410	BRAMH20142340	BRAWH20147290	BRAWH20149340	BRAWH20155050	BRAWH20158530	BRAWH20160280	RRAMH20162690	BRAM120166790	BRAWH20171030	BRAWH20173050	BRAWH20182060	BRAWH20185060	BRCAN 1000 1490	BRCAN20003460	BRCAN20006200	BRCAN20006390	BRCAN20054490	BRCAN20060190	BRCAN20064010	BRCAN20071190	BRCAN20091560	BRCAN20103740	BRCAN20124080	BRCAN20126130	BRCAN20143700	BRCAN20147880	BRCAN20216690	BRCAN20224720	BRCAN20237240	BRCAN20263400	BRCAN20273100	BRCAN20273340	BRCAN20273550	BRCAN20275130	BRCAN20279700

Table 24

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_					_							_		_	_	_	_	_	-		_	_	_	,		_		_				_			_	_
0	0	0	0	0	0	0	0	0	0.643	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	19.596	0	0	0	0	0	0	0	11.987	0	0	0
0	0	0	0	0	61.115	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2. 836	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	48.439	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.854	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	c	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16.392	0	0	0	0	0
0	0	0	0	0	0	100	10. 537	2	1.026	100	77.986	100	100	76, 977	100	<u>6</u>	5	83, 309	20, 131	2. 786		75. 977	100	34, 465	65. 299	100	100	100	100	100	56.917	3.881	38, 292	100	100	100
100	60.666	29.858	100	100	38.885	o	0	0	0.665	0	0	0	0	0	0	0	0	0	0	1.804	0	0	0	0	0	0	0	0	0	0	0	2.513	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	22.014	0	0	0	0	0	0	0	0	0. 786	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17.805	0	0	0	0	0	16. 189	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	٥	0	0	٥	0
0	0	0	0	0	0	0	4. 222	0	0	0	0	0	0	0	0	0	0	16.691	0	0.558	9	0	٥	0	0	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	0	٥	0	0	0	0	0	0	٦	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٩	0	0	0	0	0	0	0	0	0	0	0
90210	80400	20283190	20283380	20284600	0285450	00000870	20001860	20004040	20004870	20006370	20008160	20008500	0020850	20021550	20023230	COC20026640	COC20027510	31000	331250	COC20031870	35130	37320	337400	)41750	)55420	59510	069770	390520	091960	93800	399370	101230	107300	110100	114180	117690
BRCAN20280210		BRCAN202	BRCAN20,	BRCAN202	BRCAN202	BRCOC10(	BRCOC200	BRCOC20C	BRCOCZOC	BRCOCZOC	BRCOCZOC	BRCOCZOC	BRC0C20C	BRCOCZOC	BRC0C200	BRCOCZOC	BRCOC200	BRC0C20031000	BRC0C20031250	BRCOCZO	BRC0C20035130	BRC0C20037320	BRC0C20037400	BRC0C20041750	BRC0C20055420	BRC0C20059510	BRC0C20077690	BRC0C20090520	BRC0C20091960	BRC0C20093800	BRC0C20099370	BRC0C20101230	BRC0C20107300	BRC0C20110100	BRC0C20114180	BRC0C20117690

Table 25

0	3 119	0	0	0	0	0	٥	٥	0	0	0	0	9		7. 299	٦	0	2	٥	52.083	0		٥		23, 948		ō	0	٩	52.083		52. 083	0	٥		2
0	0	0	0	0	0	0	0	0	0	0	0				0	0		0	0	9	9	9	0	0	9		9	9	٩	0	0	0	0	7	0	5
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	24. 496	0	0	=	0	0	0	0	0	28. 568	0	9	9	0	0	0	0	0	0		0	5
0	2.87	0	0	0	0	0	0	0	0	0	0	0				38, 155	9	7. 269		47.917	31.42	5	100	15. 661		19, 559		60.949	5	47.917	2	47.917	17. 468	ë	9	8
100	9. 965	100	60.694	100	100	100	59.512	100	100	74.813	100	48, 902	5	0	0	0	0	٥	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	0	0	٥	0
0	0	0	39, 306	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		37, 398	0	7. 124	0	0	0	0	0	15, 351	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	6	6	0	0	0	0	49.688	6.632	0	0	0	0	0	16.515	0	0	7.734	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	6	0	0	0	0	0	0	0	0	0	0		23. 78	0		0	0	0	0		0			0		0	0	0	0	0	0	0	0	0
6	1.996	c		6	c	te	te	0	C	0	0	0	0	0	0	0	0	0	0	0	21.859	0	0	32, 686		13, 607	0	0	0	0	0	0	0	0	0	0
	0	6	le	6	6	te	de	-	le	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			0
6	to	10	10	1	6	10	10	•	10	9	6	e	0	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	,	10	10	0		1	1	1	90	10	1	0	0	0	0	0	0	0	0	0	6	10	P	0	0	0	C	-		0	0	0	0	0	0
09001100000	3BC0C20121720	20000000000000000000000000000000000000	DDC00000000000000000000000000000000000	DDC000134480	00245000000	00/00/00/00/00/00/00/00/00/00/00/00/00/	BRC0C20130130	000410100000	005/14/00000	BACOCZ0148330	BBC0C20158240	BBC0C20176520	RRC0C20178560	RRH 1 P 1 0 0 1 2 9 0	BRH   P20000870		BRH 1 P 2 0 0 9 6 1 7 0	BRH 1 P20096850	BRH 1 P20 103090	RRH 1 P 2 0 1 0 4 4 4 0	RAH 1 P 2 0 1 0 5 7 1 0	BBH 1020106100	DOI 02010201000	BRH 1020111200	80H 1020115080	RRH 1 P 20 1 1 5 7 60	REM   P20118380	BBH   P20118010	200	1020	02012	200	BRH 1920132860	BRH 1 P 20 1 3 5 1 0 0	RRH   P20137230	BRH 1P20139720

Table 26

0	0	426	0	0	0	0	0	0	10	0	0	0	0	0	0	10	0	0	0	0	0	0	0	6	6	0	612	0	0	0	0	0	0	0	0	1
		37.							L						Ľ	L		L		L			L		L		5.								L	1
0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0	ľ	0	ľ	0	°	0	ľ	0	0	ľ	0	0	0	0	0	٥	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3. 967	100	1, 432			100	100	8	100	100		001	901	8	100	100	100	9	0	100	1. 267	8		<u>0</u> 01	8		100	6. 143	100	100	100	0.312	15.312	3. 004	, ,	6. 438	Ł
36.		34.	_	_	0	0	0	0	0	0 14.	0	0	0	0	0	0	0	0	0	1	0	0 74	0	0	0 19.	0	0 36.	0	0	0	0 50	0	0 23.	0 26.	0 36	1
5	0	0	0	0	0	0	0	0	0	0	0	0	0.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.061	0	0	0	0	0	1.666	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5. 298	0	0	0	49. 688	0	0	0	0	
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	æ	0	0	0	Į	ଞ	0	0	0	0	0	8. 28	0	0	
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0 25	0	0	0		9	0	0	0	0	0	0	9	0	
٥	0	0	0	0	0	0	0)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-
٥	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	0	0	
-	-											_							-	-		_			4		-	_	-		_	_		4		
1720140530	BRH   P20142850	BRH 1 P 2 0 1 4 3 7 3 0	RH I P 20143860	RH I P 2014 9540	BRH 1 P 20153560	20153600	BRH1P20167880	BRH 1 P 2 0 1 6 9 6 8 0	20169900	BRH 1 P 2 0 1 7 0 1 0 0	RH 1P20173150	RH I P 20174040	3RH I P 20175420	3RH IP20180140	HIP20183690	3RH I P 20186 120	BRH 1 P 2 0 1 8 6 5 0 0	BRH I P20189980	BRH 1 P 2 0 1 9 0 0 7 0	BRH I P 2019 1490	BRH IP20191770	RH IP20194940	RH I P 20195890	RH IP20196410	RH1P20205090	RH I P 20207430	P20207990	P20208420	P20208590	P20227080	1P20230710	P20232290	P20233090	PZ0234380	P20236950	
1	BRHIP	됥			불	BRH IP	<b>BRH1P</b>	3RH I P	3RH1P201	SH P	A E	SE P	E E	3	E E	A E	E E	E E	E E	딅	틝	딅	E E	뙲	를	딅			E	픮	딅	픮	E E	E E	BRHIP	

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Table 27

	T	ds	1€	9 7	27																																	
5		849	ণ	9	9	5 0	7	ग	7	7	7	ग	7	<b>3</b>	0	7			6. 695		٦	7	9	9	- 4	6.8/8	ग	7	7	<u> </u>	0	3		7	2	7	070	9
		39	-	-			1										$\perp$	- }	- [	$\perp$	1	$\perp$	1	1	ı,	-1	1	1						1			-	
10		0	0	0	0	5	3	ग	9	٥	٥	9	O	١	0	9				0					5													1
		0	0	0	9			9	न	5	9	3	-					3	=	9	- 1		-	ŀ	3	8		eا	2	1	83.985	4		1	1	9	٠,	Ξ.
15		36.	31.		တ	4			2		12	3	1		İ					0	1					-		١	۱					1	1	1	1	10
				0	١		١		١	-		1	١	1					1		ı		1		1		۱	1	- {	ł	- 1		1	1	-	뛰	1	
20		0	0	0	0	0	0	0	0	0	0	0	0	0	.0	0	0	0	6.925	0	0	0	О	0	0	0	0	٥	0	0	0	0	0	0		0	0	5
25		0	0	0	0	0	D	0	0		0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					1	١	
		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	21, 304	0	0	0	12.077	9	9	9	0		3.597
30		0	0	0	0	0	Э	0	0	0	0	٥	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	43.31	0	0	٥	9		0
35		0	0	0	0	0	0	0	0	0	0	0	0	0	0	ō	0	0	2, 142		0	0	0	0	0	0	0	0	0	0	16.015	0	0	0	0	٥		5 068
33		0		0																																		
40				0																																		
		c	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	O	0	0	0	0	
45		P20238690	D20240460	P20243470	P20249110	P20252450	P20253660	P20277620	P20283030	P20284800	P20285830	P20285930	P30004880	N10000920	N20013420	N20014260	N20015030	N20015790	SW20018GDO	SN20028570	SN20038200	SN20038410	SN20039370	SN20043040	SN20046570	SN20046790	SN20046860	SN20066110	SN20097020	SN20101100	SN20105870	SN20105960	SN20108300	SN20120810	SN20121030	SN20137020	SN20142940	ALLANTACTON

Table 28

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		· -	_	_	-	-	-	-	_	-	-	-	-	-	Ė	-	_	_	_	<b>—</b>	To:	<u></u>	<u></u>	~	6				_	-		_	<u> </u>	0	6	Te
10	ľ	0	0	0	0	0	0	°	48. 181	2	2	2	9			7.19			7. 591	9. 707	37, 32		8. 528	22. 188	35.648	_			1.91	5, 339			٦			
0	0	0	0	0	0	O	17, 396	77.945	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
83.985	20	60.467	100	100	001	001	8.678	0	0	0	0	0	0	c	0	0	0	0	0	0	0	0	28.623	0	0	0		0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	22.055	0	0	0	0	0	2.372	2.336	0	0	0	0	0	0	0	23, 537	0	0	0	0	6. 659	0	0	4. 246	0	0	0	0	-
0	0	0	0	0	0	c	25. 637	0	0	0	0	0	0	0	0	0	10.345	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5
0	0	0	0	0	0	0	33, 205	0	0	0	0	0	0	0	0	0	0	0	0	0	0	14, 506	0	0	0	0	0	0	0	0	0	0	0	0	0	-
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.845	0	0	0	0	0	0	0	0	0	3. 444	0	0	28. 439		8. 797	0	ALO AC
0	0	0	0	0	0	0	2. 431	0	0	0	0	0	0	0	0	6. 532	0	0	0	0	0	0	0	0	0	0	15, 907	0	0	0	0	0	0	0	2.619	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
16.015	0	0	0	0.	0	0	3. 424	0	0	0	0	0	0	0	0	0	0	1. 538	14.575	0	0	0	16.375	0	0	6.093	0	0	1. 222	0	2, 954	0	0	8.244	3.69	C
0	0	0	0	0	0	٥	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	c
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	0	0	0	0	
BRSSN20151990	BRSSN20159070	BRSSN20159820	BRSSN20169050	BRSSN20176820	BRSSN20177570	BRSSN20187310	BRSTN20000580	BRSTN20005360	BRTHA20000570	BRTHA20004740	BRTHA20046290	BRTHA20046390	BRTHA20046420	CD34C30001250	CD34C30004240	001000019N010	CT0NG20004690	CT0NG20027090	C10NG20050280	CT0NG20076130	CT0NG20077790	CT0NG20095290	CT0NG20095340	CT0NG20099380	CTONG20106620	CT0NG20118250	CT0NG20121010	CTONG20127450	CT0NG20128470	CT0NG20141650	CT0NG20143690	CT0NG20153300	CTON020155180	CT0NG20158150	CTONG20161850	CTONG20164990

Table 29

0	0	1.576	0	0	0	7.411	0	0	3.025	0	9.34	0	٥	0	0	0	0	0	8.821	0	0	11.41	10, 575	11, 811	0	10. 501	٥	0	11.342	9.629	0.321	19.624		9.624	0	0
0	0	0	0	0	0	0	1. 454	0	0	0	0	0	٥	0	ᅙ	0	0	0	0	0	0	0	0	0	0	9	٥	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	0	0	0	0	0	0	0	0	0	28, 534	0	0	0	0	0	٥	0	0
0	0	0	0	0	0	0	0.411	0	2. 783	0	2.864	0	0	0	0	9.669	0	27. 988	8. 116	0	0	0	0	0	0	0	0	0	0	0	0. 296	0	0	0	0	0
0	9. 153	0	16. 736	0	0	0	2. 857	0	0	0	9.845	35.892	0	0	4.74	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10. 757
0	0	0	0	0	19. 689	0	0.925	0	0	0	0	0		0	3		23. 712		0		0	23. 605	21.878	0	0	0	0	0	0	0	0	0	0	19.91	38, 222	0
0	0	0	0	0	0	Э	0.403	10.98	0	18.444	5.615	0	2. 822	0	0	0	0	0	0	0 .	22, 29	10. 289	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	7.81	1.432	0	6.953	0	9	0	0	0	0									ထ			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	10.144	0	0	0	0	0	0	0	0	o	0	0	0	0	0	0	50.895	0	0	0	0	0	0	0	0	0
5.677	0	0	0	0	0	0	1.431	0	0	0	1.993	0	0	9.618	0	0	7.336	0	0	6.571	0	7.303	0	0	16.915	0	0	0	0	0	0. 206	0	0	6.16	0	0
0	0	0	0	0	0	0	0	O	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	ō	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CT0NG20186320	D30ST10002700	D60S120003580	D90ST20000310	D90ST20035800	DFNES20010910	DFNES20071130	HCH0N20002260	HCHON20003220	HCH0N20010990	HCH0N20015350	HCHDN20022470	HCH0N20067220	HCH0N20067700	HEART20003060	HEART 20005410	HFART20061950	HFART20090000	HHDPC10000650	HHDPC20057940	HL UNG20033780	K 1 DNE 20011170	K I DNE 2002 7250	K I DNE 20104300	K I DNE 20107500	K I DNE 2012 2910	K I DNE 2012 7 100	K I DNE 201807 10	L IVER 1000 1260	1 1VFR20064100	I IVER20087510	MAMGI 10000830	WESAN20031900	WFSAN20036460	MESAN20106640	MESAN20164090	NOVAR10000150

Table 30

13.079 18.714 7. 128 9. 452 38. e. 32. Ö 0 17. 468 10. 792 19. ಬ್ œ. 5. Ö 000 8 38. 16.676 3.068 11.45 0 25.26 4. 791 0. 214 819 NTZRP 70045590
NTZRP 70063950
NTZRP 70195430
NTZRP 70195430
NTZRP 70195350
NTZRP 7019530
NTZRP 7019550
NTZRP 701950
NTZRP 7019 NT 2NE 200 10 400
NT 2NE 200 10 400
NT 2NE 200 2 16 20
NT 2NE 20 1 2 2 4 30
NT 2NE 20 1 2 6 0 50
NT 2NE 20 1 3 6 0 50
NT 2NE 20 1 3 6 0 50
NT 2NE 20 1 3 7 6 2 50 N12R | 20023590 N12R | 20041880 N12R | 20046080 N12R | 202 | 6250 N12R | 20252550 N12RP60000770

0	0	0	0	15	0	0	0	=	0	0	533	0	0	0	0	0	0	0	0	12	877	0	0	0	0	0	0	0	0	094	0	0	0	0	063
				2.8				3.7			21.5	11.61								23.91	3.8									2.0					4
0	33.893	21.086	0	0	33, 325	0	0	12.086	0	0	0	0	0	0	0	0						0	0	0	0	0	0	0	0	0	67.455	0	0	67, 455	0
9	0	0	0	0	0	0	0	0	0	0	0	0					51.									5.		0			0	0	0	0	0
0	٥	0	0	0	0	0	2.913	0	0	0	9.905	16.034	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.963	0	0	0	0	3, 738
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	32.864	0	0	0	0	0	12, 384	0	0	0	0	6.628	50.098	0	0	0	0	7. 901	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	ľ			0			0		0			0	0				0	0	0	0	0	0	0
6	0	0	0	0	0	3. 687	0	0	0	ō	0	5. 239	0	0	0	0	0	0	0	0	0	0	0					12.	0				4.078		
22 126	0	ਠ	8 18	0	ō	0	0	0	7. 259	0	0	26, 393	1. 795	3. 527	0	0	0	22. 212	0	0	0	0	0	12.051	22. 212	0	0	0	0	0	0	0	0	0	0
0	0	5	0	0	0	0	0	٥	0	39.038	0	0					H	0	0	0	0	0	0						-		0	0	0	0	10
0	0	0	0	1.802	Э	0	2.027		0	0	13. 781	11.155	0	0	0	6. 406	0	0	16, 746		0	16.746	6.546	0	0	0	0	0	0	0.67	0	0	0	0	5 201
0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
99	15120123530	950	20171280	08120175290	05120185830	640	9860	4EN20030180	000	3980	VEN20085150	NEN20108240	US20012010	ISH20062340	NT20013480	NT20042990	3300	NT20076470	NT20092330	440	NT20121220	NT20121950	20122910	NT20130320	NT20131810	NT20144800	NT20163960	EN20002220	EN20008740	EN20011410	EN20016260	EN20027440	EN20029310	EN20033960	C11000F 1000

Table 32

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0.379	6.902	0	0	2.34	5.368	0	8. 598	0	0	15.479	16.354	38.93	0	14.012	0		0	11.444	0	9. 487	0	0	0	0	11.634	0	0	0	0	0	0	0	0	37. 524	1.909	0
0	0	0	0	0	0	0	0	0	0	50.331	0	0	0	0	0	0	0	0	0	0	0	57.966	0	0	0	0	0	0	0	0	0	0	0	0	0	c
0	0	68. 148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	c
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	48.614	0	0	0	0	0	0.986	0	0	0	0	4, 135	0	0	43.832	42, 801	0	0	0	c
0	22.047	0	0	0	0	0	0	3. 23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	14. 759	0	0	0	0	35. 791	0	0	0	0	0	0	C
0 /84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	22. 629	0	0	0	0	0	0	0	47.3	0	0	0	0	0	0	0	0	0
0	9	0	2, 652	0	0	0	7.753	0	36, 501	0	14.747	0	0	0	6.012	5. 737	0	0	0	0	0	0	0	0	0	8.365	0	0	0	0	0	0	0	0	1, 722	0
0	0	9	0	0	0	0	15, 624	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4.084	0	0	0	0	0	0	0	0
0	0	Э	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0.743	3.436	28.977	0	0	0	9. 907	0	0	28.977	0	0	4.072	0	0	0	٥	6.872	٥	0	0	0	0	14.633	٥	0	8. 403		29. 776	11.599	0	1. 222	1. 762
0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	٥	0	0	0	٥	0	0	0	0	9	9	٥	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	9	٥	٥	0	0	0	9	9	0	٥	0	0
0	0	0	0	٥	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0
SPLEN201280C0			2	SPLEN20149110	SPLEN20157880	ᆲ	SPLEN20171210	SPLEN20179180	SPLEN20186430	SPLEN20204170	SPLEN20212730	SPLEN20214580	SPLEN20250390	STOWA20051200	STOWA20062290	STOWA20092890	SYNOV20003970	TESOP20005270	TEST   10000940	TEST   2000   720		TEST   20004890				TEST 120044310	TEST 120061110	TEST   20063830	TEST 120086210	TEST   20152460	IEST 120168960	TEST 1201 70350	TEST   20208400	TFST   20213580	TEST   20214250	TEST   20254220

Table 33

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22. 576	34, 12	2. 434	0	18, 384	0	0	1.504	0	30, 115	0	6.532	0	57.08	0	0	0	0	0	0	12, 293	0	0	0	0	20, 303	12.342	0	0	0	3. 16	0	0	0		34, 582	0
0	0	0	84.653	0	0	84. 653	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.476	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
77.02	0	0	0	21, 141	0	0	0	0	0	0	0	19. 023	0	0	0	0	22. 595	7. 541	0	0	0	0	0	0	0	0	-1	21.607	0	0	0	0	0	0	0	7. 219
0	0	0	0	0	0	0	0	0	0	0		0				0					0	0	0	46, 138	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0		0					0	0	25, 432	0	0	0	29.879	0	0	0	0	0	0	0	67. 193	0		17.886	6
0	0	0	0	16.578	0	0	0	0	0	0	0	0	0	54. 53	0	0	22. 147	0	0	11.085	15.94	54. 53	0	0	0	0	29. 753	0	47, 167	0	0	0	0	2, 538	0	14, 151
0	0	0	0	0	0	0	0	0	0	0	0	18. 787	0	0	0	ĝ	22, 315	0	0	0	0	0	33, 209	13, 123	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	31.972	0	0	0	0	56. 448	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	28.17	0
43, 347	0	0	0	5. 883	0	0	0	45, 981	0	0	0	0	0	0	45.981	0	0	0	29, 854	7.868	0	0	0	0	0	7, 899	0	0	0	0	5, 573	0	38, 787	0	5, 533	12, 555
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
EST120258460	EST120330310	EST120334410	EST120366910	EST120391770	EST120432750	EST120455620	HYMU20000570	HYMU20058070	HYMU20066100	HYMU20075320	HYMU20081490	HYMU20100410	THYMU20101920	HYMU20108310	THYNU20119390	HYMU20126900	THYMU20128260	HYMU20169680	THYMU20193640	THYMU20209590	THYMU20235760	THYMU20239430	THYMU20240710	THYMU20253250	THYMU20286290	TK I DN 100000 10	TK I DN20005210	TK   DN20030590	TRACH20005020	TRACH20005400	FRACH20007020	TRACH20019960	TRACH20034840	TRACH20079690	TRACH20128110	IRACH20149970

Table 34

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0	°	0.913	0	0	0	4.979	0	48. 181	3.275	0	0	24.416	5.93	0		14.093	0	0	0	1.639	0	0	9.36	0	0	14.257	0	0	0	0	0	0	0	0	12.201	
0	0	2.97	0	9.326	0	4.047	0	0	0	75, 144	0	0	0	Э	0	0	0	0	0	0	9.348	0	0	0	0	0	0	0	0	0	0	0	0	0	ō	,
0	0	0	0	0	0	4. 178	0	0	0	0	0	0	0	0	0	0	ō	0	0	0	0	0	0	0	0	0	0	33. 472	0	0	0	40.045	ō	0	0	
0	0	0	0	0	0	0	2. 601	0	1.506	0	46, 104	0	16, 367	46. 104	0	0	6. 152	46, 104	0	0	0	0	0	0	0	13, 116	0	0	2. 463	35. 577	26, 353	0	0	0	0	
0	0	2.918	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0 .	0	0	0	0	0	29.9	0	0	0	0	31.859	0	0	0	0	0	0	0	
0	0.606	1.89	0	0	0	0	5.848	0	0	0	0	0	0 ·	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5, 539	0	0	0	0	0	0	
2. 93	0	0	0	0	0	4.49	0	0	2. 953	0	0	0	26. 737	0	0	12, 709	10.05	0	0	0	0	0	0	0	0		12.401	8.993	0	0	12.915	10. 759	0	0	5, 501	
0	0	0	0	0	0	3, 393	0	0	5, 951	0	0	0	5. 388	0	24.8	0	4.05	0	0	0	0	0	0	0	0	6.477	0	9.061	4.865	0		21.682	0		5. 543	з
0	C	0	0	0	75. 184	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9. 367	0	0	0	0	0	0	0	8. 724	0	0	0	0	0	0	
0	0	0	37. 308	1.836	0	1. 593	0	0	1.048	0	0	0	0	0	0	0	0	0	10. 632	1.049	3.68	13.99	6. 99	7. 121			44.008	0	0	0	0	7. 636	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	0	0	0	0	٥	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	27. 675	2.731	4. 789	36.414	15. 593	18. 536	72: 245			16.614	4.46	64. 423	47.719	19.877	50.102	15.543	10, 163	
RACH20183170	JMVEN10001860	JMVEN20003540	JTERU20000740	JTERU20030570	JTERU20054460	JTERU20055930	JTERU20056010	JTERU20064860	JTERU20065930	JTERU20070040	JTERU20081300	JTERU20084260	JTERU20094350	JTERU20120310	JTERU20124070	JTERU20164260	JTERU20168220	JTERU20183640	STR020032120	NSTR020125520	3RACE 20039040	3RACE 20060 720	BRACE20062640	BRACE20090440	BRACE20099570	BRACE20111830	BRACE20142570	BRAWH20128270	BRCAN20280360	BRH 1 P 2 0 1 1 0 8 0 0	BRH 1 P 2 0 1 7 6 4 2 0	BRSSN20003120	CTONG20105660	CTONG20124010	CTONG20133480	

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## <sup>3</sup> 1 347 046 A1

Table 35

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Table 36

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0	0	0	0	0	0	0	0	0	0	2. 434	0	0	3, 556	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58, 507	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	8. 169	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	35. 577	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	7.775	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	3.678	0	0	0	0	0	0	0	0	0	0	0	0	55, 394	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	3. 207	0	0	0	0	0	35, 119	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	14. 727
0	0	0	0	0	0	0	0	0	0	0	0	0	5. 793	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11.34	0	0	0	0	0	11,517	0	0	0	0	0	0	10.374
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1001	43, 392	100	100	100	9	5	5	20. 784	100	4.055	100	64, 423	2.962	100	100	001	100	100	64, 881	100	100	100	29. 517	100	100	44.606	100	100	29.977	100	100	100	100	100	100	27. 002
FC88F30033050	FCBBF30039020	FCBBF30052180	FCBBF30054440	FCBBF30057290	FCBBF30062880	FCBBF300/0770	FC88F30071520	FCBBF30078290	FCBBF30083620	FCBBF30123470	FCBBF30170590	FCBBF30172550	FC88F30175310	FCBBF30178730	FCBBF30190850	FCBBF30195640	FCBBF30199610	FCBBF30215060	FCBBF30225660	FCBBF30240960	FCBBF30242250	FCBBF30243640	FCBBF30247930	FC88F30252520	FCBBF30252800	FCBBF30252850	FC8BF30262510	FCBBF30266780	FCBBF30266920	FCBBF30278630	FC88F30278030	FCBBF30281880	FCBBF30284720	FCBBF30285280	FCBBF40001730	FCBBF40005480

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Table 37

_1		_		<u> </u>	$\overline{a}$	ਨਾ	<u> </u>	<u></u>	ਾ	त	انہ		न	<u></u>	<u>_</u>	<u>a</u>	ळा	61	ਰਾ	ठा	न	ा	0	0	O)	0	<u></u>	ை	न	ा	<u>@</u>	20	<b>a</b>	_	o	5
<u> </u>		٦										14.41		8.2			- 58				12.4							1:7			3.406	19.21		33		
3		0	0	0	0.178	0	0	0			0	9	=	٥	0	0	0	٥	0	٥	0	0	32, 063	0	0	0	0	9		- 1	3, 691	3/. 113	0	0		0
11.082	6	0	٥	0	0.442	0	0	0	0	0	0		=	0	٥	0	0	0	٥	9	0	16, 193	1	0	Ì		듸		9	- 1	3.81	٥			٥	0
ı	4.942	0	0	0	0	0	0	11.583	0	0	1.836	9	0	0	0	2.069	1.461	0	0	0	٥	0	0	0	0	0	0	$\vec{\cdot}$	1	o	က	10. 201	١,	2. 187	٥	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.073	0	0	0	٥	0	0	0	0	9	0	0	0	0	3. 627		0	0	٥	<u></u>
5	0	0	0	0	5. 203	0	0	0	0	17.901	0	0	ō	0	0		6.571		0					0			0	0	0	0	2.349		0	0		18, 233
9	0	0	o	0	0	0	0	0	0	0	1.8	0	0	2. 489	0	0	1. 432	0	0	0	0	0	0	0	0	0	6.064	7, 015	28. 63	0, 342	0	0	0	1. 429	0	0
0	4.881	7. 541	0	0	0	0	0	0	0	0	0	0	0	12, 539	0	0	7.215	0	0	O	0	0	8.96	0	О	0	3.055	0	0	0		20. 742	0	1. 44	3,018	0
0	0	ō	0	0	0	0	0	0	0	0	0	0	0	8.894	0	0	0	0	0	0	0	0	0	0	0	0	10.956	0	0	0	3.699	0	0	0	0	0
õ	0	0	0	0	0	6, 141	0	0	0	0	2, 555	0	0	1.707	0	.2. 87B	1.016	0	0	0	0	3, 088	0	С	0	0	0	9.958	٥	0	0.727	0	0	3.55	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9, 237	7, 559	17.488	71.37	0.853	2.552		57. 236	3.563		10 R12
5. 501	8.949			28, 625	8.38	5, 328		20.975	16.742	14.415	3.325	24.007		4 598			2 646		۱:				32, 856		60, 769	1	0	0	0	0	0	0	0	0	0	-
ICHON20007380	1EART20072310	HDPC2006R620	H UNG20023340	(1DNE20017130	CI DNE 20028830	ESAN20014500	JT2RP 70072690	VF2RP70137640	NTDNG20067090	A ACE60004630	PROST20083600	ROST 20 189770	RECTM20003490	SKNSH20008190	SMINT20115880	SPI EN20169720	SPI FN20194050		FST   20083940	FST 120213150	EST   20254540	IEST   20265250	RACH20118940	UTERU20145480	UTERU20146680	ASTR020155290	BRAWH20030250	RRAWH20113430	RRAWH20122770	RRH 1 P 2 0 0 0 5 3 4 0	BRH 1 P30001 1 10	BRSTN20002200	CTONG20052900	CTONG20108210	DENES20031920	CCD04 1000 1000

Table 38

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0	0	0	0	0	0	0	0	24.098	0	0	0	104	0	0	0	0	4, 353	0	2. 659	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	22. 43		0	0	0	0	0	0	0	0	0	0	0	0	13,076	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	29. 041	0	0	16.019	0	0	0	0	14, 316	29.041	0	0	0	0	0	0	0	0	0	9. 701	0	8. 277	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	2. 285	0	0	ō	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	21.815	0	0	0
0	0	0	0	0	0	0	0	21.73	0	0	0	0	0	0	0	0	0	0	2.398	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	2.886	0	0	0	0	0	1. 003	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	0	0	0	0	0	0	9.581	0	0	9
0	0	0	0	0	0	0	0	0	0	0	0	3.598	0	0	0	0	0	0	0	0		50, 703	0	0		26.964	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	3.861	0	0	0	0	0	0	0. 707	0	0	0	0	11.144	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		5.758	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	٥	٥	0	0	٥	0	0	0	0	0	0	0	
100	15, 507	100	100	100	27, 125	7, 139	100	54, 171	100	8	9	2, 482	2	70, 959	9.04	100	9. 786	8		79, 225	9		70, 959	2		18.603		40.243	8	18	5		23.704	1	20, 225	8
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	٥	0	0	9	9
FEBRA20003210	FEBRA20007620	FEBRA20009090	FEBRA20010120	FEBRA20017050	FEBRA20018280	FEBRA20025270	FEBRA20025520	FEBRA20026110	FEBRA20026280	FEBRA20029860	FEBRA20034680	FEBRA20037260	FEBRA20040530	FEBRA20042190	FEBRA20052910	FEBRA20060610	FEBRA20072120	FEBRA20079310	FEBRA20082010	FEBRA20088360	FEBRA20090290	FEBRA20092890	FEBRA20093520	FEBRA20097310	FEBRA20113560	FEBRA20125070	FEBRA20132740	FEBRA20140100	FEBRA20161120	FEBRA20166540	FEBRA20167390	FEBRA20171380	FEBRA20176800	FEBRA20184330	FEBRA20192420	FEBRA20195820

Table 39

EBRA20196370	0	40.753	0	0	0	0	0	0		0	0	0	0
EBRA20196630	0	21. 712	0	0	0	0	0	0	0	0	٥	0	
EBRA20197110	0	5. 271	0	0	0	0	0		0	٥	0		2, 345
EBRA20211710	0	26.519	0	0	0	10, 719	0	24.406		0	0	38, 357	0
EBRA20214970	0	100	0	0	0	0	0	0		0	0	0	0
EBRA20215500	0	77.838	0	22. 162	0	0	0	0			0	0	0
EBRA20216360	o	50.44	0	14, 361	0	0	0	0			0	0	0
EBRA20222040	0	8	0	0	0	0	0	0			0	0	0
EBRA20223220	0	9	0	0	0	0	0		0	0	Q	0	0
EBRA20225040	0	4.094	0	0	0	0	0	3, 768	11.		0	0	0
EBRA20226010	0	77.838	0	22. 162	0	0	0	0			0	0	0
EBRA20229560	0	200	0	0	0	0	0	0		0	0	0	0
BRA20229630	0	100	0	0	0	0	0			0	0	0	0
EBRA20232850	0	100	0	0	0	0	0	•		0	0	0	0
EBRA20235500	0	40.825		0	59, 175	0	0			0	0	9	0
CHON20040020	0	1.957		0	0	1. 682	0			0	0	0	1.741
E20102650	0	5.89	0	0	0	0	2.363	0		0	0	0	0
112RP 70037240	0	23.02	0	26.217	0	0	0	0	0	0	0		0
EBLM20072960	0	4.311		0	0	0	0	0			0	0	0
PLACE60169420	0	9.752		0	0	3, 942	3.912	8.975	13.858	0	14, 56	0	4, 338
SKMUS20003610	0	2. 666		0	0	1.077	0	2.453		0	0	0	0
SM1NT20026890	0	2. 93		10,012	0	1.184	4. 702	0	0	0	0		1.304
SMINT 20033400	0	7.324	0	0	0	2.96				0	0	0	0
SPL EN20020070	0	47, 573	0	0	0	19. 229		0	0	0	0	0	0
EN20079510	0	58.898	0	0	0	0	0		0	0	9	0	9
120001000	0	48, 295		0	0	39.041	0		0	٥	0		0
120094020	0	22. 853	0	0	0	9. 237	0	-		0	0		٥
HYMU20027560	0	18. 25	0	0	0	0	0				0	0	0
HYNU20180280	0	74, 935	0	0		0		٥		0	٥		•
1YMU20271250	0	0.446	0	2. 287	2.587	0.902	0.179	0.411	0		0	4.51	0.198
RACH20003590	0	7. 434	Ō	0	0	0		٥	0	3.042	٥		0
MVEN10001560	0	2.576	0	0	0	0		0	0	0	0		0
ERU20022940	0	13.576	0	0	0	0	-			0	٥		4, 026
ERU20046640	0	4, 23	0	0	0	1.71							- 882
ERU20119060	0	17		0		13.742	13. 63						0
TERU20144640	0	-:	0		0		0				50.246		0
ERU20176130	0	51, 268				0		9	0	0	٥	9	0

Table 40

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5																											_										
J	6	0	0	0	0	8.954		13, 174	0	0	0	0	0	0	26.317		5.754	7.692	3.551		2.052		0	0.951	0	7.905	3.926	1.98	0	6, 543	0	8.471	0	6.999	18.801	5.129	0
10								0										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	ō	0	0	0
	0	0	0	c	0	0	0	11,054	0	0	0	0	0	0	0	6. 591	0	0	0	10.394	0	0	0	0	0	0	6.588	0	0	0	0	0	0	0	0	0	0
15	0	0	15, 234		ō	0	0	0	0		9.323		27. 708		0	1.807	0	1.077	0	0	0	0	0	2. 626	0	0	3.612		0	6,019	0	0	0	0	17. 297	0	6.881
	0	0	0	0	0	0	0		85.082	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	O	0	0	0	0	0	0	0	0	0	0	0	0
20		33.045	0	0	16.499	0	0	20. 44	0	0	20. 964	0	0	0	0	4.063	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	14, 931	0	0	16.148	8. 7	2.97	0	8. 671	ŀ	0	ı	21. 185		3, 542	0	6.936	0	2. 793	0	0	0	0	9	0	0	-	3. 18	0	0	0	0	0	0	4. 625	16. 862
	0	0	30.09	5, 983	43. 477	8. 135	0	5.985	0	0		30.812	٥	0	0	1. 784	0	0	0	2.814	٥	0	0	1. 729	0		٥	0	0	0	0	7.697	0	0	0	4.66	6. 796
30	0	0	0	1	25.986	0	0	10. 731	0	٥	0	0	0	0	0	0	0	0	0	0	0	- 1	35. 74	٥	9		٥	0	0	0	0	0	0	0	0	9	0
35	0	~	21. 196		5. 104	0	0	0	- 1	30.77	٥	9		15, 036	- 1	7.541	- 1	24.615	0	0	1.313	٥	9	1, 218	- 1	1	2.513		٥	0	0	21. 687	0		12.033	3, 283	7. 1811
	1.267			7.377			10.808			1	}			26.318	쀠			8.617				9.947	4.096	2. 132	26. 272			2.218		7, 329	25, 095	18.979		m)	- 1	5. 745	12. 569
40	0	0	0	0	0	0	0	0	0	0		0	=	9	9	-	0	0	0	9	0	9	0	히	0	0	0		٥	9	0		9	٥			o
	0	0	0	0	0	0	0	0	9	9	9	0	0	힉	9	9	9	0	9	7	9	0	9	0	0	0	0	힉	9	0	0	0		0	9	-	ā

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BRANT 20103480

BRH IP 20103480

BRH IP 20103480

CTONG 20103630

BRH IP 201039340

CTONG 20103630

BRH IP 20103630

BRH IP 20103630

BRH IP 20103630

BRH IP 20103630

BRH IP 20103630

BRH IP 20103630

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BRH IP 20103630

BRH IP 20103630

CTONG 20103630

HUNG 20103630

KIDNE 20103630

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KIDNE 20103630

KIDNE 2010360

Table 41

225	0	0	9	9	9	9	7	338		9	9	9	न	9	9	্	ণ	9	ণ	9		9	0	9	ণ	ণ	9	ণ	9	9	9	ী	9	न		9
က								2							j									0		0			0				0	0		
0	0	0	0	9	٩	0					ျ		9			9			٩	٥	٩	٩	0						١							
0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		74. 975	0	0	0	0	0	0	0	0	0	0	٥	0	9	0		0	0
8. 901	6. 405	9	0	0	0	0	0	0	0	0	0	0	45.093	0	0	0	0	0	٥	0	0	45, 093	0	0	45.093	0	0	0	0	0	0	0	0	0	0	<u></u>
0		3, 482	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	2. 255	0	0	0	<u> </u>	0	0	25. 211	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11, 633	0	0	0	0	0	0	0	0		0	0	0	0	0	0	44, 597	0	0	0	0	0	0	0	0	0	0	0	0	21, 156	0	0	0	0	0	0	0
5.861	0	0	0	7. 258	16.413	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4.71	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	ē
8.256	4.456	0	0	5, 112		0	0	9.817	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	c
7, 226	15, 599		100	17.896	20, 236		8.974		27, 302	100	8	65. 522		ι	8	55, 403			25, 025		8	54 907		2	54, 907		2	8	78 844		1	8	2	18	52 585	
6	0	0	0	0	0	0	0	0	0	6	0	0	0	0	6	0	0	0	0	0	0	-	0	0	0	0	0	0	10	0	0	0	0	0	F	1
6	0	0	0	0	0	0	0	0	0	ē	0	0	0	6	6	. 0	c	0	0	0	c	le	,	6	-	0	ē	0	6	, c	6	0	te	te	c	6
NIORPIONSEZEO	NT2RP70081610	NTONG20009770	0CBBF 10000540	OCBRF 10001750	OCRRF20006770	OCRRE20013890	OCRRE20019830	OCRRF 20020150	OCBBF20020830	OCBRF 20023570	OCBRF 20028050	OCRRF20028650	OCRRF 20079800	OCBE 20010280	OCBBE 20030010	OCBR 20035930	DCRRF20037440	OCRRF 20041680	OCBE 20045330	OCRRF20046120	OCRRE20046470	OCHRESONARGO	OCBBE 20040650	0CRRF20050770	OCBRF 20051610	OCBRE 2005 1430	OCRE 20053490	OCRRF 20053730	0000 1000 1000 1000 1000 1000 1000 100	00567 20034200	000000000000000000000000000000000000000	OCBBE 2006 2140	OCBBF 20062410	OCBBE 20066390	OCBBE20071210	-1-

Table 42

	_	_	_			_	_		_		_			_	_			-	·-		-	1		_	-		1			_	-	_	_		-	<u> </u>
0	1	5	0	=	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	22, 111	0	0	0	0	0	0	0	0	0	
0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20.388	0	0	0	0	0	31, 296	0	0	0	21.301	0	0	0	0	0	0
0	0	Э	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61, 158	0	0	0	0	0	0	0	0	0	0	6
0	2, 305	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9.442	3.014	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13.322	0	0	0	0	0	26.074		29,008	0	0	0	0	0	44, 597	0	_
0	1.012	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	44. 784	0	0	0	17.396	7.727	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	49. 562	0	0	0	0	0	0	O	0	0	0	0	0	0	0	0	0	0	74.416	0	0	0
6. 702	0.713	0	2. 608	0	0	0	0	0	0	0	0	0	0	0	0	0	13.005	0	0	4. 728	0	0	0	0		3, 266	0	0	0	14.819	4.12	0	. 0	0	0	36.36
11.73	1.248	59 836	195 1	8	8	100	100	100	100	100	100	2. 961	100	100	34.079		22. 763	100	180		55.216	18	100	- 1	21. 447	9. 527		- 1		25, 938	7, 211		25, 584	55, 403		63.64
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF 20072240	JCBBF 20073540	JCBR 20074140	JCBRF 20076220	DCBM 20079310	CBBf 20079460	JCBBF 200813BO	CBBF 20082830	CBBF 20085200	CBBF 20088400	CBBF 20086910	CBBF 20088140	200882	CBBF20091150	CBBF20100400	CBBF20103130	CBBF20104040	DCBBF 20105670	2	OCBBF20107920	OCBBF20108580	OCBBF20108630	낑			OCBBF20118970	띪		OCBBF20122620	OCBBF20124360	OCBBF20127040	OCBBF20127140	OCBBF20127550	OCBBF20128120	OCBBF20129360	OCBBF 20130910	OCBBF20132850
		$\sim$	_		_	_		_		_		-	_	_	)	j	$\mathbf{r}$	크	ᆵ	=	-1			=1								1				_

Table 43

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0	4.052	0	0	0	0	0	0	0	0	0	0	0	0	1.877	5.987	0	0	0	1.775	0	1.948	0	9, 419	0	0	6. 671	18.087	0	0	0	0	7. 106	0	10.517	0.579	8. 562
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Э	0	0
0	0	0	0	0	0	0	0	0	0,	0	0	0	С	0	0	0	0	0	0	0	0	0	0	0	0	11, 195	0	0	0	0	0	0	0	0	0	0
0	3. 728	0	0	0	0	0	0	0	0	0	0	0	0	C	12, 393	0	0	7, 587	0.653	5. 322	0	2.673	0	5. 203	0	0	33, 279	0	0	0	0	6, 538	0		2. 664	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.85	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10.879	0	0
19. 735	0	0	0	0	0	0	0	0	44. 597	0	0	4.41	0	0	10. 797	0	0	0	2, 24	10.432	0	0	0	0	0	9.023	0	0	0	0	0	6. 408	0	0	0. 522	0
19, 885	0	0	0	0	0	0	0	0	0	0	0	4. 443	0	1. 705	2. 72	0	0	0	0.322	0	0	0	0	0	0	0	0	0	0	10, 759	0	0	0	0	0	7. 78
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1. 156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	2. 593	0	12, 664	0	0	0	0	0	0	0	0	9.389	0	3, 604	1.916	0	ō	10.556	0.909	0	0	0	0	0	3, 363	2, 135	0	0	0	0	0	0	2.889	0	0	0
24.517	4, 539	100	44, 332	65. 522	100	8	100	100	55, 403	100	65, 522	16.434	100	2, 102	5.03	10.845	6, 763	27.713	1.59	6, 48	2. 182	1, 627	10. 552	12.671	11.772	7.473	20, 261	41.66	10. 791	13, 265	40. 221	7.961	5.057	11. 782	0.649	19.184
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	o	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20140890	0CBBF20145760	0CBBF20148280	0CBBF20151150	0CBBF20153340	0CBBF20153350	0CBBF20155060	0CBBF20164670	0CBBF20170690	0CBBF20173060	0CBBF20173250	OCBBF 20178150	0CBBF20180840	0CBBF20186870	0CBBF20189560	PEBLM20044520	PEBLN20071880	PLACE60060420	PROST20047390	PUAEN20003740	SMINT20029760	SPLEN20008820	SPLEN20084600	SPLEN20095550	SPLEN20099700	SPLEN20140800	SPLEN20173510	SPLEN20211220	SPLEN20250170	STOMA20067800	TEST 120031270	TEST 1201 16830	TEST   20121550	TEST   20234140	TEST   20442760	THYMU20039810	THYMU20070360

Table 44

3.947	8.7	0	0.511	14, 383	0	0	0	6.073	0	22. 893	1. 198	0	0	2.171	5, 143	0	0	0	0	0	0	0	0	0	0	3.46	0	0	0	0	3, 321	0	7. 069	0	11, 099	0
0	0	0	0	0	0	0	0	0	0	0	5.841	0	0	0	0	0	0	0	0	3.004	37. 423	0	15.36	0	0	2.813	0	0	0	0	7. 199	0	0	0	0	0
0	0	33.098	1.717	0	12,742	0	0	0	0	0	4.019	0	0	3.643	0	0	2.876	0	С	0	0	19, 515	0	31.84	0	2.903	0	0	0	0	7. 431	0	0	0	0	0
9.079	0	4. 536	0	13, 232	6.985	0	0	1,862	0	0	3.856	0	0	0	4. 732	4, 059	0. 788	0	19, 969	0	0	0	0	0	0	6.367	5. 259	31, 797	1,584	0	20.37	0	6.504		15, 317	0
0	5.558	o.	0	0	0	0	0	12, 934	23. 761	0	3.826	0	27, 481	0	0	0	0	8,006	0	0	0	18.574	0	0	0	0	18, 262	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	6.194	0	0	2, 246	0	0	0	0	0	0	23.811	12.029	0	0	0	0	0	0	0	0	4.581	0	0	0	0	0
7.119	0	8.892	0.461	32. 424	10.27	0	6.842	0	0	0	7, 559	0	15, 515	0	0	3.978	0	0	9. 786	0	0	0	0	0	21.675	4. 68	10, 31	10.389	1.553	0	16.971	0	19, 124	17.772	20.017	20.835
7.173	0	4.48	0	6.534	0	0	6.894	1.839	6.758	0	3. 264	0	0	1.972	4, 673	12.025	0	0	9.861	1.679	0	5. 283	0	0	10.92	3.93	2, 597	0	0	0	13.076	0	0	0	10.085	0
0	0	0	٥	0	0	0	0	0	0	0	0	0	28.03	0	0	0	0	0	0	3.011	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	1.114	15, 779	0.655	9. 205	4.859	0	43.707	2, 591	4.761	0	0.766	0	0	1, 389	0	5.647	0	0	0	0	0	0	0	0	0	7, 197	27, 441	7.374	0	0	14.879	8, 574	9.049	4. 205	21, 311	14. 788
4. 422	3.898	11.047	2. 292	8.056	8.505	33, 259	25. 5	2, 268	8. 332	25. 645	2.012	27. 189	9, 637	2. 432	5. 761	4.942	0.96	16.844	24.315	1.035				10, 627			3. 202	12.906	0.964	11.014	4.961	7.504	31,677		6, 217	25.884
0	0	22. 168	1.16	16, 166	8. 534	66. 741	17.057	9. 102	16. 72	51.462	4. 038	54. 561	19, 338	2.44	11.561	9.917	11.556	5. 634			25.873	13.071		42.651	27.016	1.945		25.898	0	0	0	0	0		0	0
0	0	0	٥	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	1.434	4.095	3.689	22, 318	11.77	10, 945	13.868	38. 493
1RACH20033230	TRACH20084720	BRACE20067430	BRAMH 10000930	BRH   P20003120	BRSSN20152380	FEBRA20024100	FEBRA20027810	FEBRA20037500	FEBRA20082100	FEBRA20098460	FEBRA20144170	FEBRA20145780	FEBRA20233770	HHDPC10000830	MESAN20025190	MESAN20089360	NT2R120048840	NT2RP70043480	OCBBF20032460	OCBBF20039250	0CBBF20049300	OCBBF20061720	OCBBF20078920	0CBBF20084660	0CBBF20087010	PR0ST20087700	PR0ST20153320	TRACH20135520	AD1PS20004250	ASTR010001650	BRACE20056810	BRACE20059370	BRACE20106690	BRACE20210140	BRAWH20103290	BRAMH20121640

Table 45

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	Tab	1 €	•	45	•																															
5	2.85	3.09	0	4, 488	0	6.476	0	0	0	2. 146	4.604	0	0	0	0	34, 763	15,693	2. 721	0	3, 959	0	14,415	2, 843	2.803	O	0	6.384	0	0	0	11.184		~ 1	3, 148	٥	0
10	0	0	0	7			7.	0															3.08							0	0	0				
	0	0	0	1.369	0	0	0	0	0	0	0	0	0	0	0	0	0											1	15.			0		10.566		
15	5. 243	11, 369	3,414	0. 751	0		9	6. 102			9					4. 569	14.	~	0		Ġ	9	ان			19	ć.		æ			0				
	0	0	0	1.303	21. 292	0	0	0	0	0	7. 354	0	0	0	0	0	0	0	0	0	0	0	6.055	0	0	0	0	0	0	0	0	0	0	0	0	
20	0	0	0	1, 688	Õ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.513	0	0
25	2.57	1 .	3, 346	2. 208	0	2. 92	6.587	11.962	0	5.806		0	0	0	0.616	17.913	0	7.361	5.675	3.57	0	0	6.837	2. 527	٥	0	5. 756	0	4. 225	4.21	0	0	0	0	0	0
	2.589	1	3.372	1,854	0	0	6.637		0	0	10.458	0	0	0	0	22, 561	0	0	5. 718	0	9. 329	0	6					0			20.	0		5. 721	0	0
30	0	0	0	0				0			0	0	0	0	0	0	0	0	0	0	0	0	0	9. 132	0	0	0	0	0	0	0	0	0	10, 258	0	0
35	1.824	7.91	4.75	2. 089	0	0	0	0	14. 427	0	2.947		1.988	0	0	6.357	0	0	16, 112	0	2. 191		1, 213	0	0	0	4.086	0	17.994	0	0	0	0	6.045	0	0
33	12. 769		8.314	3.2	14, 933	7,755	10.91	7.43	25. 252	7.212	15. 473	11, 353	3.479	40. 207	10, 704	5, 563	17.58	6.096	28. 201	4.435	5, 751	9	6.37	9.419	44.033	11.659			10.498	31.379		40.207	29. 587	3, 527	7. 532	66.858
40	0	0	0	Э	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	4.747	5.147		0.68	-1.00	۱	8.112		37.553	3. 575	7.67	16.883	31.042	59. 793	15.918	8, 273	52. 288	4. 533	10.485		2.851	12.007	1.579	9. 338		17, 338	10.635	2.51	7.806	15, 555		59. 793	44.001	5, 245	3. 734	33, 142
<b>4</b> 5	05530	17620	18580	38880	75860	29960	00240	00630	01150	04120	05740	75560	18550	125560	086440	069060	89490	33680	40020	07510	16650	95280	02520	009470	03480	55790	127380	132610	62230	01850	122900	26630	149840	092690	068490	711960

Table 46

50 ·

0	1.306	13.91	0	0	0	0	0	0	0	4. 28	0	0	4.61	4.349	0.479	0	9.401	0	3.984	6.094	0	0	0	0	0	0	0	0	0	13, 101	12. 426	0	0	0	0	0
0	4.246	0	0	0	0	0	0	0	0	0	0	0	0	0	1.558	0	0	0	0	19.814	7.514	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	4. 788	0	0	0	0	0	0	0	0	0	0	23, 268	0	0	11.054	0	0	0	0	0	0	0	0	0	0	0	0
0	12.014	0	0	0	7. 703	0	0	0	0	6. 562	0	0	2.828	0	0	0	0	11.662	3.666	0	0	3.614	13.444	3.03	4.027	6. 544	1, 55	0	0	0	0	0.721	0	3.379	0	0
0	4, 172	0	0	0	0	0	0	0	0	4. 557	0	0	0	0	0	0	0	0	0	0	0	0	23, 341	0	0	0	0	0	0	0	0	0	39, 387	0	0	0
0	2. 702	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.814	0	14, 715	0	0	0	0	0	0	0	0	0	0
0	9.42	0	0	6.898	0	0	28, 366	0	0	1	17.037	0	1.386	0	0	3, 373	2.826	17, 146	7. 186	0	0	3, 543	0	0	0	٥	0	0	10, 297	11.814	0	0. 707	0	0	0	0
0	7.119	0	0	0	22. 823	0	0	0	0	3, 888	0	2.828	0	0	0.435	0	5. 695	5. 759	0	0	4. 199	0	0		3.977	0	1.531	0	0	23.808	0	0	5. 601	3, 338	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	٥	0	32, 194		46, 351	0	0	0	0	0	0	0	0	0	0
0	6. 686	8. 903	0	29. 374	0	0	0	0	0	1.826	0	0	٥	0	0.307	0	0	0	2.55	0	2, 958	0	٥	6. 324		4. 552	0	٥	0	0	0	0	0	0	0	0
9.015	5.851	15, 583	18, 503	25. 707	9.38	77.076	17.619	40, 207	28. 747	9.588	21. 165	3.487	5. 164	4.872	2.147	4. 191	7. 021			20.48	2. 589	39.61	8, 185	٥	9	0	0	٥	0	0	0	0	0	0	0	0
٥	0	0	0	0	0	0	0	0	0	0	0	٥	0	0	o	0	0	0	0	0	0	न	9		9.84	15.989	3. 787	31.88	55	ౙ	13.966			24. 772	57.435	57. 435
13, 407	4, 351		27.517			22. 924		59, 793	71.253		31.476	5, 185	5. 12		3, 991				۲.,	10. 152			24, 344	5. 487	7. 292		5, 613	23. 626	ri.	21.826	41.402	1.306	10.27		42, 565	42. 565
0CBBF 20094240	0CBBF20097720	OCBBF20108190	OCBBF 20108430	00BBF 20126780	OCBBF 20130110	0CBBF20139260	0CBBF20148730	0CBBF20149280	OCBBF 20164050	OCBBF 20173980	OCBBF 20178880	0CBBF20180120	OCBBF20188730	PR0ST20057930	SPLEN20162680	SPLEN20211940	TEST120184620		TEST   20369690	THYMU20141670	TRACH20028030	UTERU20099720	UTERU20135860	BRACE20057190	BRH 1 P 2 0 1 9 1 8 6 0	BRH1P20214950	FCBBF10003670	FCBBF 10004370	FCBBF30013770	FCBBF30095260	FCBBF30246230	FEBRA20002100	FEBRA20034360	FEBRA20095140	FEBRA20130190	FEBRA20204060

Table 47

w

0		5. 236	0	1.306	2,218	4.061	4. 794	5, 099	5.622	0	0.864	1.80	0	0	0.898	0	6. 921	0	5. 232	0	0	0	4,054	0	6, 261	0	1.76	5, 373	0.848	-	0.889			انہ	1.245	0
0	0	0	0	0	0	0	0	0	18. 281	2.302	0	0	15. 57	0	0	0	0	0	0	0	0	0	0	0	0	٥	11.446	9		1.952	0		24. 933			0
С	0	0	٥	0	0	4.543	2. 299	0	0	0	1. 45	0	0	0	٥	0	0	0	8. 78	0	0	0	0	0	0	2, 636	0		0	4, 029	0	0	8, 434	- 1	3, 134	0
0	0	4.817	4.119	2. 403	0	1. 245	1.89	0	5. 173	1, 303	2. 781	0	0	0	0	0	19, 102	0	9. 627	23. 589	0	0	0	2. 135	8.64	0.722	3. 239	5	1.816	1, 105	0.818	0	5, 291		0.573	0
0	0	0	2, 384	ō	0	2, 162	0	16. 288	17.961	2. 262	4. 139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.918	2.84	0	0		9	0
0	4. 38	0	0	2. 702	0	1.4	1.417	0	0	0	1. 787	0	9.907	0	0	0	0	3.542	0	0	0	0	0	0	0	.3. 249	0	0	0	0	0	1.86	7. 932	0		0
0	0	0	4, 037	1.178	4.001	1.831	6.176	4. 598	0	0.638	0	0	0	0	0	0	6. 241	0	11. 795	0	0	0	3.656	0	31.051	2. 124	11.11	19, 382	1.78	0	0	0	6, 915		0.56	0
0	1.924	ပ	3 39	0	2.016	1. 23	9. 334	0	5. 108	1.93	2.747	0	0	0	0.816	0	0	Õ	4.754	0	0	0	11.051	2, 109	0	2, 141	6.397	0	0.513	0	0	4.086	6.967	-		4.062
0	0	0	0	0	0	0	0	0	0	0	1. 407	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	
0	0	3.351	6. 686	20.004	4, 250	9.097			1 -	1.36	1. 106	0.576	0	0	0	0	4.43	1.096	11.72	0	0	0	18, 164	0	28.049	1.508	5. 633	0	1.625	0	0.569	0	1. 227	0	0, 199	1. 431
0	0	0	6.687	10. 243	2, 485	1.516	15, 345	5, 712	6. 298	4, 759	4, 354	2.018	5.365	41.87	13.079	13, 434	31.013	13, 424	11, 722	28. 723	13, 381	ł	18	36.	7.013	4, 399	1.972	42, 136	5.371		0.996	1.007	2. 148	797.7	0, 349	5.008
8.819	9 518	23, 539	3, 355	2.936	4.987	1.521	4 619		25, 278	1.592	16, 505	2.024		28, 007	22. 208	26.958	15, 558		=	6	26.	23	18	15.	١.	3, 531	11.87	24, 158	ட	-	1, 999	4	17, 238	9.388		5.0
6.536	3.527	8.722	6.215	6.528	7.391	2 255		8. 494			10, 792			20, 755		39, 957	11.53	2.852	8.716		19.899	17.508	13.508	38.663	5.215	1.308	5.865	8.952	2.819		1.481	4, 495		6.957	0.519	3,724
HCH0N20008320	L I VER 20028420	IRACH20111130	ASTR020108190	BRACE 20003070	BRACE 20060550	BRAWH20004600	BRAWH20011710	BRAWH20016620	BRH I P 10001740	BRSTN 10000830	CTONG 10000940	CTONG20150910	D30ST10002670	FCBBF 10000380	FCBBF 10000770	FCBBF 10003770	FCBBF20059090	FCBBF30016320	FCBBF30016570	FCBBF30049550	FCBBF30083820	FCBBF30238870	FCBBF 40001420	FEBRA10001880	FEBRA20004620	FEBRA20080810	FEBRA20086620	FEBRA20095880	HHDPC20034390	HI ING 10000550	NT2R   20023160	NT2R120023910	NT2R   20025400	NT2R120028470	NT2R120054050	NT2R120076290

Table 48

F.	_	6	8		6	പ്ര	6	0	6	4	<u></u>
	1. 237	•	4.913	2, 12					4, 109	3. 43	
	0	0	0	0	0	0	4. 229	4.925	0	0	3.062
	0	0	0	7. 139	0	0	4.365	10, 167	0	0	0
	1. 138	1.003	0	1. 957	0	1. 62	2. 393	4. 18	3. 78	0	0
1	0	0	0	0	0	0	0	0	13. 125	3.657	3.009
1	0	0	0	0	5.686	0	2. 691	0	8.5	0	3.897
4	0	1.965	3.692	0	0	0	0	0	3. 705	2.064	1, 699
	1. 124	0.99	6.696	0	2. 497	6. 399	1, 182	1.376	11.2	4.16	0.856
1	0	0	0	6.93	8.955	0	4. 238	0	0	0	3.069
	0	0	4	4	3.518	Ġ	0	0	2. 63	1. 465	3.014
	1.386	9. 767	8. 256	2, 383	12, 315	21. 697	4.371	3, 394	9. 202	2. 565	1.055
	5. 561	9. 799	1,841	4. 781	30.89	7.916	11.695	10, 215	9. 236	5.146	4. 234
	2. 061	1.816	2. 728	3.543	18.314	11. 733	4, 333	2. 523	6.845	3.814	3, 138
	NT2R   20091730	NT2R120091940	NT2RP70036880	NT2RP70078420	OCBBF20047570	OCBBF 20080050	OCBBF20125530	OCBBF20140640	TRACH20032720	TRACH20141240	UTERU20004240

Table 49

	CCUDT I	HEART
CionelD	FEHRT	- TEAR!
FEHRT20003250	100	0
OCBBF20189560	35.243	0
BRAWH20029630	0	79.6
CTONG201509	0	5.418
HCHON20007510	- 0	23.818
HEART20003060	0	90.384
HEART20005410	0	53.555
HEART20021840	0	100
HEART20025980	0	100
HEART20034320	0	100
HEART20037810	0	100
HEART200494	0	100
HEART20049410	0	63.375
HEART20049800	0	100
HEART20061950	0	63.227
HEART20063340	0	100
HEART20067870	0	- 100
HEART20067890	. 0	100
HEART20072310	0	32.316
HEART20074430	0	100
HEART20077670	0	100
HEART20089940	0	100
HEART20090000	0	68.952
HEART20095990	0	100
HLUNG10000550	0	3.611
HLUNG20017120	0	21.996
KIDNE20028390	0	48.974
KIDNE20028830	0	15.131
NTONG20029480	0	44.44
OCBBF10001750	0	48.053
PROST20127800	0	48.531
SKMUS20001980	0	21.074
SKMUS20003610	0	7.134
SMINT20026890	0	7.842
SMINT20121220	0	23.322
SMINT20122910	0	30.763
SMINT20183530	0	65.405
SPLEN20008740	0	3.252
SPLEN20027440	0	14.879
SPLEN20162680	0	2.882
STOMA20062290	0	40.108
TESTI20254220	0	16.559
THYMU20271250	0	3.582
TRACH20141240	0	6.886
UTERU20004240	0	5.666

Table 50

CloneID	FEKID	KIDNE
ASTRO10001650	0	7.727
ASTRO20108190	0	2.346
BGGI120006160	. 0	3.117
BRACE20039040	0	9.038
BRACE20060550	. 0	6.974
BRAMY20102080	0	63.37
BRAWH20004600	0	2.128
BRAWH20125380	0	35.37
BRAWH20162690	0	4.596
BRHIP20115760	0	66.835
BRHIP20205090	0	65.282
BRHIP20238880	0	1.283
CTONG20052650	0	65.178
CTONG20108210	0	2.491
CTONG20128470	0	6.004
CTQNG20133480	0	19.179
CTONG20139070	0	. 7.516
D9OST20000310	0	16.47
DFNES20001530	0	11.162
FCBBF10001820 .	0	59.128
FEBRA20002100	0	4.929
HCHON20008980	0	35.524
HCHON20016650	0	5.38
HLUNG20033780	0	32.277
KIDNE20002520	0	2.979
KIDNE20003940	О	100
KIDNE20006780	0	100
KIDNE20007210	0	73.728
KIDNE20007770	0	19.958
KIDNE20008010	0	100
KIDNE20009470	o	8.811
KIDNE20011170	o	77.71
KIDNE20011400	0	100
KIDNE20013730	0	24.839
KIDNE20017130	o	54.019
KIDNE20018730	o	100
KIDNE20018970	0	100
KIDNE20020150	0	100
KIDNE20021680	0	100
KIDNE20021910	0	24.85
KIDNE20021980	0	100
KIDNE20022620	0	100
KIDNE20024830	0	100
KIDNE20027250	0	35.87
KIDNE20027950	0	100
KIDNE20028390	0	25.593
KIDNE20028830	0	7.907
KIDNE20029800	0	10.988
KIDNE20067330	l 0	100

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Table 50 (continued)

Table 50	(continued)	
CloneID	FEKID	KIDNE
KIDNE20079440	0	35.045
KIDNE20096280	0	100
KIDNE20096470	0	100
KIDNE20100070	0	100
KIDNE20100840	0	100
KIDNE20101370	. 0	100
KIDNE20101510	0	100
KIDNE20102650	0	8.237
KIDNE20102710	0	100
KIDNE20104300	0	33.246
KIDNE20106740	0	100
KIDNE20107390	0	100
KIDNE20107500	0	74.264
KIDNE20107620	0	100
KIDNE20109730	0	100
KIDNE20109890	0	100
KIDNE20112000	0	100
KIDNE20115080	0	65.178
KIDNE20118580	0	100
KIDNE20120090	0	33.186
KIDNE20121880	0	62.256
KIDNE20122910	0	83.085
KIDNE20124400	0	6.171
KIDNE20125630	0	100
KIDNE20126010	0	100
KIDNE20126130	0	100
KIDNE20127100	0 -	33.012
KIDNE20127450	0	100
KIDNE20127750	0	100
KIDNE20130450	0	100
KIDNE20131580	0	63.24
KIDNE20132180	0	100
KIDNE20137340	o	100
KIDNE20138010	o	100
KIDNE20141190	0	49.697
KIDNE201441890		100
KIDNE20148900	0	100
KIDNE20163880	0	100
KIDNE20180710	0	49.105
KIDNE20181660	0	100
KIDNE20182690	0	100
KIDNE20182690 KIDNE20186780	0	100
KIDNE20180780 KIDNE20190740	0	100
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		28,683
LIVER20035110		16.169
MESAN20025190		2.166
NOVAR20000380	0	2.100
NT2RI20054050	1	7.879
NT2RP70043480	0	ľ
PROST20107820	0	1.696 32.771
PROST2012353	0	32.//1

Table 50 (continued)

CloneID	FEKID	KIDNE
PROST20161950	0	20.387
PUAEN20030180	0	46.744
SKMUS20003610	0	3.728
SMINT20033400	. 0	10.243
TBAES20000590	0	5.253
TESTI20044310	· 0	29.162
TESTI20082330	0	45.847
TRACH20032720	0	12.917
UTERU20099720	0	12.351
BRACE20003070	25.479	0
BRCOC20031870	34.023	0
CTONG20125640	85.462	0
FCBBF30016320	33.393	0
HCHON20002	8.723	0
HLUNG10000550	11.709	0
PROST20130530	64.069	0
SPLEN20169720	43.864	0
SPLEN20194050	30.978	- 0
KIDNE20028720	12.368	1.993

50 °

Table 51

CloneID	FELNG	HLUNG
BRACE20096200	0	70.38
BRAWH20004600	0	2.238
BRAWH20030250	0	11.121
BRCAN20006390	0	61.519
BRCAN20280360	0	8.855
BRH1P20238880	0	1.35
CTONG10000940	0	1.428
CTONG20103480	0	6.495
CTONG20129960	0	10.709
CTONG20155180	0	48.707
FCBBF10001210	0	36.439
FEBRA20144170	0	1.98
FEBRA20197110	0	7.756
HHDPC20034390	0	0.933
HLUNG20016330	0	29.367
HLUNG20016770	0	12.888
HLUNG20017120	0	12.093
HLUNG20023340	0	33.714
HLUNG20033780	0	33.957
HLUNG20084390	0	100
IMR3220002430	0	3.147
LIVER20028420	0	14.004
N0VAR2000	0	2.278
NT2RI2005405O	0	2.059
NT2RI20091730	0	4.091
NT2RP70044280	0	12.369

Table 51 (continued)

CloneID	FELNG	HLUNG
OCBBF20020830	0	40.304
OCBBF20125530	0	4.302
PLACE60004630	0	28.618
PROST2005793	0	14.383
PROST20107820	0	0.892
PROST2018583	- 0	33.898
PUAEN20030180	0	12.294
SMINT20121220	0	12.822
SPLEN20002220	0	44.799
SPLEN20054290	0	26.875
SPLEN20128000	0	1.253
SPLEN20157300	0	51.319
SPLEN20176200	0	18.8
SPLEN20179180	0	3.344
SPLEN20211940	0	12.373
STOMA20013890	) 0	21.183
TBAES20000590	0	5.527
TESTI20094230	0	59.311
TESTI20184620	. 0	10.365
TESTI20334410	0	8.049
THYMU20000570	0	4.974
THYMU20039810	0	1.915
TRACH20007020	0	14.4
TRACH20141240	0	3.786
TRACH20183170	0	10.745
D9OST20033970	61.464	0
FELNG20002410	100	0
HCHON20016650	33.188	0
KIDNE20029800	67.783	0
OCBBF20145760	78.585	0
SPLEN20162680	9.292	0
TESTI20214250	37.027	0
TRACH20005400	30.64	0
HCHON20002	8.672	2.958
. HLUNG10000550	11.642	3.971
NT2RI20023910	34 882	8.923
SPLEN20008740	10.483	1.788

50 °

#### Table 52

Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with Helicobacter pylon, ctl TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours: ct1, Hp. and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without Helicobacter pylon, in the cells co-cultured with cag PAI-positive Helicobacter pylon (TN2) (at a ratio of MKN45 TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45: TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	٠.	THP-1		MKN45			
	ct1	TNF_1h	TNF_3h	ct1	Нр	∆cagE	
3NB6920014080	4	4	4.1				
ADRG_20013010	0.1	0.1	0.1	0.04	0.04	0.04	
ADRG_20067670				0	2.6	0	
ADRG_20083310	0.3	0.3	0.3				
ASTRO20032120	1.4	1.7	0.6	1.2	0	1	
ASTRO20084250	1.2	1.1	0.4	0.1	0.04	0.1	
ASTRO20152140	0.1	. 0.9	0.4	1.6	1.8	1.6	
ASTRO20166810	0.7	0.7	0.2	. 4.3	3.5	4.4	
ASTRO20181690	1.5	1.9	0.2	1.8	2.2	0.2	
BLADE20004630	3.3	2.9	2.2	0.3	0.8	0	
BRACE20006400	3.6	3.5	. 3.6				
BRACE20019540	0.7	0	0				
BRACE20038480	0.5	0.6	0.3	0.2	0.2	0.2	
BRACE20039040	2.5	2.2	2.3	0.1	0.7	1.1	
BRACE20039440	0.3	0.3	0.2				
BRACE20052160	2.7	2.3	1.9	1.3	0.8	1	
BRACE20053630	0.2	0.2	0	3.4	3	2.6	
BRACE20057620	0	3.7	0.5	0	0	0.3	
BRACE20058810	3.8	2	2.8	0.6	0	0.9	
BRACE20060720	0	1.3	0	0	0	0.04	
BRACE20060840	2.2	1.7	1.6	3.9	3.8	1.6	
BRACE20061740	1.9	2.1	2.7				
BRACE20062640	1.9	0.2	2.4	2.3	1.2	1	
BRACE20063780	0	0.1	0	0.4	0.2	0.2	
BRACE20067430	2.4	0	1.7	0.04	. 0	0	
BRACE20090440	1.1	1.8	2.2	1	0.5	1.3	
BRACE20101700	3.1	1.8	1.7	0.5	0.4	1	
BRACE20114780	1	1.5	0.6	1.2	0.4	0.2	
BRACE20151320	0	0	0.1	0.1	0.2	0	
BRACE20152870	0.6	1.3	1.5	0.4	0.3	0.3	
BRACE20163150	1.5	1.7	0.9	1.4	1.4	1.7	
BRACE20165830	2.6	4.9	3.3				
BRACE20201570	0	0	0	0	0	0	
BRACE20210140	1.7	1.4	1	1	0.6	0.5	
BRACE20223330	0.1	0	0	0	0.1	0	
BRACE20224500	· 0.2	0	0.2	0	0	0.1	
BRACE20229280	0.2	0.04	0.4	0	2.1	0	
BRACE20235400	1.8	0.6	1	0.3	0.6	0.1	
BRACE20266750	1.8	2.1	1	1.3	1.1	0.9	
BRACE2026/250	1			0.8	0.8	0	

#### Table 52 (continued)

Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ctl, TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours; ct1, Hp, and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45: TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45: TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

	Class Nome	THP-1			MKN45			
	Clone Name	· · · · · · · · · · · · · · · · · · ·			!			
		ct1	TNF_1h	TNF_3:	ct1	Нр	∆cagE	
	BRACE20269710	0.9	0.9	0.7	0.4	0.2	0.1	
15	BRALZ20018340	1.1	1	0.5	0.3	0.4	0	
	BRALZ20058880				1 1	3.1	2.5	
	BRALZ20059500	1.7	1.5	2.3		İ	_	
	BRALZ20064740	1.9	2.8	1.2	8.9	0	0	
20	BRALZ20069760	1.3	0.4	0	0.04	0.04	0.04	
	BRALZ20075450	1.3	. 0	0	0.04	0.04	0.04	
	BRALZ20088690	1.8	1.4	1.5	. 0	0	1.6	
	BRAMY20002770	0.8	2.4	0.3	1.2	0	0	
	BRAMY20004110				0.8	0	0	
25	BRAMY20060920			}	0.3	11.8	12.2	
	BRAMY20103570	0	0.1	0.1	0.6	0	0	
	BRAMY20144620	0.7	0	0.9				
	BRAMY20152110	1.8	1.7	1.2	2.5	2.3	8.0	
30	BRAMY20162510	0.1	0	0	0.7	0.7	0	
30	BRAMY20163250	3.4	4.2	2.4	2.2	1.5	0.9	
	BRAMY20163270	3.8	0.7	4.5				
	BRAMY20168920	2.4	2.5	2.2	0.2	0.04	0.1	
	BRAMY20178640	1.7	1.6	1.9	0.9	1	0.5	
35	BRAMY20184670	0.4	0.3	0.2	0.04	0.2	0.6	
	BRAMY20204450	3.6	3.6	1.6	0	0	0	
	BRAMY20210400	0.5	0.5	0.5	1	0.2	0.9	
	BRAMY20215230	1	0.7	1.1	1.9	0.8	1	
	BRAMY20218670	1.6	0	1.5	0.2	2.6	0.1	
40	BRAMY20229800	5	3.9	0.5	1.4	4	1	
	BRAMY20229840	0.04	0	0.04	0.3	0	0.2	
	BRAMY20231720	1.1	1.3	1.6			1	
	BRAMY20247280	3.5	2.2	1.9	2	0.7	0.5	
45	BRAMY20261680	5.2	4	3	3.5	3.2	2.5	
	BRAMY20266850	0.4	4.4	6.9	2.2	2.9	2.7	
	BRAMY20267130				13.7	0	0	
	BRAMY20277140	3.3	2.5	3	0.7	0.8	0	
	BRAMY20280720	0	9.8	1.1			İ	
50	BRAWH10000930	2.6	1.3	1.9	0	0	0	
	BRAWH20015350				0	0	0	
	BRAWH20017010	0.9	0	0	0.6	0.2	0.9	
	BRAWH20029630	1.9	2.4	1.8	1.4	0.2	0.04	
55	BRAWH20100690				3.2	0.9	0.8	
	BRAWH20106180	0	2.7	0.5		1		
	BRAWH20107540	2.1	1.3	0.8	1.1	1.1	0.6	

### Table 52 (continued)

Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ctl. TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours; ct1, Hp. and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45: TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45: TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	٠,	THP-1			MKN45	
	ct1	TNF_1h	TNF_3h	ct1	Нр	∆cagE
BRAWH20110660	1.7	2.1	2.4	1.4	1.4	0.9
BRAWH20118230	0	0	0.04	2.3	0.9	1.9
BRAWH20122770	0	0	0.8			
BRAWH20126190	0 0		0	0	0	0
BRAWH20132190	2.2	2.2	1	1.8	1.5	0.4
BRAWH20138660	3.3	2.2	2.1			
BRAWH20139410	0.9	1.7	0.2	2.1	1.9	0.7
BRAWH20155950	1.5	1.8	1.5	0.9	0	o
BRAWH20158530	58.9	19.3	41.1			
BRCAN20060190				0.2	0	0.2
BRCAN20147880	0.3	0.3	0	0.5	1	1.3
BRCAN20273340	2.8	3.5	0	0.3	0.3	0.3
BRCAN20273640	0.3	0.4	0.2	0.7	0.8	0.3
BRCAN20275130	3.9	3.6	2.3	0.2	0	0
BRCAN20280210	0	0	0	0.8	0	О
BRCAN20280400	3	3.6	2.6	1.8	1.7	1
BRCOC20021550	0.7	0	0.2	0.3	0.3	0
BRCOC20037400	1.5	1	1.2	0.1	0	0.2
BRCOC2010510				3.8	1	1.5
BRHIP10001740	0.8	0.7	0.9	0.4	0	0
BRHIP20001630	0.5	0	0	1		
BRHIP20096170	0	0.4	0.3			
BRHIP20103090	1	1	1.3	0.9	0	0.7
BRHIP20105710	1.5	0	1.9	0.7	0.7	0.9
BRHIP20110800	1.9	2.7	2.2	0.8	0	0
BRHIP20111200	0.3	0.9	1.1			
BRHIP20118910		1		0	0	0
BRHIP20129720	0	0.1	0	0	o	0
BRHIP20143860	6.2	5.3	6.7	3.6	2.7	2.4
BRHIP20173150	0	0.04	0	0.9	1.6	2.8
BRHIP20175420	2.4	2.4	2.5	0.6	0	0
BRHIP20186120	1.2	2.9	0			
BRHIP20194940	0.04	0.7	0.3		1	
BRHIP20196410	1.7	2.6	1.8	0.9	2	1
BRHIP20207430	0	0	0.2	0	0	0.1
BRHIP20218580	1.1	1.8	0.9	1.2	0.6	0.3
BRHIP20233090	2.8	1.5	1.8	0.5	0	0.4
BRHIP20284800	2.3	1.5	1.7			
BRHIP30004880				0.04	0.2	0.04
BRSSN20046570	2.5	2	1.7	2.6	1	1.2

### Table 52 (continued)

Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ctl TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours; ct1, Hp. and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45: TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45: TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

	Clone Name	THP-1		MKN45			
		ct1	TNF_1h	TNF_3h	ct1	Нр	∆cagE
	BRSSN20142940	0	0	0.04	1.2	1.3	1.2
15	BRSSN20152380	0.5	1	0.7	0.04	0.04	0.04
	BRSSN20176820	1.2	0.5	0.04	1.5	1	1.4
	BRSSN20187310				2.5	9.6	27.6
	BRTHA20046390	2	2.1	2	3.2	3.2	2.4
20	CD34C30004240	1	1.3	1.8	2	1.7	1.3
	CD34C30004940				0	2.9	0
	COLON20043180				. 7.2	6.6	7.2
	CTONG10000620	0.04	0.04	0.04			
	CTONG20014230	0.4	0.5	0			
25	CTONG20095270	0	1.9	. 1.6	0	0	0
	CTONG20045240	1.5	0.5	0.8	0	0	0
	CTONG20096750	0	0.1	0	0	0	0
	CTONG20100240	0.2	0.8	0.04	0.2	0.04	0.04
30	CTONG20103480	2.7	2.9	3.7	. 0	0.1	0
	CTONG20105660	7.2	4.3	3.7	3.1	2.8	3.1
	CTONG20121010	0	0	0	1.7	1.6	0
	CTONG20128470	0.8	1	1	0.2	0.3	0.2
	CTONG20138030	2.7	2.1	1.9	2.2	0.8	1.8
35	CTONG20139070	2.4	2.3	2.2	0.9	0.4	1.1
	CTONG20146970	7	6.9	5.4	7.3	2.7	6.8
	CTONG20158150	0.2	3	0.4	1.6	0	1
	CTONG20186320	3.6	2.5	3.8	1.8	1.8	0.6
40	CTONG20265130	1.2	2.2	6.3	0.8	6	20.3
	D3OST20005540	0.7	1.7	0.4	0.7	0.2	0.9
	D3OST20037970	2.7	2.7	1.7	1.9	0.6	1.3
	D9OST20031370	0.8	2.9	1.1	0.04	0.04	0.04
	DFNES10001850				0.0		0
45	DFNES20031920	2.1	2.2	0.8	1.2	2.9	0.8
	FCBBF10005060				0.9	0	1
	FCBBF20032970	3.1	3.6	3.6	1.6	0.9	2
	FCBBF20035280				0	0	0
50 ·	FCBBF20054260	2	2	2.4			2.24
	FCBBF20071860	0.9	1.1	1.9	0	0	0.04
	FCBBF30001840	1	1.6	1.5	2.5	0	0
	FCBBF30016320	- 1	1.9	0.6	1.3	1.5	0.3
	FCBBF30016570	2.4	1.8	1.7	0.4	0.2	0.4
55	FCBBF30033050	4.1	0	3.2	1	0	0.3
	FCBBF30071520	2	0	1.2		1.0	0.5
	FCBBF30083820	2.9	3.5	1.4	2.2	1.6	0.5

### Table 52 (continued)

Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ctl. TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours; ct1, Hp. and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45: TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45: TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

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Clone Name	٠.	THP-1			MKN45	
	ct1	TNF_1h	TNF_3h	ct1	Нр	∆cagE
FCBBF30215060				0.5	0.5	0.5
FCBBF30251420	0	2.6	0	0.3	0.1	0.6
FCBBF30252520	1	3.8	2.4	0.4	0	0
FCBBF30262360				0.0	0.04	0.04
FCRBF30266920				0.3	0.4	2
FCBBF30278630				1.3	3.6	0
FCBBF30285280	0 0	1	0	0	0	0
FCBBF40001420	0.3	0.7	0.3	0.1	0.7	0.1
FEBRA10001880	0.5	0.4	0.4	0.4	0.4	0.5
FEBRA20010120	4.2	6.4	3.5	0.7	0	0
FEBRA20017050	0	0.8	0.8	0.04	0	0
FEBHA20034360	0.8	0.9	0.7	0.1	0.1	0.1
FEBRA2C037260	1.2	1.4	0.9			-
FEBRA2C037500	0.04	0	0.1	4.4	4	3.4
FEBRA20082100	0.2	0.3	0.5	2.1	0.7	0.5
FEBRA20095880	0.9	0	0.5	0.7	0.3	0.7
FEBRA20167390	0.3	0	0	0.9	0.3	0.6
FEBRA20175800	0.9	0	0	0.04	0	0
FEBRA20225010	0.9	0.2	0.2	0	0	0
HCASM10000530	2.7	2.7	3.1	0.9	0.8	0.4
HCHON2000226	0.1	0	0	0.8	0.6	0.9
HCHON2008980	1.8	2.4	0.2			1
HCHON20009350	0	0	0			
HCHON20010990				0.3	0.3	0.3
HCHON20011160	0.04	0.2	0.04			
HCHON23015230	2.6	2.3	2.4	1.2	1.7	0.6
HCHON23022470	2	1.2	0.7	1.6	1.1	1.1
HCHON20035130	1.9	2	2.4	1.3	0	2
HCHON23043590	2.6	2.4	1.8	1.5	0.3	0.6
HCHON23067220	1.5	2.1	2.3	2.1	0	0.9
HCHON20076500	2.1	2.4	2.1	0	0.1	0
HEART20021840	0.6	0.4	0			
HEART20067870	0	0	0	0	0	0
HEART20083640	0.8	0.2	0.2			
HHDPC10000650	1.4	1.4	1.1	0.7	0.4	0.3
HHDPC20034390	1.1	0.5	1.2	0.3	0.04	0.04
HHDPC20095280	0.8	0.7	0.5	0	0.5	0
HLUNG10000550	7.6	7	6.9	2.1	1.4	1
KIDNE20018970	1.5	1.2	0.9	1.4	0.9	0.9
KIDNE20028720	1.5	1.2	0		1	

#### Table 52 (continued)

Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ctl. TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours; ct1, Hp, and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45: TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45: TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

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	Clone Name		THP-1			MKN45	
		ct1	TNF_1h	TNF_3h	ct1	Нр	∆cagE
i	KIDNE20079440	1.4	1.8	0			
15	KIDNE20096470	2.1	2.6	2.3	1.3	1	0.7
	KIDNE20106740	0.2	0.1	0	0	0	0
	KIDNE20120090	0.2	0	0			
	KIDNE20127750	1.9	0.6	0.4			
20	KIDNE20130450	0.9	0.9	1.3	0.1	0.8	0.4
	KIDNE20132180				0.7	0	0
	KIDNE20141190	0.1	0.2	0	. 0.4	0.3	0
	KIDNE20148900	4.6	0	4.7.		į	
	KIDNE20163880	0.6	1.5	0	2.2	1.8	1.2
25	KIDNE20182690	0.5	0.4	. 3.9	2.5	3.1	3.1
	LIVER10004790	1.5	3.3	1.6	0	0	0
	LIVER20011130	2.4	0.8	0	0.2	1.9	0.2
	LIVER20038540	0	5.1	0	1.2	4.9	0
30	LIVER20055440	0.5	0.5	0.4	0.3	0.1	0.1
	LIVER20062510	. 1	1.1	1.2	0	0	0.9
	LIVER20085800	0	0.8	0.5			
	MAMGL10000830	5.4	4.3	0.1	0.6	0.6	0.7
	MESAN20031900	0.7	0.3	0.4	0.1	0.1	0.1
35	MESAN20121130	2.6	2.8	2.2	0.1	0.04	0.04
	MESAN20127350	1.6	0.7	0.3			
	MESAN20130220	0.9	2.3	2.2			
	MESAN20154010	2.6	2.2	2	2.9	2.4	2.5
40	MESAN20174170	0	0	0.7	0	0	0
	NOVAR10001020				0.3	0.04	0.04
	NT2NE20053580				0.8	0	0
	NT2NE20089610	0.9	1.3	1.5	0.1	0.04	0.04
	NT2NE20089970	0.7	0	0	0	0	0
45	NT2NE20146810				2.8	2.3	1.9
	NT2NE20155110	2.5	2.6	2.9			-
	NT2NE20156260	1.3	1.3	1.7	0.3	0.1	1
	NT2NE20158600	0.8	3.4	3			_
50 .	NT2NE20172590				0	0.8	0
	NT2NE20174920	1.8	1	1.1	1.4	0	0
	NT2NE20181650	1	1.1	0.5	0.2	0.1	0.04
	NT2RI20005750	- 0	0.4	0	0.6	0.04	0.8
	NT2RI20009870	3	2.3	2.3	7.3	2.1	3.4
55	NT2RI20023160	3.5	1.1	2.8	1.7	0.4	1.8
	NT2RI20040930	0.7	0.6	0.5	0.3	0.1	0.1
	NT2RI20046080	1.8	1.8	1.5	1.2	0.8	0.9

### Table 52 (continued)

Alteration of the expression level of each clone due to TNF- $\alpha$  stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ctl. TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- $\alpha$  for 1 hour, and in the cell stimulated with 10 ng/mL TNF- $\alpha$  for 3 hours; ct1, Hp. and  $\Delta$ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45: TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 $\Delta$ cagE) (at a ratio of MKN45: TN2 $\Delta$ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	٠.	THP-1		MKN45			
	ct1	TNF_1h	TNF_3h	ct1	Нр	∆cagE	
NT2RI20055790	0.9	0.9	0.9	0.8	0.6	1	
NT2RI20069730	2.4	2.1	1.7	2.1	1.4	1.4	
NT2RI20203900	0	0	0	0	0	0	
NT2RP70062230				1.8	0	1.5	
NT2RP70102350	1.7	0.04	0.04				
NT2RP70110860	0	0	0.6	0	0	0	
NT2RP70111320				3.2	4.4	2.8	
NT2RP70130020	0	0	0	. 1	0	0.1	
NT2RP70143480	1.2	2	1.7	0.8	1.1	0.6	
NT2RP70150800				0.8	0.3	0.3	
NT2RP70157890	4.6	1.1	0.3	2.2	1.8	0	
NT2RP70169110	0.5	1.3	1.7	1	3.3	2.5	
NT2RP70175670	0.3	0.1	1.4	4.3	3.3	3.3	
NT2RP70188020	2.5	. 2.8	2.6	0	0	0	
NT2RP70188710	0	0.1	0.2	4.3	2.8	2.9	
NT2RP70190640				0.4	0.4	0.9	
NTONG20029480	3.1	0.7	2.2				
NTONG20064840				1.5	1	1	
NTONG20067090	2.5	2.1	2.3	0.4	0.1	0.2	
NTONG20070340	0.1	0	0	6.3	1.3	0.7	
NTONG20077560				0.5	0.5	0.5	
NTONG20083650	2.9	2.9	2.7	2.5	2.5	1.9	
NTONG20090680	2.1	2	2.4	2	1.3	1.6	
OCBBF20005230	1.7	1.3	2.3	0.9	0.7	0.7	
OCBBF20019380	0.6	0.6	0.5	0	0	0	
OCBBF20020150	4.2	3.2	3	1	0	0.6	
OCBBF20020830	2.7	2.7	1.3	4.4	2.3	2.1	
OCBBF20039250	1.	1.2	0.9	0.4	0.1	0.5	
OCBBF20041680	1.4	0	0				
OCBBF20047570	0.04	0	0	0.3	0.2	0.6	
OCBBF20051610	0	0.04	0.04	0	0	0	
OCBBF20054200	0.4	0.3	0	0.04	0.04	0.04	
OCBBF20061720	1.3	2	0.2	0.7	1.2	0	
OCBBF20062140	3.3	3.1	5				
OCBBF20071960				0.1	0	0	
OCBBF20072320	- 0.04	0	0.04	0.04	0.04	0.04	
OCBBF20079310	0.04	0	0	0	0.04	1	
OCBBF20081380	6.3	6.1	5.1	0.8	0.4	0.6	
OCBBF20085200				0.1	0.5	1.3	
OCBBF20094240	0.9	1.5	1.6	1.1	0.3	0	

#### Table 52 (continued)

Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ctl, TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours; ct1, Hp, and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45: TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45: TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

	Clone Name		THP-1			MKN45	
		ct1	TNF_1h	TNF_3h	ct1	Нр	∆cagE
	OCBBF20107920	2.9	2.9	2.6	2.6	0.7	0.3
15	OCBBF20127040	1.4	1.3	0.5	0.2	0.04	0
	OCBBF20130110				3.2	2.4	1.8
	OC3BF20139260	2.1	0.7	0.2			
	OC3BF20164050	0.3	0.3	0.2	0.2	0	0.04
20	OC3B=20178990	2.1	0.7	0.2	0.9	0	o
	OC3BF20180840	3.7	2.7	3.1	0.1	0.3	0.3
	PEBLM10000240	2.1	2.2	1.6	. 0	0.3	0
	PEBLM20013120	3.3	0.5	3			
	PEBLM20024550	0.1	0	0	3	2.2	0.7
.25	PEBLM20052820	1.9	2.1	. 2.2	1	0.6	0.8
	PEBLM20074370	0.9	0.9	1.7	3.7	3.1	3
	PERIC20002140	0.04	0.9	0.4	0.7	0.3	0.8
	PERIC20004780	0	0.04	0.1	0.04	0	0.04
Je	PLACE60003480	4.1	1.5	4.8	0.6	1.6	5.1
	PLACE60136720	0.5	0.7	0.7	0.6	0.7	0.2
	PLACE60155130	0.7	2.3	0			
	PLACE60169420	1.2	1.4	1.6	0.6	0	0.8
	PLACE60181070	42.3	10	28.2			
35	PROST10004800	3.1	3.2	1.8			
	PROST20120160	0	8.0	0	0	0.3	0.9
	PROST20144220	2.5	2.8	2.4	1.6	0.5	0.2
	PROST20149160	0.7	0	0.4	1.6	0.6	0.6
40	PROST20149250	0	0.9	0.4	0	0	0
	PROST20151240	1.3	0.7	0	0	1.2	0
	PROST20153320	1.4	1.2	1.8	1.4	0.3	1.2
	PROST20161950	0	0	0.6	2.2	1.4	1.2
	PHOST20189770	1.1	1.4	0.8	2.8	2.8	2.1
45	PUAEN20003740	3.1	0.5	2.8	1.4	0.5	2.4
	PUAEN20011880	1.3	2.4	0.4	0.1	0.3	0
	PUAEN20015260	0.04	0.04	7.4			
	PUAEN20025680	1.9	1	2.3	3.1	0.9	1.1
50	PUAEN20040670	0.3	0.5	0.2	1.3	0.5	1
	PUAEN20045250	1.8	1.6	1.6	1.9	1.6	1.1
	PUAEN20078980	1.1	0.3	0.7	0.5	0	0.1
	PUAEN20085150	2	1	2.3	1.6	1.1	0.2
	SKMUS20018230	1.9	2.2	1.8	0.8	0.5	0.6
55	SKMUS20028210	1.6	2.7	2.2	0	0	1.3
	SKMUS20031680	0.9	0	0	1.2	2.4	0.3
	SKMUS20046670	0.3	0.3	0.3			

### Table 52 (continued)

Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helico-bacter pylori*, ctl. TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours; ct1, Hp. and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45: TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45: TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

	Clone Name		THP-1			MKN45	
		ct1	TNF_1h	TNF_3h	ct1	Hp	ΔcagE
	SKNSH20062340				0.6	0.5	0
15	SKNSH20080430	1.1	2.6	0.5	0	1.3	0
	SMINT20001760	1.8	1.5	0.7	0.3	0.1	0.3
	SMINT20013480	1.3	2.1	0.9			
	SMINT20014580	2.7	2.1	1.4	1.2	0	0.6
20	SMINT20033400	2.6	1.7	1.4			
	SMINT20047810	2.2	0.7	0.5			
	SMINT20051610	0.1	0.1	0.3	. 0.4	0.1	0.5
	SMINT20056210				0.9	1.8	0
	SMINT20060780	0.2	0.6	0.5	0.04	0.04	0.04
25	SMINT20080540				0	0	0
	SMINT20105000				0	1.1	0.3
	SMINT20108530	1.3	1.5	0	0.04	0.04	0.04
	SMINT20122850	0.04	0.04	0.04	0.04	0.04	0.04
30	SMINT20122910				0.3	0.3	0.3
	SMINT20153530	4.8	4.6	5.6	2.7	1.5	1.8
	SMINT20161220	8.5	6.2	19.5	2	1.1	1
	SMINT20163960	0.6	0.5	1.4	0	0	0
	SMINT20164770	2.4	2.1	1.6	1.8	1.2	1
35	SMINT20168570	0	0	0			
	SPLEN20008820	2.5	2.3	2.7	1.6	1.3	8.0
	SPLEN20011410	0.4	0.4	0.1	i		
	SPLEN20013540	1.6	0.9	1.1	2.4	1.4	1.8
40	SPLEN20019450	1	1.8	1.2	0.2	0.6	0.4
	SPLEN20022230	4.5	6.2	3.9	1.4	1.1	1.6
	SPLEN20040600	3.2	4.5	3.6	0	0	0
	SPLEN20076530	0.04	0.04	0.04	0	0	0
	SPLEN20101190	0.3	0.2	0.6	1.6	0	0
45	SPLEN20126190	2.5	3.4	2.8	5.2	3.5	3.1
	SPLEN20152760	4.2	3	3.2	1.2	0.8	1.6
	SPLEN20157300	0.4	0.5	2.5	}		
	SPLEN20158990	1.9	0.9	2.6	1.1	1.1	1.3
50	SPLEN20163560	0.3	0.6	0.3	0	0	0
	SPLEN20174260	0.4	0	0	0.3	0.1	0.1
	SPLEN20211570	2.3	2.3	2.2	1	2.1	1.4
	SPLEN20214580	- 0.04	0.6	0.9	1.4	1.3	2.6
	SPLEN20245300	3.1	2.6	1.9	0.6	0	0.2
55	SPLEN20279950	0.8	2.1	0.3			
	SPLEN20280660	0.6	. 0.5	1	0	0	0
	SPLEN20283650	1.8	1	0.8	0.8	0	0

#### Table 52 (continued)

Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ctl. TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours; ct1, Hp. and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45: TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45: TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

	Clone Name		THP-1	······································		MKN45	
		ct1	TNF_1h	TNF_3h	ct1	Нр	∆cagE
	SPLEN20329240				0.2	0	0
15	STOMA20010250	2	0.9	1	0	0	0.7
	STOMA20032890	0.9	1.5	0.4			
	STOMA20048520	0.04	2	0.4	0	0.9	0
	STOMA20057820	1.3	1	0	4.3	4.1	0
20	STOMA20062290	0.4	0.6	0.4	0.3	0.3	0.2
	STOMA20076800	1.1	. 0.7	0.6	1.2	0.6	0.3
	TESTI20001170	0	0	0	. 0.8	0.6	0.7
	TESTI20002780				0	0	0
	TESTI20004890	1.1	0.7	0.6	0	0.2	0.4
25	TESTI20011200	6.3	3.7	5.9	0.5	0.04	0.2
	TESTI20018230	0	0	0	0.04	0.04	0.04
	TESTI20035960	0.1	0	0	0.04	0.04	0.04
	TESTI20038270				0	0	0
30	TESTI20044230	0	0	0	0.6	0.2	0.2
00	TESTI20046750	0.4	0.04	0.04	1	8.0	0
	TESTI20060400	1.2	2	0.2	0.7	0.5	0.04
	TESTI20066770	0	0	0	0.04	0.04	0.04
	TESTI20076850	0	0.6	0	0.04	0.04	0.04
35	TESTI20083940	0.9	1.5	1.4	0	1.2	1.3
	TESTI20087620	0.8	2.3	0.8	1.1	0.04	0.1
	TESTI20098530				5.3	1.2	0
	TESTI20105720	2.7	3.5	2.5	0.04	0.1	0.04
40	TESTI20108720	0.04	1.5	1.1	2.5	2.1	1.8
10	TESTI20123080	1			6	0	0
	TESTI20128350		}		1.4	1.6	0
	TESTI20136100	3.1	1.9	2.1		'	
	TESTI20137670				0.4	0.4	0.4
45	TESTI20143240	0.2	0.1	0.1	0.3	0.04	0.3
	TESTI20143620	0.04	0	0			
	TESTI20156100	0.1	0.04	0.1		ĺ	
	TESTI20161970	1.2	0.7	0	1.1	0.4	1
50	TESTI20168480				0.5	5.7	0.5
50	TESTI20168960				0.5	0.5	0.5
	TESTI20178160	0.04	0.04	0.04	0.04	0.04	0.04
	TESTI20185810	-			0.9	0	0
	TESTI20199170	0.7	0	0	0.9	0.8	0
<i>55</i>	TESTI20200260				0.3	0	0
	TESTI20200710	3.9	2.6	2.4	2.5	3.5	2.9
	TESTI20202650	0.04	0.04	0.04	1	1.2	0.3

### Table 52 (continued)

Alteration of the expression level of each clone due to TNF- $\alpha$  stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ctl, TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- $\alpha$  for 1 hour, and in the cell stimulated with 10 ng/mL TNF- $\alpha$  for 3 hours; ct1, Hp. and  $\Delta$ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45: TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 $\Delta$ cagE) (at a ratio of MKN45: TN2 $\Delta$ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

	Clone Name		THP-1			MKN45	
		ct1	TNF_1h	TNF_3h	ct1	Нр	ΔcagE
	TESTI20220100	0	5.7	0			
15	TESTI20224620				0	0	1.5
	TESTI20229600	0	0	0	Į		
	TESTI20230850	0.04	0.04	0	0.04	0.04	0.04
	TESTI20231920				0.5	0.5	0.5
20	TESTI20234140				1.8	0.3	0.3
	TESTI20234270	2.6	2.8	2.9	0.5	0.04	0.3
	TESTI20238000	0.2	0	0.04	0.04	0.04	0.04
	TESTI20238610				0.04	0.04	0.04
	TESTI20239510	0	0.2	0	0.04	0.2	1 1
25	TESTI20242990	1.8	2.1	1.8	0	0	0
	TESTI20265250	2.1	1.6	1.9	1.5	0.8	0.4
	TESTI20265370	0.04	0.04	0.04	0.04	0.04	0.04
	TESTI20266740	0.2	0	0.7	0.04	0.04	0.04
30	TESTI20272390	1.3	1.2	0.8	0.2	0.2	0.4
	TESTI20275030	0	0	0	0	0	0.3
	TESTI20275620	1.3	0.04	0.7			
	TESTI20277360	0	0	0			
	TESTI20282540	0.04	0	0.1	0.2	0.04	0.3
35	TESTI20284880	0.4	0.2	0.1	0.04	0	0.1
	TESTI20285830	0.04	0.04	0.04			
	TESTI20288110				1.2	0	0
	TESTI20289850	0.04	0	0	0.04	0.04	0.04
40	TESTI20307540				0.6	0.8	0
	TESTI20308600				0.5	1.2	0.5
	TESTI20311290	0	0	0	0 .	0	0.7
	TESTI20317600	0	0	0	0.04	0.04	0.04
	TESTI20319190	0.2	0	0	0.04	0.04	0.3
45	TESTI20332420	0.6	0.1	0.9			
	TESTI20335200				0.9	1.4	0.9
	TESTI20342430	0	2.8	0	0.6	0.6	0.5
	TESTI20345060				0.1	0	0.04
50 ·	TESTI20347300	0.9	0.6	1.4	0.04	0	0
50	TESTI20357960	1	1	1.7	2.7	1.3	1.7
	TESTI20361140	0.04	0.04	0.04	0.2	0	0
	TESTI20369220	0.04	0.04	0.04			
	TESTI20369690	1.5	0	1.3	1.3	1.4	1
55	TESTI20370020	0.4	1.7	0.1	1		
	TESTI20371030	1.3	1.3	1	0.8	0.5	0.5
	TESTI20386230	2	0.2	0.3			

#### Table 52 (continued)

Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ctl, TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours; ct1, Hp, and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45: TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45: TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

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	Clone Name	· · · · · · · · · · · · · · · · · · ·	THP-1			MKN45	
	Ī	ct1	TNF_1h	TNF_3h	ct1	Нр	ΔcagE
-	TESTI20391210	0.6	2.3	4.9	3.1	0	2.4
15	TESTI20392090	0	0	0.04	0.04	0.04	0.7
	TESTI20392250	9.3	7.8	3.8			
	TESTI20392270	1.8	1.4	1.6	1.1	1.6	1.1
	TESTI20401020	0.2	0.5	0.8	0	0	0
20	TESTI20401430	4.3	4.8	4.3			
	TESTI20409440	1.4	. 0.5	0.3	0.5	0	0.3
	TESTI20415640	8.0	2.5	1	. 0	0	0
	TESTI20424000	0.2	0.04	0.04	0	0	0
	TESTI20424730	1.8	0.7	2.9	3.8	0	3.3
25	TESTI20425070	2.3	2.4	2.6	1.9	1.4	1.2
	TESTI20433130				0	0	0
	TESTI20438570	0.8	0.6	0.6	0.8	0.6	1.2
	TESTI20443090	0.1	0.1	0.1	0.3	0.5	0.6
30	TESTI20463520				0	0	0
	TESTI20465520	0.6	0.6	0.5	0.2	0	0.1
	TESTI20478010	0.9	1.7	0.7	0	0.3	0
	TESTI20478180	0.04	0.04	0.04	0.04	0	0
	THYMU20029100	1.9	1.2	2.3	2	2.9	2.5
35	THYMU20061700	0	0	0	0.7	0.2	0.2
	THYMU20095960	2.9	2.4	0.5	1		
	THYMU20111180	1.1	0.6	0.5	0	0	0
	THYMU20118060	0.2	0	0.2	0.04	0.04	0.04
40	THYMU20130890	0.6	1.3	3.3			
	THYMU20142040	1	1.1	0.7	1.3	1.1	1
	THYMU20142970	4	3.5	3.8	1.6	2	0.6
	THYMU20153160	1	0.7	1	0.1	0.1	0.04
	THYMU20158250	10.4	7	5.5	1.1	0	0
45	THYMU20187720	3.2	3.2	2.8	2.4	2.2	2.3
	THYMU20194360	1.8	2.1	1.7	0.4	0.3	1.3
	THYMU20208300	1.9	1.9	1.6	0.3	0.2	0.3
	THYMU20226600	3	0	1.4	1.1	0.3	2.6
50	THYMU20239000	2.1	2.3	2.8	1.4	8.0	1.1
30	THYMU20253250	1.1	0.3	0.3			0.04
	THYMU20272490	2.7	1.4	0.6	0.04	0.04	0.04
	THYMU20284120	3.8	4.1	4	0.4	0.04	0.5
	THYMU20286290	0	2.1	0.4	3.1	2.5	1.7
55	TKIDN10000010	2.2	2.2	2.5	1.2	1	1.1
	TRACH20005020	0	0	0	2.8	0.9	0.5
	TRACH20032720	0.1	0	0	0.6	0.04	0.1

### Table 52 (continued)

Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helico-bacter pyloni*, ctl TNF\_1h, and TNF\_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours; ct1, Hp, and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45: TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45: TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	• .	THP-1		-	MKN45	
Ī	ct1	TNF_1h	TNF_3h	ct1	Нр	∆cagE
TRACH20041830				0.8	0.2	0.9
TRACH20060150	0.2	0.9	2			
TRACH20076760	5.1	4.9	4.5	0.6	0.5	0.4
TRACH20082780				0	0	0
TRACH20091230	0.4	0	0.2	2.1	1.1	1.2
TRACH20099340	1.8	3.8	4.9	1.9	2.5	0.9
TRACH20109650	3.5	3.3	3.5	3.7	3.7	3.4
TRACH20115740	0.04	0.04	0.04			
TRACH20134950	5.6	5	4	3.5	1.2	1.9
TRACH20135520	1	0.9	0.6	0.9	0.9	0.5
TRACH20153810	2.1	0	0			
TRACH20184490	2.2	3.2	2.8	1.6	0	0
TSTOM20001390	1.5	2.1	1.8	2.5	0.4	2.5
TSTOM20005690	1.3	0.8	1.1	0.3	0	0.1
UMVEN10001550	2.4	2.6	3.3	0.6	0	0.04
UMVEN20003540	5.2	3.9	4.9	3.1	2.4	2.8
UTERU20004240	0.04	0.2	0.1	0.04	0	0.04
UTERU20046980				0	0	0
UTERU20055930	2.5	3.6	2.9	2.3	, 1.6	2.5
UTERU20068990	0.04	1.3	0.04	0.1	0	0
UTERU20070810	2.7	1.9	2.4	1.9	1.3	1.1
UTERU20115740	3.1	3.2	5	2.3	1.9	0
UTERU20119060	0.8	1.9	0	1.9	0.3	1.6
UTERU20124070	2	2.7	1.8	2.8	2.1	1.8
UTERU20126880				0	2.2	0.1
UTERU20134910	2.5	2.7	2.3	2.9	1.4	1.3
UTERU20146680	0	0.1	0	0.5	0	0.04
UTERU20176130	2.9	1.3	1.6	1.9	0.6	0.8
UTERU20185230	3.1	3.2	1.8	1.6	1.1	0.6
UTERU20186740	1.9	1.4	0.7	0.04	0	0

Homology Search Result Data

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[0322] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences.

[0323] In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared

[0324] Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

3NB6910001910//ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE--TRNA LIGASE) (ALARS).//3.10E-20//

	392aa//24%J/067323
	3NB6920014080
	3NB6920014590//HOMEOBOX PROTEIN DLX-6//1.00E-91//226aa//78%//Q98877
	ADIPS10000640//Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds.//1.60E-169//303aa//
5	100%//AF222742
	ADIPS20004250//ZINC FINGER PROTEIN OZF.//6.60E-27//223aa//32%//Q15072
	ADRGL10001470//CYTOCHROME P450 11B1 PRECURSOR (EC 1.14. 15.4) (CYPXIB1) (P450C11) (STEROID
	11-BETA-HYDROXYLASE).//1.60E-38//84aa//98%//P15538
	ADRGL20000640
10	ADRGL20011190//spectrin, beta, non-erythrocytic 1 [Homo sapiens].//1.00E-36//250aa//38%//NP_003119
	ADRGL20012870
	ADRGL20013010
	ADRGL20013520
	ADRGL20018300//KINESIN LIGHT CHAIN (KLC).//1.20E-207//566aa//70%//Q07866
15	ADRGL20018540
	ADRGL20028570//Rattus norvegicus MG87 mRNA, complete cds.//2.90E-69//250aa//53%//AF095741
	ADRGL20035850//CYTOCHROME P450 17 (EC 1.14. 99.9) (CYPXVII) (P450-C17) (STEROID 17-ALPHA-HY-
	DROXYLASE/17,20 LYASE).//7.30E-52//99aa//100%//P05093
	ADRGL20044590  BNA for requiriling, complete cds //0//67333//899///AB025258
20	ADRGL20048330//Mus musculus mRNA for granuphilin-a, complete cds.//0//673aa//89%//AB025258
	ADRGL20061930//transposon-derived Busterl transposase-like protein//6.00E-65//500aa//33%//NP_067034
	ADRGL20067670
	ADRGL20068170
	ADRGL20068460
25	ADRGL20073570 ADRGL20076360
	ADRGL20078360  ADRGL20078100//NADPH:ADRENODOXIN OXIDOREDUCTASE PRECURSOR (EC 1.18. 1.2) (ADRENODOX-
	IN REDUCTASE) (FERREDOXIN-NADP(+) REDUCTASE).//3.10E-147//276aa//99%//P22570
	ADRGL20083310
30	ASTRO10001650//DREBRIN E.//4.80E-293//540aa//99%//Q16643
50	ASTRO20001410
	ASTRO20005330
	ASTRO20008010//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//6.00E-57//143aa//
	70%//Q03923
35	ASTRO20012490
	ASTRO20027430//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//2. 20E-18//178aa//
	34%//Q15404
	ASTRO20032120
	ASTRO20033160//BRAIN MITOCHONDRIAL CARRIER PROTEIN-1.//2.70E-125//291aa//80%//095258
40	ASTRO20055750//Human elastin gene, exon 1.//2.70E-293//654aa//88%//M17282
	ASTRO20058630
	ASTRO20064750//Homo sapiens BM-003 mRNA, complete cds.//6.10E-69//214aa//64%//AF208845
	ASTRO20072210//PERIAXIN.//2.10E-25//87aa//56%//Q63425
	ASTRO20084250//Ciona savignyi mRNA for PEM-3, complete cds.//3.50E-56//154aa//64%//AB001769
45	ASTRO20100720
	ASTRO20105820//ACTIN INTERACTING PROTEIN 2.//2.60E-111//392aa//56%//P46681
	ASTRO20106150//H.sapiens mRNA for calpain-like protease.//1.80E-291//473aa//98%//Y10552 ASTRO20108190//TUBERIN (TUBEROUS SCLEROSIS 2 PROTEIN) //5.30E-278//513aa//100%//P49815
	ASTRO20111490 ASTRO20114370//Mus musculus SMAR1 mRNA, complete cds.//1.30E-213//461aa//89%//AF235503
50 °	
	ASTRO20114610 ASTRO20125520//dnaj protein [Schizosaccharomyces pombe]//7.80E-37//260aa//38%//CAB59885
	ASTRO20130500//UBIQUITIN-ACTIVATING ENZYME E1.//2.70E-157//815aa//42%//Q29504
66	ASTRO20136710
55	ASTRO20138020 ASTRO20141350//Mus musculus mRNA for granuphilin-b, complete cds.//7.40E-12//169aa//30%//AB025259
	ASTRO20141330//Mus musculus mirita for grandpiniini 8, semplete seesavas a
	ASTRO20143630 ASTRO20145760//TUBULINTYROSINE LIGASE (EC 6.3.2.25) (TTL).//1.60E-14//233aa//27%//P38584
	1011102017010011000EH 1111020170 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

ASTRO20152140			
ASTRO20155290			
ASTRO20166810			
ASTRO20168470//ZINC	FINGER PROTEIN 135.//4.80E	-103//289aa//59%//P52742	
ASTRO20173480			
ASTRO20181690//oocy	te-specific protein P100//1.60E-7	'0//554aa <b>//3</b> 6%//S23468	
ASTRO20190390	•		
BEAST20004540			
BGGI110000240			
BGGI110001930			
BGGI120006160//isome	rase-like protein (Arabidopsis tha	aliana].//1.00E-52//187aa//47%//BAB0	0076
BLADE20003400//ZINC	FINGER PROTEIN 177.//2.50E-	33//205aa//38%//Q13360	
BLADE20003890//ZINC	FINGER PROTEIN 135.//1.50E-	264//471aa//95%//P52742	
BLADE20004630			
BNGH420088500			
BRACE20003070//Ratt	us norvegicus neurabin mRNA, co	omplete cds.//2.30E-40//172aa//46%//	U72994
BRACE20006400			
BRACE20011070//Mus	musculus F-box protein FBX15 m	nRNA, partial cds.//9.60E-142//471aa/	//56%//AF176530
BRACE20019540			
		THIOESTER HYDROLASE, INDUCI	
(LONG CHAIN ACYL-	COA THIOESTER HYDROLASE	E) (LONG CHAIN ACYL-COA HYDI	ROLASE) (CTE-I)
	E-148//423aa//65%//088267		
BRACE20037660		•	
		melanogaster].//3.80E-8.3//426aa//4	
BRACE20038470//Ratt	us norvegicus neurexophilin 4 (	Nph4) mRNA, complete cds.//1.70E	-57//109aa//98%//
AF042714			
BRACE20038480//Hum	an SEC14L mRNA, complete cds	s.//2.60E-93//179aa//99%//D67029	
BRACE20038850			
BRACE20039040			
BRACE20039440//Dros	ophila melanogaster CHARYBD	E (charybde) mRNA, complete cds.//	6.50E-17//142aa//
35%//AF221109			
BRACE20039540//MH0	class I chain-related gene /	A protein [Homo sapiens]//2. 00E-	116//246aa//90%//
NP_000238			
BRACE20050900			
BRACE20051380			
BRACE20051690			
BRACE20052160//Xen	ppus laevis bicaudal-C (Bic-C) ml	RNA, complete cds.//2.10E-13//208aa	//30%//AF224746
BRACE20053280//Mus	musculus Pdz-containing protein	n (Pdzx) mRNA, complete cds.//5.20E	-63//223aa//64%//
AF229645			
BRACE20053480//Mus	musculus erythroblast macroph	nage protein EMP mRNA, complete	cds.//1.70E-133//
145aa//97%/iAF263247	•		
BRACE20053630//BRI	ITLE-1 PROTEIN PRECURSOR.	.//1.20E-24//208aa//31%//P29518	
BRACE20054500			
BRACE20055180			
BRACE20056810			
	LEOPLASMIN.//5.20E-42//215aa	a//45%//P05221	
BRACE20057420		•	
	ARYOTIC TRANSLATION INITIA	TION FACTOR 4E (EIF-4E) (EIF4E) (I	MRNA CAP-BIND-
	25 KDA SUBUNIT).//1.00E-22//6		
BBACE20057730//toxir	sensitivity protein KTI12 homolo	og//1.10E-10//173aa//26%//A64492	
BBACE20058580//Hom	o sapiens HCMOGT-1 mRNA for	sperm antigen, complete cds.//2.10E-	178//358aa//96%//
AB041533	o depiction to the definition for		
BRACE20058810 -			
	OTEIN 4.1 (BAND 4.1) (P4. 1).//6.	70F-52//400aa//32%//P11171	
BDACE20039370//PDC	YRIN HOMOLOG PRECURSOR	R.//1.30E-14//139aa//44%//Q06527	
BRACE20060550//ANA	, ITHIN HOMOLOG FRECONSOR	1.30L 1711 133day177 /a/1 4000L/	
BRACE20060720 BRACE20060840			
	C EINGER DROTEIN ZICA (ZINC	FINGER PROTEIN OF THE CEREB	FITUM 4) //4 00F=
ロコムしにといいのいからい/と言い	J FINGER PROTEIN AICH (ZINC	LINGED LUCITIN OF THE OFFIED	ON ~).//~.UUE-

```
131//264aa//87%//Q61467
        BRACE20061050
        BRACE20061740
        BRACE20062400
        BRACE2C062640//HYPOTHETICAL 93.7 KDA PROTEIN F48E8.6 IN CHROMOSOME III.//9.10E-90//343aa//
        45% J/Q09568
        BRACE20062740
        BRACE20063630
        BRACE20063780
10
        BRACE20063800
        BRACE20063930
        BRACE20064880//POLY(RC) BINDING PROTEIN 2 (PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLE-
        OPROTEIN X) (HNRNP X) (CTBP) (CBP).//1.80E-129//207aa//81%//Q61990
        BRACE20067430
        BRACE20068590//HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961.//2.70E-155//504aa//56%//Q9Y2G7
15
        BRACE20069090
        BRACE2C081720
        BRACE2C082950
        BRACE2C090440
        BRACE2C096200//Homo sapiens sir2-related protein type 7 (SIRT7) mRNA, complete cds.//1.00E-162//305aa//
20
        991a//AF233395
        BRACE20096540
        BRACE20097320
        BRACE20099570
        BRACE2C101700
        BRACE2C101710
        BRACE20106690
        BRACF2C106840//Rattus norvegicus partial mRNA for CRM1 protein.//9.00E-59//120aa//100%//AJ238278
        BRACF2C107530//Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR-AKL) mRNA, com-
        plete cds //1 70E-48//108aa//91%//AF044574
30
        BRACE2C103130//Homo sapiens RAB-like protein 2B (RABL2B) mRNA, complete cds.//1.60E-43//92aa//100%//
         AF095352
         BRACE2C108880//MALEYLACETOACETATE ISOMERASE (EC 5.2.1.2) (MAAI) (GLUTATHIONE TRANS-
         FERASE ZETA 1) (EC 2.5.1.18). //5. 90E-11//27aa//100%//043708
         BRACE2C109370
35
         BRACE2C109830
         BRACE2C111830
         BRACE2C114780
         BRACE20115450
         BRACE2C115920//RHO-GTPASE-ACTIVATING PROTEIN 4 (RHO-GAP HEMATOPOIETIC PROTEIN C1) (P115)
40
         (KIAA0131) //9.70E-73//291aa//52%//P98171
         BRACE20116110
         BRACE2C116460//ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34).//1.00E-20//
         48aa//100°a/P30049
         BRACE2C118380
         BRACE2C121850
         BRACE20136240
         BRACE20141080
         BRACE20142320
50 -
         BRACE20142570
         BRACE20147800
         BRACE20148210
         BRACE2C143240//Gsplp [Saccharomyces cerevisiae].//1.00E-05//75aa//35%//NP_013396
         BRACE2C151320//Drosoohila melanogaster Oregon R cytoplasmic basic protein (deltex) mRNA, complete cds.//
 55
         6 10F-35//202aa//41%//U09789
         BRACF20152870
         BRACE2C153680//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//4.10E-107//209aa//
```

	99%//AF078779
	BRACE20154120//Shb=Src homology 2 protein//2.60E-23//79aa//48%//AAB29780 BRACE20163150
	BRACE20163350//MYELIN PO PROTEIN PRECURSOR.//8.20E-08//92aa//33%//P20938
5	BRACE20165830
	BRACE20171240
	BRACE20172980//translation initiation factor eIF3 [Schizosaccharomyces pombe]//5.60E-06//136aa//30%/
	CAB11250
	BRACE20175870
10	BRACE20177200//RAN-SPECIFIC GTPASE-ACTIVATING PROTEIN (RAN BINDING PROTEIN 1) (RANBP1).//
	9.90E-32//63aa//100%//P34022
	BRACE20179340 BRACE20185680//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATECOA LIGASE) (ACYL- AC-
	TIVATING ENZYME).//1.40E-16//94aa//40%//Q01576
15	BRACE20188470//ATP-binding cassette, sub-family A member 8//1.70E-115//457aa//50%//NP_009099
	BRACE20190040
	BRACE20190440
	BRACE20192440//TRANSLATION INITIATION FACTOR IF-3 //1.20E-09//161aa//26%//P47438
	BRACE20195100
20	BRACE20201570
	BRACE20210140
	BRACE20220300
	BRACE20223280 BRACE20223330
24	BRACE20224480
	BRACE2C224500
	BRACE20228480
	BRACE20229280 -
	BRACE20230700
<i>3</i> 0	BRACE2C232840//ATP-binding cassette, sub-family E, member 1//0//560aa//75%//NP_002931
	BRACE2C235400
	BRACE2C237270//Human WW domain binding protein-2 mRNA, complete cds.//6.10E-21//50aa//88%//U79458
	BRACE2C238000 BRACE2C240740
35	BRACE2C248740  BRACE2C248260//H. sapiens PR264 mRNA.//1.50E-13//78aa//48%//X62447
	BRACE2C253160//putative trna-splicing endonuclease subunit [Schizosaccharomyces pombe]//1.10E-11//
	148-ra/ 32°-d/CAA21061
	BRACE2C253330//Homo sapiens Na+/H+ exchange regulatory co-factor (NHERF) mRNA, complete cds.//5.50E-
	88/157aa/i99%i/AF036241
40	BRACE2C257100//transcription factor (SMIF gene)//2.00E-37//110aa//94%//NP_060873
	BRACE20262930
	BRACE20262940
	BHACE20266750 BHACE20267250
45	BRACE20269200
	BRACE2C269710
	BRACE2C273890//Human phosphotyrosine independent ligand p62B B-cell isoform for the Lck SH2 domain mR-
	NA partial cds.//5.70E-25//100aa//65%//U46752
	BRACE20274080
50 .	BRACE20276430//Homo sapiens retinoblastoma-associated protein RAP140 mRNA, complete cds.//4.70E-106/
	203aa/100%J/AF180425
	BRACE20283920 BRACE20284100//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds.//7.20E-121//237aa//100%/.
	AF022728
55	BRACE20286360
- <del>-</del>	BRACE20287410
	BRALZ20013500//Homo sapiens prostate stem cell antigen (PSCA) mRNA, complete cds.//3.30E-06//122aa/
	32%//AF043498

	BRALZ20014450
	BRALZ20017430//H.sapiens mRNA for protein phosphatase 5.//1.70E-41//99aa//87%//X89416
	BRALZ20018340//H.sapiens mRNA for glutamine transaminase K.//4.70E-93//114aa//98%//X82224
	BRAL 720019660
5	BRALZ20054710//Mus musculus mRNA for cysteine and histidine-rich protein (Chrp gene).//1.70E-163//280aa//
	99%//AJ251516
	BRALZ20058880 .
	BRALZ20059500
	BRALZ20064740
10	BRALZ20065600
10	•
	BRALZ20069760 BRALZ20073760//MONOCYTE TO MACROPHAGE DIFFERENTIATION PROTEIN.//8.40E-41//76aa//69%//
	Q15546
	BRALZ20075450
15	BRALZ20075760
	BRALZ20077900//anaphase-promoting complex 1; meiotic checkpoint regulator//3.00E-91//190aa//92%//
	NP_073153
	BRALZ20077930//Xenopus laevis 4g2 mRNA, complete cds.//1.20E-191//501aa//71%//AF182319
	BRALZ20080310
20	BRALZ20088690
	BRAMY10001300//Homo sapiens MAGE-E1b mRNA, complete cds.//5.40E-78//140aa//97%//AB040528
	BRAMY10001570 .
	BRAMY20000520//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HNRNP C1 AND HNRNP
	C2).//7.10E-70//293aa//53%//P07910
25	BRAMY20000860
	BRAMY20002770
	BRAMY20004110
	BRAMY20011140
	BRAMY20025840//H.sapiens mRNA from TYL gene.//7.10E-103//198aa//98%//X99688
30	BRAMY20039260
	BRAMY20045240
	BRAMY20054880//Rattus norvegicus KPL2 (Kpl2) mRNA, complete cds.//1.40E-43//155aa//59%//AF102129
	BRAMY20060920//reduced in osteosclerosis transporter//1.50E-09//60aa//53%//NP_112471
	BRAMY20063970
35	BRAMY20071850
	BRAMY20102080
	BRAMY20103570
	BRAMY20104640//Mus musculus mRNA for serine/threonine protein kinase.//1.80E-140//345aa//75%//AJ250840
	BRAMY20110640
40	BRAMY20111960
	BRAMY20112800
	BRAMY20116790
	BRAMY20120910//GRG PROTEIN (ESP1 PROTEIN) (AMINO ENHANCER OF SPLIT) (AES-VAES-2).//1.60E-
	97//188aa//100%//Q08117
<b>45</b>	BRAMY20121190
_	BRAMY20121620//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//1.80E-256//500aa//85%//
	AF055666
	BRAMY20124260//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//2.80E-286//
	554aa//92%/iU87306
50 ·	BRAMY20134140//ATPase, H+ transporting, lysosomal (vacuolar proton pump) 9kD//4.60E-29//52aa//59%//
50	
	NP_003936 BRAMY20135900//CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN.//2.00E-07//146aa//23%//P55060
	BRAMY20136210
£.F	BRAMY20137560
55	BRAMY20144620
	BRAMY20147540
	BRAMY20148130

BRAMY20152110

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BRAMY20153110//TRYPTOPHAN 5-MONOOXYGENASE (EC 1.14.16.4) (TRYPTOPHAN 5-HYDROXYLASE).//
8.50E-58//201aa//58%//Q92142
BRAMY20157820//PUTATIVE KINESIN-LIKE PROTEIN C2F12.13.//1.10E-90//341aa//50%//014343
BRAMY20160700
BRAMY20162510//MELANOMA-ASSOCIATED ANTIGEN B2 (MAGE-B2 ANTIGEN) (DAM6).//1.30E-33//209aa//
35%//015479
BRAMY20163250
BRAMY20163270
BRAMY20167060
BRAMY20167710
RRAMY20168920
BRAMY20170140
BRAMY20174550//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochon-
drial protein, complete cds.//0//648aa//98%//AF047690
BRAMY20178640
BRAMY20181220
BRAMY20182730
BRAMY20183080
BRAMY20184670//Homo sapiens mRNA for ALEX1, complete cds.//6.40E-14//139aa//27%//AB039670
BRAMY20195090
BRAMY20196000
BRAMY20204450
BRAMY20205740
BRAMY20210400//Homo sapions thyroid hormone receptor-associated protein complex component TRAP150
mRNA. complete cds.//2.80E-16//141aa//39%//AF117756
BRAMY20211390//seven in absentia (Drosophila) homolog 1 [Homo sapiens]//3.70E-156//282aa//99%//
NP 003022
BRAMY20211420//Homo sapiens mRNA for LAK-4p, complete cds.//3.00E-31//224aa//33%//AB002405
BRAMY20213100//Xenopus laevis Mi-2 histone deacetylase complex protein 66 mRNA, complete cds.//2.10E-
66//394aa//44%//AF171099
BRAMY20215230
BRAMY20217460//Homo sapiens cardiac voltage gated potassium channel modulatory subunit mRNA, complete
cds. alternatively spliced.//3.70E-81//158aa//98%//AF295530
BRAMY20218250//putative four repeat ion channel [Rattus norvegicus]//0//588aa//99%//AF078779
BRAMY20218670
BRAMY20229800
BRAMY20229840
BRAMY20230600
BRAMY20231720
BRAMY20240040//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds.//3.20E-
301//642aa//90%//AF042800
BRAMY20242470//CORONIN-LIKE PROTEIN P57 (CORONIN 1A).//1.60E-70//210aa//66%//P31146
BRAMY20245300//Homo sapiens putative prostate cancer susceptibility protein HPC2/ELAC2 mRNA, complete
cds.//0i/737aa//99%//AF304370
BRAMY20247110//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, com-
plete cds.//6.00E-117//366aa//63%//AF127084
BRAMY20247280
BRAMY20248490
BRAMY20250240
BRAMY20250320
BRAMY20252180
BRAMY20252720//Homo sapicns mRNA for thioredoxin reductase II alpha, partial cds.//1.60E-84//161aa//99%//
BRAMY20260910//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//811aa//
99%//AF125158
BRAMY20261680
BRAMY20266850//Homo sapiens oxidation protection protein (OXR1) mRNA, complete cds. //4. 50E-57//193aa//
56%//AF309387
```

	BRAMY20267130
	BRAMY20268990
	BRAMY20270730//Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and
	vasotocin genes, complete cds://7.80E-155//398aa//66%//U90880
5	BRAMY20271400//RHO-GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHOGEF) (RIP2).//0//946aa//80%//
	P97433
	BRAMY20273960
	BRAMY20277140
	BRAMY20277170//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.2 (KSHIIIA).//1.00E-290//538aa//
10	97%//P22462
	BRAMY20280720
	BRAMY20284910
	BRAMY20285160//COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN].//1.90E-79//148aa//
	100%//P01024
15	BRAMY20285930
	BRAMY20286820
	BRAWH10000930
	BRAWH20002320//Manduca sexta death-associated small cytoplasmic leucine-rich protein SCLP mRNA, com-
	piete cds.//3.50E-18//167aa//31%//AF250910 BRAWH20004600//Mus musculus mRNA for NAKAP95, complete
20	cds://8 40E-184//336aa//84%//AB028921
	BRAWH20011710//cytoplasmic linker 2//1.60E-96//316aa//59%//NP_034120 BRAWH20012390//Trichomonas
	vaginalis mRNA for centrin (cel gene).//4.70E-14//153aa//28%//AJ249457
	BRAWH20012410
	BRAWH20014920
25	BRAWH20015350
	BRAWH20015890
	BRAWH20016620//Homo sapiens mRNA for MOK protein kinase, complete cds.//3.40E-82//160aa//99%//
	ABC22694
	BRAWH20016660
30	BRAWH20016860
	BRAWH20017010//Homo sapiens testes development-related NYD-SP22 mRNA, complete cds. //1.00E-23//
	5644/92° J/AF367474
	BRAWH20018730//HYPOTHETICAL 56.4 KDA PROTEIN IN SRS2-SIP4 INTERGENIC REGION.//1.90E-46//
	5034a//31°d/P47026
35	BRAWH20028110/iHomo sapiens actin-binding double-zinc-finger protein (abLIM) mRNA, complete cds.//9.40E-
	168/416aa//61%//AF005654
	BRAWH20029630//Homo sapiens bet3 (BET3) mRNA, complete cds.//2.40E-47//96aa//100%//AF041432
	BRAWH20030250 BRAWH20064050//FIBULIN-1, ISOFORM C PRECURSOR.//6.30E-42//337aa//33%//P23144
	BRAWH20054050//FIBULIN-1, ISOFORM C FRECORSON://d.30E-42//337aa//357/ii/ 160E-159//332aa//84%//P08042
40	BRAWH20096780//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.00E-140//514aa//52%//Q99676
	BRAWH20100690
	BRAWH201C1360
	BRAWH20103180 BRAWH20103290//GUANINE NUCLEOTIDE EXCHANGE FACTOR DBS (DBL'S BIG SISTER) (MCF2 TRANS-
45	FORMING SEQUENCE-LIKE PROTEIN) (KIAA0362) (FRAGMENT).//0//756aa//99%/015068
	BRAWH20105840//HYPOTHETICAL 27.0 KDA PROTEIN IN SPO0A-MMGA INTERGENIC REGION.//1.70E-21//
	156aa//32%/P54527
·	BRAWH20106180
50	BRAWH20107540
	BRAWH20110660
	BRAWH20110790 BRAWH20110960//Homo sapiens mRNA for 26S proteasome subunit p40.5, complete cds.//1.50E-175//378aa//
55	90%//AB009398 BRAWH20111550
55	BRAWH20112940//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-
	WI HAVE TO THE TAXABL

UDPACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAM-

INYLTRANSFERASE) (GALNAC-T1).//1.10E-59//369aa//36%//Q07537

BRAWH20113430//COLD-INDUCIBLE RNA-BINDING PROTEIN (GLYCINE-RICH RNA-BINDING PROTEIN CIRP) (A18 HNRNP).//9.30E-52//104aa//96%//Q14011 BRAWH20114000//GLUTAMATE DEHYDROGENASE 1 PRECURSOR (EC 1.4.1.3) (GDH).//5.90E-233//426aa// 98%//P00367 BRAWH20117950//LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (PROLINE-BETA-NAPHTHYLAM-IDASE).//1.80E-78//364aa//42%//Q29550 BRAWH20118230//BONE MORPHOGENETIC PROTEIN 7 PRECURSOR (BMP-7) (OSTEOGENIC PROTEIN 1) (OP-1).//7.60E-74//85aa//98%//P18075 BRAWH20121640//transporter protein; system N1 Na+ and H+-coupled glutamine transporter//1.00E-106// 450aa//61%//NP\_006832 BRAWH20122580 BRAWH20122770 BRAWH20125380//DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDPS).//6.40E-15//121aa//35%// Q57695. BRAWH20126190 BRAWH20126980 BRAWH20128270//BH3 INTERACTING DOMAIN DEATH AGONIST (BID).//2.70E-100//195aa//99%//P55957 BRAWH20132190//Homo sapiens putative N-acetyltransferase Camello 2 (CML2) mRNA, complete cds.//1. 80E-17//110aa//44%//AF185571 BRAWH20137480//actin binding LIM protein 1//2.80E-70//181aa//55%//NP\_006710 BRAWH20138660//Homo sapiens stonin 2 mRNA, complete cds.//1.50E-171//322aa//99%//AP255309 BRAWH20139410 BRAWH20142340 BRAWH20147290 BRAWH20149340//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP) (P140 RAS-GRF).//4.10E-129// 290aa//83%//P28818 BRAWH20155950 BRAWH20158530 BRAWH20160280 BRAWH20162690 BRAWH20164460//TAT-BINDING HOMOLOG 7.//1.60E-96//366aa//54%//P54816 BRAWH20166790 BRAWH20171030//Homo sapiens putative helicase RUVBL mRNA, complete cds.//2.80E-209//324aa//100%// AF218313 BRAWH20173050 BRAWH20182060 BRAWH20185060 BRCAN10001490//chromobox homolog 6//2.10E-40//82aa//100%//NP\_055107 BRCAN20003460//outer arm dynein intermediate chain 1//5.60E-57//159aa//49%//T02761 BRCAN20006200 BRCAN20006390 BRCAN20054490//Sus scrofa mRNA for 54 kDa vacuolar H(+)-ATPase subunit, beta isoform.//1.00E-117//229aa// 96%//AJ223758 BRCAN20060190 BRCAN20064010 BRCAN20071190//FAF1 PROTEIN (FAS-ASSOCIATED FACTOR 1).//4.00E-225//433aa//96%//P54731 BRCAN20091560//Xenopus laevis mRNA for Nfrl, complete cds.//1.20E-256//605aa//77%//D86491 BRCAN20103740//P2X PURINOCEPTOR 7 (ATP RECEPTOR) (P2X7) (PURINERGIC RECEPTOR) (P2Z RE-CEPTOR).//2. 20E-18//60aa//78%//Q99572 50 BRCAN20124080 BRCAN20126130 BRCAN20143700 BRCAN20147880 BRCAN20216690 BRCAN20224720//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO).//4.40E-132//254aa//100%// P50336 BRCAN20237240

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BRCAN20263400

	BRCAN20273100
	BRCAN20273340
	BRCAN20273550
5	BRCAN20273640//lymphocyte specific formin related protein//3.00E-80//350aa//56%//NP_062653 BRCAN20275130
-	BRCAN20279700//Homo sapiens copine I mRNA, complete cds.//2.10E-32//82aa//68%//U83246
	BRCAN20280210//H.sapiens HZF10 mRNA for zinc finger protein.//3.30E-54//219aa//49%//X78933
	BRCAN20280360//Homo sapiens phosphatidic acid phosphohydrolase type-2c mRNA, complete cds.//8.20E-22//
	213aa//28%//AF047760
10	BRCAN20280400
	BRCAN20283190//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.20E-131//235aa//
	99%//014646
	BRCAN20283380//Mus musculus mRNA for serine hydrolase protein, isoform 2 (serh1 gene).//6.50E-45//103aa//
	80%//AJ245737
15	BRCAN20284600
	BRCAN20285450
	BRCOC10000870
	BRCOC20001860//Homo sapiens endoplasmic reticulum alpha-mannosidase I mRNA, complete cds.//6.30E-
	154//282aa//99%//AF145732
20	BRCOC20004040//Rattus norvegicus sphingosine 1-phosphate receptor Edg-8 (Edg-8) mRNA, complete cds.//
	4.80E-108//265aa//81%//AP233649.
	BRCOC20004870 .
	BRCOC20006370//PUTATIVE SURFACE GLYCOPROTEIN C210RF1 PRECURSOR (C210RF3).//4.00E-67//
	144aa//88%//P53801
25	BRCOC20008160//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//4.20E-155//777aa//
	40%//AB029290
	BRCOC20008500//Human ras inhibitor mRNA, 3' end.//4.60E-229//428aa//100%//M37190
	BRCOC20020850
	BRCOC20021550//Rattus norvegicus mRNA for Nadrin, complete cds.//1.90E-56//247aa//55%//AB042827
30	BRCOC20023230
	BRCOC20026640
	BRCOC20027510//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//2.20E-18//178aa//
	34%//Q15404
	BRCOC20031000
35	BRCOC20031250//TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM).//7.10E-38//92aa//82%//P48500
	BRCOC20031870
	BRCOC20035130//14-3-3 PROTEIN EPSILON (MITOCHONDRIAL IMPORT STIMULATION FACTOR L SUBU-
	NIT) (PROTEIN KINASE C INHIBITOR PROTEIN-1) (KCIP-1) (14-3-3E).//1.00E-29//71aa//88%//P42655
	BRCOC20037320//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.00E-75//
40	937aa//26%//060100
	BRCOC20037400
	BRCOC20041750
	BRCOC20055420//GLYCYLPEPTIDE N-TETRADECANOYLTRANSFERASE 2 (EC 2. 3. 1. 97) (PEPTIDE N-
	MYRISTOYLTRANSFERASE 2) (MYRISTOYL-COA:PROTEIN N-MYRISTOYLTRANSFERASE 2) (NMT 2)./
<b>45</b>	7.90E-229//421aa//99%//060551
	BRCOC20059510//B. taurus myosin IB mRNA, complete CDS://1.40E-29//117aa//53%//Z22852
	BRCOC20074760//CDC4-LIKE PROTEIN (FRAGMENT).//4,50E-90//366aa//48%//P50851
	BRCOC20077690
	BRCOC20078640
50	BRCOC20090520
	BRCOC20091960//CDC42-binding protein kinase beta (DMPK-like) [Homo sapiens]//1.50E-71//140aa//100%/
	NP_006026
	BRCOC20093800 '
	BRCOC20099370//Homo sapiens SPG protein (SPG) mRNA, complete cds.//0//576aa//97%J/AF302154
<b>5</b> 5	BRCOC20101230///7.40E-32//227aa//35%//
	BRCOC20105100
	BRCOC20107300//Homo sapiens GTT1 mRNA, complete cds.//3.60E-44//90aa//98%//AF270647
	BRCOC20110100

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BRCOC20114180
        BRCOC20117690
        BRCOC20119960
        BRCOC20121720
        BRCOC20122290
        BRCOC20128130
        BRCOC20134480
        BRCOC20135730
        BRCOC20136750
        BRCOC20144000//DNA REPAIR PROTEIN RAD8.//5.50E-14//111aa//36%//P36607
        BRCOC20147480
        BRCOC20148330
        BRCOC20155970
        BRCOC20158240
        BRCOC20176520//Rattus norvegicus mRNA for type II brain 4.1, complete cds.//2.30E-127//269aa//79%//
15
        AB032827
        BRCOC20178270//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.90E-101//272aa//64%//
        P51522
        BRCOC20178560//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//9.50E-130//
20
        247aa//85%//P48059
        BRHIP10001290//Homo sapiens GalNAc-T9 mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltrans-
        ferase, complete cds.//1.10E-108//299aa//63%//AB040672
        BRHIP10001740
        BRHIP20000870
25
        BRHIP20001630
        BRHIP20003120//Homo sapiens reticulon gene family protein (RTN3) mRNA, complete cds.//2.20E-92//190aa//
        98%//AF059524
        BRHIP20005340//GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID
        DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR).//2.10E-157//407aa//77%//Q16666
        BRHIP20005530//UBIQUITIN-ACTIVATING ENZYME E1 1.//1.00E-59//318aa//41%//Q02053
30
        BRHIP20096170//Homo sapiens cellular repressor of E1A-stimulated genes CREG mRNA, complete cds.//9.70E-
        35//174aa//39%//AF084523
        BRHIP20096850//ALANINE AMINOTRANSFERASE (EC 2.6.1.2) (GLUTAMIC--PYRUVIC TRANSAMINASE)
        (GPT) (GLUTAMIC--ALANINE TRANSAMINASE).//1.60E-166//423aa//69%//P25409
        BRHIP20103090//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45
35
        SUBUNIT).//2.00E-12//82aa//47%//P40682
        BRHIP20104440
        BRHIP20105710
        BRHIP20106100//GAR2 PROTEIN.//1.50E-19//199aa//31%//P41891
40
        BRHIP20107440
        BRHIP20110800
        BRHIP20111200
        BRHIP20115080//DYNAMIN 2 (DYNAMIN UDNM).//4.80E-63//123aa//95%//P39054
        BRHIP20115760
45
        BRHIP20118380
        BRHIP20118910
        BRHIP20119330//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//6.80E-207//651aa//
        54%//Q05481
        BRHIP20121410
50
        BRHIP20123140
        BRHIP20129720
        BRHIP20132860//Homo sapiens rhophilin-like protein mRNA, complete cds.//5.40E-144//298aa//93%//AF268032
        BRHIP20137230//Homo sapiens mRNA for paralemin.//1.70E-37//352aa//35%/Y16278
55
        BRHIP20139720
        BRHIP20140630
        BRHIP20142850
        BRHIP20143730
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BRHIP20143860
        BRHIP20149540
        BRHIP20153560
        BRHIP20153600//Xenopus laevis RRM-containing protein SEB-4 mRNA, complete cds.//1.50E-72//148aa//93%//
        BRHIP20167880//Mus musculus left-right dynein (Lrd) mRNA, complete cds.//8.10E-22//119aa//54%//AF183144
        BRHIP20169680
        BRHIP20169900
        BRHIP20170100
10
        BRHIP20173150
        BRHIP20174040//CGMP-DEPENDENT 3', 5' -CYCLIC PHOSPHODIESTERASE (EC 3.1.4:17) (CYCLIC GMP
        STIMULATED PHOSPHODIESTERASE) (CGS-PDE).//0//857aa//99%//000408 BRHIP20175420//Mus musculus
        partial mRNA for stretch responsive protein 278 (sr278 gene).//6.60E-36//170aa//50%//AJ250191
        BRHIP20176420//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HNRNP C1 AND HNRNP
15
        C2).//9.30E-68//292aa//52%//P07910
        BRHIP20179200
        BRHIP20180140
        BRHIP20183690
        BRHIP20186120
20
        BRHIP20186500
        BRHIP20189980//FLAGELLAR WD-REPEAT PROTEIN PF20.//2.90E-41//210aa//46%//P93107
        BRHIP20190070
        BRHIP20191490//interferon, alpha-inducible protein 27//2.60E-36//92aa//95%//NP_005523
        BRHIP20191770
        BRHIP20191860//TRANSCRIPTION FACTOR 4 (IMMUNOGLOBULIN TRANSCRIPTION FACTOR 2) (ITF-2)
25
        (SL3-3 ENHANCER FACTOR 2) (SEF-2).//0//569aa//99%//P15884
        BRHIP20194940//Homo sapiens A-kinase anchoring protein 220 mRNA, complete cds.//1.30E-23//190aa//37%//
        AF176555
        BRHIP20195890//FORKHEAD BOX PROTEIN D2 (FORKHEAD-RELATED PROTEIN FKHL17) (FORKHEAD-
        RELATED TRANSCRIPTION FACTOR 9) (FREAC-9).//9.10E-07//104aa//31%//060548
30
        BRHIP20196410
        BRHIP20198190
        BRHIP20205090
        BRHIP20207430
35
        BRHIP20207990
        BRHIP20208270
        BRHIP20208420
         BRHIP20208590
         BRHIP20214950
         BRHIP20217620
40
         BRHIP20218580//Mus musculus betaPix-b mRNA, complete cds.//5.10E-100//196aa//94%//AF247654
         BRHIP20222280//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.70E-217//505aa//
         75%//Q03923
         BRHIP20227080
45
         BRHIP20230710
         BRHIP20232290
         BRHIP20233090
         BRHIP20234380
         BRHIP20238600//WD-REPEAT PROTEIN SAZD://3.30E-95//182aa//99%//Q12788
50
         BRHIP20238690
         BRHIP20238880
         BRHIP20240460
         BRHIP20243470//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PRO-
         TEIN) (35 KDA LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN).
55
         (LECTIN L-29).//1.10E-16//114aa//42%//P38486
         BRHIP20249110//hexokinase 1//0//912aa//71%//NP_000179
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BRHIP20252450//Mus musculus Syne-1B mRNA, partial cds.//1.40E-159//980aa//33%//AF281870

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BRHIP20253660//Rattus norvegicus mRNA for Proline Rich Synapse Associated Protein 1A (ProSAP1A gene).//
1.90E-120//239aa//92%//AJ249562
BRHIP20254480
BRHIP20277620
BRHIP20283030//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//1.40E-88//
881aa//29%J/P33450
BRHIP20284800
BRHIP20285830//TYPE III INTERMEDIATE FILAMENT.//8.20E-10//88aa//35%J/P23729
BRHIP20285930//Homo sapiens IL-1 receptor accessory protein mRNA, complete cds.//3.30E-08//104aa//32%//
AE029213
BRHIP30001110
BRHIP30004570//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//3.60E-32//281aa//31%//
BRHIP30004880//H.sapiens mRNA for titin protein (clone hh1-hh54).//9.60E-85//812aa//26%//X90568
BRSSN10000920
BRSSN20003120//METABOTROPIC GLUTAMATE RECEPTOR PRECURSOR.//7.00E-08//257aa//22%//P91685
BRSSN2C006340
BRSSN2C013420//histone deacetylase 6 [Homo sapiens] //0//811aa//99%//NP 006035
BRSSN2C014260//RIBONUCLE INHIBITOR //1.70E-10//195aa//29%//P29315
BRSSN2C015790//ORNITHINE DECARBOXYLASE (EC 4 1.1.17) (ODC).//9.00E-102//352aa//53%//P00860
BRSSN2C013690//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.30E-41//88aa//100%//AF155103
BRSSN2C021600//RING CANAL PROTEIN (KELCH PROTEIN).//3.60E-59//510aa//31%//Q04652
BRSSN2C038200//RAL GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR-LIKE 2 (RALGDS-LIKE FAC-
TOR) (RAS-ASSOCIATED PROTEIN RAB2L).//3.90E-18//458aai/25%//015211
BRSSN20038410
BRSSN2C039370//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HE
16).//2 50E-38//94aa//52%//P17097
BRSSN2C043040
BRSSN2C046570
BRSSN20046790//ZINC FINGER PROTEIN 135.//8.60E-81//231aa//60%//P52742
BRSSN2C066110//Homo sapiens mRNA for mucolipidin, short form (ML4 gene).//1.70E-26//121aa//49%//
AJ293659
BRSSN2C097020
BRSSN2C1011C0//GRG PROTEIN (ESP1 PROTEIN) (AMINO ENHANCER OF SPLIT) (AES-1/AES-2).//2.50E-
10//70aa//51°J/Q08117
BRSSN2C105870
BRSSN20105960
BRSSN20108300
BRSSN20117990
BRSSN2C120810//SERINE PROTEASE HEPSIN (EC 3.4.21.-) (TRANSMEMBRANE PROTEASE, SERINE 1).//
9.80E-144//254aa//100%//P05981
BRSSN2C121030
BRSSN2C137020
BRSSN20142940
BRSSN2C146100//ADENYLATE CYCLASE, OLFACTIVE TYPE (EC 4.6.1.1) (ADENYLATE CYCLASE TYPE III)
(ATP PYROPHOSPHATE-LYASE) (ADENYLYL
CYCLASE).//0//389aa//90%//P21932
BRSSN20151990
BRSSN20152380
BRSSN2C159070
BRSSN2C159820
BRSSN2C169050
BRSSN2C176820//Mus musculus p300 transcriptional cofactor JMY mRNA, complete cds.//8. 50E-297//640aa//
89% J/AF201390
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50 °

BRSSN20177570
BRSSN20187310//ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).//3.20E-
26//306aa//30%//P16157
BRSTN10000830
BRSTN20000580
BRSTN20002200
BRSTN20005360//TRANSLATION INITIATION FACTOR IF-2.//1.20E-07//205aa//26%//060841
BRTHA20000570
BRTHA20004740//HYPOTHETICAL 41.6 KDA PROTEIN IN IMP1-HLJ1 INTERGENIC REGION (RF1095).//
1.60E-16//310aa//27%//P28625
BRTHA20046290//NOVEL ANTIGEN 2 (NAG-2) (TSPAN-4).//7.30E-84//153aa//100%//014817
BRTHA20046390
BRTHA20046420
CD34C30001250
CD34C30003140
CD34C30004240//H. sapiens graf gene.//1.10E-140//270aa//100%/Y10388
CD34C30004940
COLON10001350//IG ALPHA-1 CHAIN C REGION.//1.70E-196//353aa//99%//P01376
COLON20043180
COLON20093370
CTONG10000100//GUFA PROTEIN.//2.10E-31//156aa//45%//Q06916
CTONG10000220//Mus musculus cerebellar postnatal development protein-1 (Cpd1) mRNA, partial cds.//1.80E-
101//220aa//90%//U89345
CTONG10000620
CTONG10000930
CTONG10000940//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4
INHIBITOR C) (P18-INK4C).//7.20E-13//131aa//35%//Q60772
CTONG10001650
CTONG10002770//PLECTIN.//12.00E-49//284aa//28%//P30427
CTONG20002180
CTONG20004690//CYTOCHROME B561 (CYTOCHROME B-561).//2.80E-50//101aa//100%//P49447
CTONG20009770//26S PROTEASOME REGULATORY SUBUNITS2 (P97) (TUMOR NECROSIS FACTOR TYPE
1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN).//0//908aa//99%//Q13200
CTONG20014280//Xenopus laevis fizzyl mRNA, complete cds.//2.00E-82//479aa//38%//AF034578
CTONG20027090
CTONG20028410
CTONG20038890
CTONG20049410
CTONG20050280//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//8.00E-149//490aa//55%//P16415
CTONG20052650//BYSTIN.//5.10E-60//120aa//99%//Q13895
CTONG20052900//FASCIN (ACTIN BUNDLING PROTEIN).//7.30E-257//437aa//98%//Q16658
CTONG20075860//Homo sapiens mRNA for SPIN protein.//3.90E-123//204aa//69%//Y14946
CTONG20076130//ZINC FINGER PROTEIN 185 (LIM-DOMAIN PROTEIN ZNF185) (P1-A).//1.10E-158//327aa/
89%//015231
CTONG20077790
CTONG20082690 CTONG20085950//ZINC FINGER PROTEIN 191.//5.80E-91//346aa//53%//014754
CTONG20085950//ZING FINGER FROTEIN 191//3.00E 51//04064/05/3/3/4/1/064317
CTONG20091320
CTONG20092570//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//1.00E-55//300aa/
49%//AF044201
CTONG20092580
CTONG20092680//Rattus norvegicus protein associating with small stress protein PASS1 (Pass1) mRNA, com
plete cds.//1.40E-11//98aa//40%//AF168362
CTONG20092700//Mus musculus transcriptional repressor RP58 (rp58) mRNA, complete cds.//6.60E-18//162aa
35%/AF140224
CTONG20093950//Mus musculus zfh-4 mRNA for zinc-finger homeodomain protein 4, complete cds.//0//473aa
90%// <b>A</b> B024499

CTONG20095270
CTONG20095290
CTONG20095340//PROBABLE CATION-TRANSPORTING ATPASE WO8D2.5 IN CHROMOSOME IV (EC
3.6.1).//3. 90E-134//500aa//37%//Q27533
CTONG20096430
CTONG20096750
CTONG20097660
CTONG20098440
CTONG20099380
CTONG20099550//TRICHOHYALIN.//4.20E-16//534aa//25%//Q07283
CTONG20099630
CTONG20100240//Mus musculus radial spokehead-L protein (RshI1) mRNA, complete cds. //1.60E-185//520aa//
63%//AF329192
CTONG20101480
CTONG20103480
CTONG20105080
CTONG20105660
CTONG20106230
CTONG20106520//THREONINE SYNTHASE (EC 4.2.99.2).//6.70E-77//347aa//40%//Q42598
CTONG20108210
CTONG20114290//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//1.30E-75//
937aa//27%//060100
CTONG20114740//Homo sapiens NY-REN-57 antigen mRNA, partial cds.//1.70E-37//72aa//100%//AF155114
CTONG20118150//HYPOTHETICAL 100.6 KDA TRP-ASP REPEATS CONTAINING PROTEIN C1672.07 IN
CHROMOSOME III.//2.10E-150//910aa//36%//014053
CTONG20118250//CARBONIC ANHYDRASE (EC:4.2.1.1) (CARBONATE DEHYDRATASE).//3.30E-88//257aa//
62%//Q92051
CTONG20119200//Homo sapiens NY-REN-57 antigen mRNA, partial cds.//1.00E-18//41aa//100%//AF155114
CTONG20120770
CTONG20121010//ZINC FINGER PROTEIN 29 (ZFP-29).//7.80E-131//380aa//58%//Q07230
CTONG20121580//KINESIN-LIKE PROTEIN KIF1A.//3.50E-148//395aa//59%//P33173
CTONG20124010
CTONG20124220//STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULA-
TORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1).//0//691aa//98%//P36956
CTONG20124470
CTONG20124730
CTONG20125540//PTB-ASSOCIATED SPLICING FACTOR (PSF).//6.90E-07//144aa//29%//P23246
CTONG20125640//60S ACIDIC RIBOSOMAL PROTEIN PO (L10E).//7.50E-137//306aa//89%//P05388
CTONG20126070
CTONG20127450//H.sapiens mRNA for Ndr protein kinase.//4.50E-11//37aa//89%//Z35102
CTONG20128430//Human non-lens beta gamma-crystallin like protein (AIM1) mRNA, partial cds. //8. 40E-127//
616aa//40%/iU83115
CTONG20128470
CTONG20129960//Mus musculus F-box protein FBX18 mRNA, partial cds.//0//905aa//92%//AF184275
CTONG20131490
CTONG20131560//NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK (DESMOYOKIN)
(FRAGMENTS) //0//632aa//99%//Q09666
CTONG20132220
CTONG20133390//ZINC FINGER PROTEIN 135.//1.00E-139//416aa//57%//P52742
CTONG20133480
CTONG20133520//ZINC FINGER PROTEIN 228.//1.50E-163//670aa//50%//Q9UJU3
CTONG20136300
CTONG20138030 ·
CTONG20139070
CTONG20139340
CTONG20139860//Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16 mRNA, complete cds.//
3.50E-17//162aa//36%//AF121775
CTONG20140320

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CTONG20140580//HepA-related protein//8.80E-61//345aa//42%//NP_054859
CTONG20141650
CTONG20143690
CTONG20146300
CTONG20146970
CTONG20147050
CTONG20149460//RING CANAL PROTEIN (KELCH PROTEIN).//1.20E-56//556aa//27%//Q04652
CTONG20149950
CTONG20150910
CTONG20153300//H.sapiens mRNA for tre oncogene (clone 210).//4.80E-214//259aa//78%//X63546
CTONG20153580//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//
4.80E-37/326aa//28%//AF186273
CTONG20155180
CTONG20155400
CTONG20156780//Rattus norvegicus PGC1 mRNA for PPAR gamma coactivator, complete cds.//1.80E-72//
176aa/46~JrAB025784
CTONG20158040//UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) (ANTIGEN X)
(AGX) (AGX-1) (SPERM-ASSOCIATED ANTIGEN 2).//4.90E-126//376aa//61%//Q16222
CTONG20158150
CTONG20158660//Rattus norvegicus mRNA for seven transmembrane receptor, complete cds.//5.90E-99//
632aa//361a/AB019120
CTONG20159530//GLYPICAN-1 PRECURSOR://3.40E-118//222aa//100%//P35052
CTONG20160560
CTONG20161850
CTONG20162170
CTONG20163550
CTONG20164990
CTONG20165050
CTONG20186320//RING CANAL PROTEIN (KELCH PROTEIN) //3.70E-19//290aa//26%//Q04652
CTONG20200310//mitotic control protein dis3 homolog //1.20E-113//655aa//36%//JE0110
CTONG20265130
CTONG20267700
CTONG20273610
D3OST1000*090
D3OST10002670
D3OST10002700
D3OST20006180//Drosophila melanogaster slingshot mRNA, complete cds.//9.20E-114//358aa//56%//AB036834
D3OST20006540
 D3OST20007340
 D3OST20013280//ARP2/3 COMPLEX 16 KDA SUBUNIT (P16-ARC).//1.10E-48//103aa//99%//015511
 D3OST20024170
 D3OST20024360//Homo sapiens neuroendocrine differentiation factor mRNA, complete cds.//4.70E-35//80aa//
 100% J/AF219226
 D3OS120024520
 D3OST20036070
 D3OST20037970
 D3OST20038560
 D3OST30002580
 D6OST20003580//H.sapiens mRNA for aminopeptidase P-like.//7.40E-70//103aa//99%//X95762
 D6OST20004450
 D6OST20005070
 D9OST20000310
 D9OST20002780
 D9OST20015470//Mus musculus MPS1 gene and mRNA, 3' end.//4.60E-147//329aa//79%//L20315
 D9OST20023970//CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KDA SYNOVIAL PROTEIN)
 (YKL-40) (CHITINASE-3 LIKE 1).//1.30E-17//44aa//90%//P36222
 D9OST20026730//Homo sapiens caspase recruitment domain protein 7 mRNA, complete cds.//2.40E-141//
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524aa//40%//AF298548
D9OST20031370//Homo sapiens mRNA for partial putative TCPTP-interacting protein (ptpip5 gene).//3.40E-39//
176aa//48%//AJ242719 D9OST20033970//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.50E-152//541aa//
52%//Q05481
D9OST20035800
D9OST20035800  D9OST20035940//BRAIN MITOCHONDRIAL CARRIER PROTEIN-1.//9.10E-93//216aa//80%//095258
D9OST20040180//OLFACTORY RECEPTOR-LIKE PROTEIN OLF4.//1.20E-106//301aa//64%//Q95157
DFNES10000030
DFNES10001850
DFNES20001530//ATAXIN 7 (SPINOCEREBELLAR ATAXIA TYPE 7 PROTEIN).//2.30E-25//98aa//57%//015265
DFNES20010910
DFNES20014040//TRICHOHYALIN. //1.70E-17//380aa//26%//P37709
DFNES20025880
DFNES20031920//Drosophila melanogaster mRNA for fucosyltransferase homologue (FucTB gene).//8.40E-18//
133aa//36%//AJ302046
DFNES20037420//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN
GST1-HS).//1.00E-274//499aa//99%//P15170
DFNES20055270
DFNES20071130//PHOSPHOTRIESTERASE RELATED PROTEIN (PARATHION HYDROLASE-RELATED PROTEIN) 14 405 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 14 405 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 15 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 15 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 15 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN) 16 1441/2003 - 1/2003 (PARATHION HYDROLASE-RELATED PROTEIN HYDROLASE-RELATED PROTEIN HYDROLASE (PARATHION HYDROLASE-RELATED PROTEIN HYDROLASE (PARATHION HYDROLASE-RELATED PROTEIN HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PARATHION HYDROLASE (PA
TEIN) //4.40E-141//233aa//86%//Q60866 DFNES20082800
FCBBF10000240
FCBBF10300380
FCBBF10000630//Homo sapiens huntingtin interacting protein HYPB mRNA, partial cds.//3.70E-16//36aa//100%//
AF049610
FCBBF10000770//Homo sapiens REC8 mRNA, partial cds.//6.10E-266//528aa//96%//AF132734
FCRRF1000:150//Homo sapiens protocadherin beta 14 (PCDH-beta14) mRNA, complete cds.//4.10E-308//
717-1A: 79" A/AF152493
FCBBP10001210//Homo sapiens mRNA for SHPS-1, complete cds.//6.90E-22//135aa//43%//D86043
FCBBF10001550
FCBBF10001710//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.90E-131//397aa//59%//
P51522
FCBBF1000*820//CITRATE LYASE BETA CHAIN (EC 4.1.3.6) (CITRASE) (CITRYL-COA LYASE SUBUNIT) (EC 4.1.3.34) //3 70E-32//294aa//27%//053078
FCBBF10302430
FCBBF10302700
FCBBF10302800
FCBBF10003220
FCBBF10003670//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCO-
SYLASE) (GUANINE INSERTION ENZYME).//2.60E-195//308aa//100%//P54578
FCBBF10303740
FCBBF10303760
FCBBF10003770//Homo sapiens mRNA for GRIP1 protein.//0//572aa//99%//AJ133439
FCBBF10304120
FCBBF10004370//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAG-
MENT) //3 30E-96//292aa//52%//Q06730 FCBBF10005060//CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP).//8.40E-51//260aa//41%//
P10123
FCBBF10005460//Mus musculus putative neuronal cell adhesion molecule (Punc) mRNA, complete cds.//9.20E-
275://484aa//94%//AF026465
FCBBF10005500
FCBBF10005740//MITOCHONDRIAL CARRIER PROTEIN YMC2 PRECURSOR.//1.10E-27//194aa//38%//
P38087
FCBBF20006780
FCBBF20014270//ACYL-COA-BINDING PROTEIN (ACBP) (DIAZEPAM BINDING INHIBITOR) (DBI) (EN-

DOZEPINE) (EP).//1.40E-34//85aa//81%//P45882

FCBBF20023700

FCBBF20032970

	FCBBF20035280
	FCBBF20042170//Homo sapiens NIBAN mRNA, complete cds.//1.90E-177//345aa//100%//AB050477
	FCBBF20042560
5	FCBBF20049300//NEUR OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL)
	(1B426B). //7.70E-64//187aa//63%//Q62609
	FCBBF20051220
	FCBBF20054280
	ECRRE20056370
0	FCBBF20059090//ZINC FINGER PROTEIN 44 (ZINC FINGER PROTEIN KOX7) (FRAGMENT).//2.00E-08//
•	96aa//34%//P15621
	FCBBF20064520//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HNRNP C1 AND HNRNP
	C2).//5.50E-70//293aa//53%//P07910
	FCBBF20067810//SP00B-ASSOCIATED GTP-BINDING PROTEIN.//1.30E-51//275aa//42%//P20964
15	FCBBF20068820//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.50E-74//216aa//62%//
15	
	P51522
	FCBBF20071860
	FCBBF20072650
	FCBBF20075560
20	FCBBF20076330
	FCBBF30001840 FCBBF30007680//Homo sapiens general transcription factor 2-I (GTF2I) mRNA, alternatively spliced product,
	FCBBF3000/6800/Homo sapiens general transcription factor 2-1 (GT12) in first, discinatively episce process
	complete cds.//4.80E-56//141aa//72%//AF038968
	FCBBF30008470 FCBBF30010810//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//7.10E-173//436aa//
25	
	70%//Q03923 FCBBF30012350//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II GAMMA CHAIN (CAM-
	FCBBF30012350//CALCIDM/CALMODULIN-DEPENDENT FROTEIN (MASSE 17) E 17 GAMMA CHAIN (EC 2.7.1.123) (CAMK-II, GAMMA SUBUNIT). //8. 80E-143//291aa//92%//P11730
	FCBBF30012810//Homo sapiens ubiquitin-specific processing protease mRNA, complete cds.//1.10E-123//
30	450aa//49%/iAF229438
	FCBBF30013770//Rattus norvegicus dnchc2 mRNA for cytoplasmic dynein heavy chain, complete cds.//0//806aa//
	93%//AB041881
	FCBBF30015940//Chlamydomonas reinhardtii dhc1 gene for 1-alpha dynein heavy chain.//4.90E-228//831aa//
	52%//AJ243806
35	FCBBF30016320
	FCBBF30016570
	FCBBF30018550//Homo sapiens putative zinc finger protein mRNA, complete cds.//9.40E-90//560aa//35%//
	AF251039
	FCBBF30019120
40	FCBBF30024750//SEMAPHORIN 4F PRECURSOR (SEMAPHORIN W) (SEMA W).//2.00E-73//129aa//100%//
	095754
	FCBBF30025560//NERVOUS-SYSTEM SPECIFIC OCTAMER-BINDING TRANSCRIPTION FACTOR N-OCT 3
	(BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 2) (BRN-2 PROTEIN) [CONTAINS: N-OCT 5A; N-OCT
	5B].//4.30E-171//203aa//100%//P20265
45	FCBBF30028180
	FCBBF30033050
	FCBBF30039020//GROWTH-ARREST-SPECIFIC PROTEIN 2.//1.80E-68//194aa//64%//043903
	FCBBF30049550//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).//0//1016aa//
	99%//Q01484
50 °	FCBBF30052180
	FCBBF30054440
	FCBBF30057290//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete
	cds.//8.90E-258//642aa//68%//AB021644
	FCBBF30062880
<i>55</i>	FCBBF30070770
	FCBBF30071520
	FCBBF30078290
	FCBBF30083620//PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX).//5.80E-146//344aa//77%//

P51805	
FCBBF30083820//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//1.50E-14	1//
142aa//38%//AF159567	
FCBBF30086440	
FCBBF30090690//Homo sapiens HT017 mRNA, complete cds://8.60E-541/311aa/138%//AF225421	
FCBBF30095260	
FCBBF30123470 .	
FCBBF30129630//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//9.50E-98//228aa//73%	.//
Q03923	
FCBBF30170590	
FCBBF30172550	
FCBBF30175310//ETHÁNOLAMINEPHOSPHOTRANSFERASE (EC 2.7.8.1) (ETHPT).//2.10E-38//401aa//28%	//
P22140	
FCBBF30178730	
FCBBF30189490	
FCBBF30190850//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE	1)
(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//6.10E-30	
275aa//31%//P16581	
FCBBF30195640//Homo sapiens ALR-like protein mRNA, complete cds.//9.10E-188//331aa//99%//AF264750	
FCBBF30199610	
FCBBF30215060	
FCBBF30225660	
FCBBF30233680	
FCBBF30238870//PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2).//0	)//
641aa//99%//Q99435	
FCBBF30240020	
FCBBF30240960//ZINC FINGER PROTEIN 136.//8.30E-131//338aa//65%//P52737	
FCBBF30242250	
FCBBF30243640//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1).//6.40E-53//102aa//100%	s//
P55345	
FCBBF30246230//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//7.10E-17	′//
141aa//40%//AF159567	
FCBBF30246630//H.sapiens mRNA for ZYG homologue.//4.80E-60//562aa//29%//X99802	
FCBBF30247930//Rattus norvegicus clone C42 CDK5 activator-binding protein mRNA, complete cds.//2.70E-73	3//
162aa//87%//AF177477	
FCBBF30250730//TRICHOHYALIN.//1.30E-10//240aa//27%//P22793	
FCBBF30251420	.,,
FCBBF30252520//Homo sapiens bicaudal-D (BICD) mRNA, alternatively spliced, partial cds.//2.50E-47//103aa	У/
98%//U90030	_
FCBBF30252800//NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1) (REDUCIN	
AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN)	N
CAP43).//1.30E-134//260aa//97%//Q92597	•-
FCBBF30252850//Mus musculus peripherial benzodiazepine receptor associated protein (Pap7) mRNA, comple	ŧе
cds.//2.90E-46//185aa//50%//AF022770	
FCBBF30262360	
FCBBF30262510	
FCBBF30266780	
FCBBF30266920	
FCBBF30278630	٦r
FCBBF30279030//Homo sapiens BNPI mRNA for brain-specific Na-dependent inorganic phosphate cotransported	; i ,
complete cds.//2.40E-120//222aa//100%//AB032436	
FCBBF30281880//regulator of G-protein signalling 7 [Homo sapiens].//2.00E-05//100aa//33%//NP_002915	
FCBBF30284720 FCBBF30285280 FCBBF3028520 FCBBF30285280 FCBBF30285280 FCBBF30285280 FCBBF30285280 FCBBF3028520 FCBBF30285280 FCBBF30285280 FCBBF30285280 FCBBF30285280 FCBBF30285280 FCBBF30285280 FCBBF3028520 FCBBF302800000 FCBBF30280 FCBBF30280000 FCBBF3028000000 FCBBF302800000 FCBBF30000000 FCBBF30000000 FCBBF30000000000000000000000000000000000	
FCBBF40001420 FCBBF40001730//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 (P20	5١
1 CODI 40001730//GUANNIVE NUCLEO FIDE-DINADING FITO FEIN DETA SODONITI-ENCE I NOTEIN 12.5 (120	٠,

FCBBF40005480

(RECEPTOR OF ACTIVATED PROTEIN KINASE C 1) (RACK1).//4.20E-120//265aa//84%//P25388

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FEBRA10001880//Homo sapiens serine/threonine kinase mRNA, complete cds.//4.60E-106//344aa//53%// AF005046 FEBRA10001900 FEBRA20002100//D-XYLOSE-PROTON SYMPORTER (D-XYLOSE TRANSPORTER).//2.00E-13//159aa//27%// 052733 FEBRA20003210 FEBRA20004620//RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) //1.50E-46//208aa/143%//P47736 FEBRA20007620//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPBC16H5.10C.//2.30E-126//692aa//39%//042945 FEBRA20009090 FEBRA20010120//CLEAVAGE STIMULATION FACTOR, 64 KDA SUBUNIT (CSTF 64 KDA SUBUNIT) (CF-1 64 KDA SUBUNIT).//1.10E-73//137aa//97%//P33240 FEBRA20017050 FEBRA20018280 FEBRA20018690//ZINC FINGER PROTEIN 44 (ZINC FINGER PROTEIN KOX7) (FRAGMENT).//2.00E-08// 96aa//34%//P15621 FEBRA20024100//Rattus norvegicus myosin heavy chain Myr 8 mRNA, complete cds.//0//863aa//78%//AF209114 FEBRA20025270 FEBRA20025520 FEBRA20026110//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-217//810aa// 481J/Q05481 FEBRA20026280 FEBRA20027810 FEBRA20029860 FEBRA20034680//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.60E-93//481aa//35%// P51523 FFRRA20037260 FFBRA20037500 FEBRA20040530//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.30E-115//335aa//54%// P51523 FEBRA20042190 FFBRA20052910 FFBRA20060610 FFBRA20072120 FEBRA20079310 FEBRA20080810//Rattus norvegicus mRNA for peptide/histidine transporter, complete cds.//1.30E-107//239aa// E7"J/AB000280 FEBRA20082010//ZINC FINGER PROTEIN 195.//0//482aa//99%//014628 FEBRA20082100 FEBRA20086620//NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL) (1B426B) //3.80E-165//453aa//65%//Q62609 FEBRA20088360//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KDA COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN AL-PHA C SUBUNIT).//5.60E-05//58aa//53%//P17427 FEBRA20090290 FEBRA20092890//Rattus norvegicus neural cell adhesion protein BIG-2 precursor (BIG-2) mRNA, complete cds.// 0//697aa//93%//U35371 FEBRA20093520 FEBRA20095140 FEBRA20095880 FEBRA20097310//Human Hsp27 ERE-TATA-binding protein (HET) mRNA, complete cds.//0//597aa//97%// U72355 FEBRA20098460 FEBRA20111460 FEBRA20113560//R.norvegicus mRNA for DRM protein.//5.10E-65//157aa//80%//Y10019 FFRRA20125070 FEBRA20130190//UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3//8.20E-65//345aa//42%//

NP_055071
FEBRA20132740//Homo sapiens mRNA for CDEP, complete cds.//3.70E-16//40aa//92%//AB008430
FEBRA20140100//RER1 PROTEIN.//3.20E-106//196aa//99%//015258
FEBRA20144170//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1) (S6KII-ALPHA 2) (P90-RSK 2)
(RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//1.30E-269//495aa//99%//Q15349
FEBRA20145780
FEBRA20161120
FEBRA20166540
FEBRA20167390//Mus musculus ST6GalNAc V mRNA for GD1 alpha synthase, complete cds.//9.40E-64//134aa/
91%//AB030836
FEBRA20171380//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946)
(FRAGMENT).//6.30E-127//415aa//48%//Q06730
FEBRA20174410//Mus musculus mRNA for nuclear protein ZAP, complete cds.//2.30E-193//543aa//69%/
AB033168
FEBRA20176800
FEBRA20184330//Rattus norvegicus glutamate receptor interacting protein 2 (GRIP2) mRNA, complete cds.//
8.10E-72//161aa//88%//AF072509
FEBRA20192420
FEBRA20195820//ZINC FINGER PROTEIN 132.//2.60E-47//134aa//63%//P52740
FEBRA20196370
FEBRA20196630//RNA helicase-related protein//0//317aa//100%//NP_031398
FEBRA20197110
FEBRA20204000
FEBRA20204060
FEBRA20211710
FEBRA20214970
FEBRA20215500//Mus musculus Nulpl (nulpl) mRNA, complete cds.//1.80E-38//146aa//64%//U94988
FEBRA20216360
FEBRA20222040
FEBRA20223220//Homo sapiens mRNA for fibulin-4.//9.20E-110//202aa//100%//AJ132819
FEBRA20225040//high-glucose-regulated protein 8//1.40E-110//514aa//51%//NP_057342
FEBRA20226010
FEBRA20229560
FEBRA20229630
FEBRA20232850
FEBRA20233770//NEURONAL PAS DOMAIN PROTEIN 2 (NEURONAL PAS2) (MEMBER OF PAS PROTEIN 4 (MOP4), //6.30E-62//164aa//81%//Q99743
FEBRA20235500//P3 PROTEIN.//5.20E-74//391aa//39%//P09131
FEBRA20237640//Rattus norvegicus neurabin mRNA, complete cds.//9.10E-29//172aa//46%//U72994
FEHRT20003250//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KI
NASE) (PI4K-ALPHA).//2.20E-146//269aa//100%//P42356
FELNG20002410
HCASM10000500//TOPOISOMERASE 1-RELATED PROTEIN TRF5.//3.70E-09//193aa//22%//P48561
HCHON10001760//histone deacetylase 5//1.00E-133//320aa//67%//NP_005465 HCHON20000380
HCHON20001560//TRANSCRIPTION FACTOR-LIKE PROTEIN MORF4.//7.20E-116//235aa//93%//Q9Y690
HCHON20002260
HCHON20003220//10-FORMYLTETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.6) (10-FTHFDH
(FBP-CI).//2.30E-302//731aa//72%//P28037
HCHON20003440//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//1.30E-64//155aa/
87%//AF084530
HCHON20007380//Homo sapiens mRNA for HELG protein.//3.90E-129//331aa//76%//AJ277291
HCHON20007510//rab6 GTPase activating protein (GAP and centrosome-associated)//0//765aa//62%/
NP_036329
HCHON20008150
HCHON20008180
HCHON20008320//ZINC FINGER PROTEIN 135.//2.20E-130//345aa//62%//P52742
HCHON20008980
HCHON20009350

	HCHON20009560//ZINC FINGER PROTEIN 74.//1.50E-22//113aa//46%//Q16587 HCHON20010990 HCHON20011160
	HCHON20011180
5 .	HCHON20015230//Homo sapiens nuclear pore-associated protein (NPAP60L) mRNA, complete cds.//1.40E-78// 158aa//97%//AF107840
	HCHON20015350//PUTATIVE RRNA METHYLTRANSFERASE SPB1 (EC 2.1.1).//1.90E-117//771aa//36%//
	P25582 HCHON20015980//Homo sapiens integrin alpha 11 subunit precursor (ITGA11) mRNA, complete cds.//1.00E-227//
o	419aa//99%//AF137378
	HCHON20016040//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IBP-3) (IGF-BINDING PROTEIN 3).//2.00E-21//45aa//97%//P17936
	HCHON20016650//Mus musculus seven-pass transmembrane receptor precursor (Celsr1) mRNA, complete cds.//6.20E-27//343aa//27%//AF031572
5	HCHON20022470 HCHON20035130//ZINC FINGER PROTEIN 22 (ZINC FINGER PROTEIN KOX15) (FRAGMENT).//1.10E-18//
	64aa//56%//P17026 HCHON20036420//Homo sapiens mRNA for PED phosphoprotein.//1.30E-64//130aa//100%//Y13736
20	HCHON20036760 HCHON20040020//TNF-INDUCIBLE PROTEIN CG12_1.//8.80E-40//302aa//36%//095236
	HCHON20043590
	HCHON20059870//Hypothetical protein.//4.20E-204//667aa//56%//AL163279 HCHON20064590//ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) .//5.00E-38//654aa//27%//P01023
	HCHON20067220 HCHON20067700//Homo sapiens gremlin mRNA, complete cds.//5.70E-76//106aa//99%//AF045800
?5	HCHON20068410//Drosophila melanogaster microtubule associated protein (asp) mRNA. complete cds.//8.10E-
	47//803aa//27%//U95171 HCHON20068710
	HCHON20074820
30	HCHON20076500
	HCHON20086720//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IBP-3) (IGF-BINDING PROTEIN 3).//4.10E-113//205aa//100%//P17936
	HCHON20097490//dedicator of cyto-kinesis 1//1.00E-154//860aa//37%//NP_001371
	HCHON20100740//LACTADHERIN PRECURSOR (MILK FAT GLOBULE-EGF FACTOR 8) (MFG-E8) (HMFG)
35	(BREAST EPITHELIAL ANTIGEN BA46) (MFGM) [CONTAINS: MEDIN].//1.60E-205//363aa//99%//Q08431 HEART20003060//BASIGIN PRECURSOR (LEUKOCYTE ACTIVATION ANTIGEN M6) (COLLAGENASE STIM- ULATORY FACTOR) (EXTRACELLULAR MATRIX METALLOPROTEINASE INDUCER) (EMMPRIN) (5F7)
	(CD147 ANTIGEN).//1.30E-132//248aa//100%//P35613
40	HEART20005410 HEART20017730//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).//2.40E-25//
	368aa//30%//Q01484
	HEART20021840 HEART20025980//Homo sapiens smoothelin large isoform L2 (SMTN) mRNA, complete cds.//9.00E-152//223aa//
	97%//AF064238
<b>4</b> 5	HEART20034320//ENDOGLUCANASE Z PRECURSOR (EC 3.2.1.4) (ENDO-1, 4-BETA-GLUCANASE) (THER-
	MOACTIVE CELLULASE) (AVICELASE I).//1.20E-64//480aa//32%//P23659
	HEART20037810
	HEART20049400
	HEART20049410//Homo sapiens cerberus-related protein (CER1) gene, complete cds.//1.10E-12//144aa//29%//
50	AF090189
	HEART200498C0 HEART20061950//Homo sapiens mRNA for myopodin.//1.30E-28//327aa//35%//AJ010482
	HEART20063340
55	HEART20067870
	HEART2007830
	HEART20074430
	HEART20077670//Mus musculus mRNA for E-MAP-115 protein.//1.70E-50//363aa//41%//Y15197

HEART20083640//Mus musculus Xin mRNA,	complete cds.//3.10E-63//272aa//58%//AP051945
HEART20089940	

HEART20090000//Rattus norvegicus PIPP mRNA for proline-rich inositol polyphosphate 5-phosphatase, complete cds.//0//639aa//91%//AB032551

HEART20095990

HHDPC10000650

HHDPC10000830//HYPOTHETICAL 24.9 KDA PROTEIN C16C10.7 IN CHROMOSOME III.//1.50E-23//56aa//60%//Q09463

HHDPC20001040

10 HHDPC20006920

HHDPC20014320//ADAM 12 PRECURSOR (EC 3.4.24.-) (A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 12) (MELTRIN ALPHA).//1.20E-14//139aa//38%//043184

HHDPC20030490//LIPOPOLYSACCHARIDE-INDUCED TUMOR NECROSIS FACTOR-ALPHA FACTOR (LPS-INDUCED TNF-ALPHA FACTOR) (P53-INDUCED PROTEIN 7).//1.90E-69//134aa//95%//Q99732

HHDPC20031130//Kruppel-type zinc finger (C2H2) [Homo sapiens]//3.30E-196//607aa//57%//NP\_005806 HHDPC20034390

HHDPC20034720//CHLORIDE INTRACELLULAR CHANNEL PROTEIN 4 (INTRACELLULAR CHLORIDE ION CHANNEL PROTEIN P64H1).//1.50E-121//213aa//99%//Q9Y696 HHDPC20057420//Mus musculus proline-rich protein (Bprp) mRNA, complete cds.//5.40E-45//143aa//69%//AF085348

20 HHDPC20057940

HHDPC20064600//SUPPRESSOR PROTEIN SRP40.//8.00E-05//175aa//24%//P32583

HHDPC20068620//lg kappa chain precursor V region (0-81VL) - human (fragment)//8.10E-06//132aa//31%// S22658

HHDPC20084140//Homo sapicns polyadenylate binding protein-interacting protein-1 (PAIP1) mRNA, complete cds.//8.10E-12//230aa//23%//AF013758

HHDPC20091140//Homo sapiens gremlin mRNA, complete cds.//2.20E-60//105aa//100%//AF045800 HHDPC20091780//coagulation factor V (proaccelerin, labile factor)//2.00E-26//170aa//40%//NP\_000121 HHDPC20092080//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IGF-BINDING PROTEIN 3).//3.30E-100//185aa//94%//P17936

30 HHDPC20095280

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HLUNG10000550

HLUNG20016330//Homo sapiens actin filament associated protein (AFAP) mRNA, complete cds.//6.70E-130// 531aa//49%//AF188700

HLUNG20016770

HLUNG20017120//PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2).//8.40E-11//82aa//40%//Q53915
HLUNG20023340//Mus musculus SLM-1 (S1m1) mRNA, complete cds.//8.80E-141//270aa//95%//AF098796
HLUNG20033780//Rho guanine nucleotide exchange factor 5//6.00E-60//440aa//38%//NP\_005426
HLUNG20084390

IMR3220002430//CHROMATIN ASSEMBLY FACTOR 1 P48 SUBUNIT (CAF-1 P48 SUBUNIT) (RETINOBLAST-OMA BINDING PROTEIN P48) (RETINOBLASTOMA-BINDING PROTEIN 4) (MSI1 PROTEIN HOMOLOG).//7.10E-09//303aa//24%//Q09028

KIDNE20002520//glutamyl tRNA synthetase homolog//9.90E-156//290aa//100%//T00743

KIDNE20003940//RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).//1.80E-151//582aa//51%//

KIDNE20006780

Q06496

KIDNE20007210//Xenopus laevis mRNA for RPA interacting protein alpha (ripalpha gene).//8.30E-17//104aa//47%//AJ243177

KIDNE20007770//CARCINOEMBRYONIC ANTIGEN CGM6 PRECURSOR (NONSPECIFIC CROSS-REACTING ANTIGEN NCA-95) (ANTIGEN CD67) (CD66B ANTIGEN).//1.20E-17//326aa//27%//P31997

KIDNE20008010//Homo sapiens mRNA for putative protein kinase (WNK1 gene).//2.50E-25//460aa//29%//AJ296290

KIDNE20009470

KIDNE20011170

KIDNE20011400

KIDNE20013730

KIDNE20017130//Oreochromis niloticus sex-determining protein DMO mRNA. complete cds.//5.10E-43//252aa//

	43%//AF203490
	KIDNE20018730
	KIDNE20018970
	KIDNE20020150//HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).//9.90E-251//458aa//98%//
5	P08107
	KIDNE20021680//SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE PRECURSOR (EC 1.1.1.35)
	(HCDH).//7.10E-141//273aa//98%//Q16836
	KIDNE20021910//Homo sapiens MRS1 mRNA, complete cds.//2.30E-30//339aa//27%//AF093239
	KIDNE20021980
10	KIDNE20022620//like-glycosyltransferase//8.50E-253//633aa//70%//NP_004728
	KIDNE20024830//Homo sapiens copine I mRNA, complete cds.//1.30E-46//134aa//47%//U83246
	KIDNE20027250//ZINC FINGER PROTEIN 41 (ZFP-41) (CTFIN92) (FRAGMENT).//3.80E-55//105aa//91%//
	Q02526
	KIDNE20027950//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.
15	16).//2.40E-40//82aa//100%//P17097 KIDNE20028390//GALACTOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.10).//16.00E-70//85aa//
	90%//P43424 KIDNE20028720//Mus musculus Ac39/physophilin mRNA, complete cds.//2.70E-130//345aa//68%//U21549
	KIDNE20028830
20	KIDNE20029800 KIDNE20067330
	KIDNE20079440
	KIDNE20096280
	KIDNE20096470
25	KIDNE20100070//Rattus norvegicus kidney-specific protein (KS) mRNA, complete cds. //1.20E-253//572aa//77%//
23	AF062389
	KIDNE20100840
	KIDNE20101270//GOLGIN-95 //3 40F-20//76aa//68%//Q08379
	KIDNE20101510//UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP).//0//
30	519aa//95%//P07911
	KIDNE20102650
	KIDNE20102710//Mus musculus mRNA for Shank3b protein (shank3 gene).//1.20E-81//203aa//71%//AJ245904
	KIDNE20104300
	MIDNEGO106740
35	KIDNE20106740 KIDNE20107390//Homo sapiens CHRAC17 (CHRAC17) mRNA, complete cds.//1.50E-40//105aa//86%//
	AF226077
	KIDNE20107500
	KIDNE20107620//Rattus norvegicus protein kinase WNK1 (WNK1) mRNA, complete cds.//8.70E-140//266aa//
	74%//AF227741
40	KIDNE20109730//Mus musculus orphan transporter isoform B9 (Xtrp2) mRNA, alternatively spliced, complete
	cds://8.70E-34//103aa//65%//AF075266
	KIDNE20109890//Rattus norvegicus TGF-beta resistance-associated protein (TRAG) mRNA, complete cds.//
	2.60E-141//774aa//37%//AF305813
	KIDNE20112000 KIDNE20115080//Homo sapiens mRNA for hNBL4, complete cds.//6.20E-115//226aa//96%//AB030240
45	KIDNE20118080/Horno sapiers in INVA for invocation for the Service Substitution of the
	KIDNE20120090 KIDNE20121880//Mus musculus claudin-19 mRNA, partial cds.//6.10E-97//193aa//95%//AF249889
	KIDNE20122910
50	KIDNE20124400//Homo sapiens mRNA for ALEX1, complete cds.//1.10E-18//167aa//28%//AB039670
50	KIDNE20125630
	KIDNE20126010
	WIDNESS COLORS
	KIDNE20126130 KIDNE20127100//Drosophila melanogaster Diablo (dbo) mRNA, complete cds.//1.10E-10//254aa//26%//
<b>5</b> 5	AF237711
	MIDNE 20127450
	KIDNE20127430 KIDNE20127750//Homo sapiens partial mRNA for transport-secretion protein 2.1 (ITS-2, 1 gene). //6. 50E-45//
	178aa//46%//AJ278475

	KIDNE20130450 KIDNE20131580//Homo sapiens mRNA for LAK-4p, complete cds.//1.80E-111//211aa//100%//AB002405
	KIDNE20132180 KIDNE20137340//HYPOTHETICAL 49.1 KDA PROTEIN C11D3.06 IN CHROMOSOME I.//5.80E-13//149aa//
5	30%//Q10085
	KIDNE20138010
	KIDNE20141190
	KIDNE20144890 KIDNE20148900
10	KIDNE20146500 KIDNE20163880
	KIDNE20180710
	KIDNE20181660
	KIDNE20182690//Homo sapiens mRNA for RERE, complete cds.//3.50E-222//401aa//99%//AB036737
	KIDNE20186780
15	KIDNE20190740//Rattus norvegicus SNIP-b mRNA, complete cds.//6.70E-20//51aa//92%//AF156982
	LIVER10001260
	LIVER10004790
	LIVER20002160//HEAT SHOCK COGNATE 71 KDA PROTEIN.//0//585aa//95%//P11142 LIVER20011130//Homo sapiens F-box protein FBL9 mRNA, partial cds.//5.50E-107//210aa//99%//AF176701
20	LIVER20011910
	LIVER20028420
	LIVER20035110
	LIVER20035680
	LIVER20038540
25	LIVER20045650
	LIVER20055200//Homo sapiens leucocyte immunoglobulin-like receptor-8 (LIR-8) mRNA. complete cds.//2.50E-
	43//132aa//71%//AF025534 LIVER20055440//Homo sapiens Rho GAP p190-A mRNA, complete cds.//2.90E-101//195aa//98%//AF159851
	LIVER20059810//UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE
30	4-EPIMERASE).//1.60E-15//39aa//100%//Q14376
	LIVER20062510
	LIVER20064100//Ciona intestinalis mRNA for myoplasmin-C1, complete cds.//2.90E-14//167aa//26%//D42167
	LIVER20064690//PLASMA SERINE PROTEASE INHIBITOR PRECURSOR (PCI) (PROTEIN C INHIBITOR)
25	(PLASMINOGEN ACTIVATOR INHIBITOR-3) (PAI3) //1.70E-146//319aa//89%//P05154
35	LIVER20075680  LIVER20080530//Drosophila melanogaster forked mRNA for large Forked protein, complete cds.//1.10E-11//
	198aa//32%//D21203
	LIVER20084730
	LIVER20085800
40	LIVER20087060//Mus musculus putative purine nucleotide binding protein mRNA, complete cds.//2.70E-233//
	619aa//70%//U44731
	LIVER20087510
	LIVER20091180  MAMGL10000830//Drosophila melanogaster L82B (L82) mRNA, complete cds.//3.00E-27//231aa//38%//
45	AF125385
	MESAN10001260//Drosophila melanogaster Crossveinless 2 (CV-2) mRNA, complete cds.//6.50E-104//628aa//
	35%//AF288223
	MESAN20004570//MEDIAN BODY PROTEIN.//3.00E-07//343aa//23%//Q08014
	MESAN20014500//Drosophila melanogaster Dispatched (dispatched) mRNA, complete cds.//1.60E-46//225aa//
50	37%//AF200691
	MESAN20025190//Mus musculus cell cycle checkpoint control protein Mrad9 gene, complete cds.//7.30E-19//
	43aa//97%//AF045662
	MESAN20027090 ** MESAN20029400
55	MESAN20031900//Homo sapiens mRNA for zinc-binding protein (Rbcc728 gene).//2.90E-161//724aa//43%//
	AJ272269
	MESAN20035290
	MESAN20036460

	MESAN20038510
	MESAN20089360
	MESAN20101140//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//2.30E-25//
e	52aa//98%//P48059
5	MESAN20103120//Homo sapiens sodium/calcium exchanger NCKX3 (SLC24A3) mRNA, complete cds.//4.10E-
	66//289aa//37%//AF169257
	MESAN20106640
	MESAN20115970
10	MESAN20121130 MESAN20125860//MELANOTRANSFERRIN PRECURSOR (MELANOMA-ASSOCIATED ANTIGEN P97).//
70	1.30E-40//81aa//100%//P08582
	MESAN20127350//myelin expression factor-3//2.80E-15//227aa//29%//JE0163
	MESAN20130220//Homo sapiens testis-specific chromodomain Y-like protein (CDYL) mRNA, alternatively proc-
	essed, complete cds.//2.10E-126//319aa//63%//AF081258
15	MESAN20132110
-	MESAN20136110//Ciona savignyi mRNA for PEM-3, complete cds.//1.90E-85//236aa//65%//AB001769
	MESAN20138450
	MESAN20139360
	MESAN20141920//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete
20	cds.//0//691aa//97%//U53445
	MESAN20152770 .
	MESAN20153910 .
	MESAN20154010//Homo sapiens mRNA for putative ribulose-5-phosphate-epimerase, partial cds.//9.10E-60//
	69aa//100%//AJ224326
25	MESAN20157080
	MESAN20161590
	MESAN20164090
	MESAN20171520//Homo sapiens TNF intracellular domain-interacting protein mRNA, complete cds. //9. 30E-30//
	198aa//40%//AF168676
30	MESAN20174170//REGULATOR OF G-PROTEIN SIGNALING 4 (RGS4) (RGP4).//1.80E-39//80aa//98%//
	P49798
	MESAN20182090
	MESAN20186700
	NESOP10001080
35	NOVAR10000150
	NOVAR10000910//COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).//6.00E-199//392aa//98%//
	P23508
	NOVAR10001020
40	NOVAR20000380 NOVAR20003520
40	NT2NE20003740
	NT2NE20010050
	NT2NE20010210
	NT2NE20010400//Homo sapiens GL013 mRNA, complete cds.//2.90E-51//223aa//60%//AF267859
45	NT2NE20010490//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.30E-194//464aa//
	72%//Q03923
	NT2NE20015240
	NT2NE20021620//Saccharomyces cerevisiae Vps9p (VPS9) ger. pmplete cds.//1.00E-13//250aa//24%//
	U20373
50	NT2NE20043780
	NT2NE20053580
	NT2NE20068130//CELL SURFACE GLYCOPROTEIN 1 PRECURSO JTER LAYER PROTEIN B) (S-LAYER
	PROTEIN 1).//2.50E-34//377aa//40%//Q06852
	NT2NE20072200
55	NT2NE20074250
	NT2NE20080170//HUNTINGTIN-ASSOCIATED PROTEIN-INTERACTING PROTEIN (DUO PROTEIN) (KALI-
	RIN) (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//6.60E-57//661aa//27%//P97924
	NT2NE20089610

	NT2NE20089970//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.60E-29//77aa//81%/
	Q05481
	NT2NE20108540
	NT2NE20110360
;	NT2NE20118960//DOLICHYL-DIPHOSPHOOLIGOSACCHARIDEPROTEIN GLYCOSYLTRANSFERASE 63
,	KDA SJBJNIT PRECURSOR (EC 2.4.1.119) (RIBOPHORIN II).//9.30E-274//562aa//94%//P04844
	NT2NE20122430//GLYOXYLATE-INDUCED PROTEIN.//7.70E-25//144aa//38%//P30147
	NT2NE20124480
	NT2NE20125050//Gallus gallus mRNA for avena, complete cds.//5.80E-199//468aa//84%//AB017437
0	NT2NE20130190
	NT2NE20131890
	NT2NE20132170//Rattus norvegicus lysosomal amino acid transporter 1 mRNA, complete cds.//3.70E-97//357aa/
	52°a//AF361239
	NT2NE20142210//SINGLE-MINDED HOMOLOG 2 (SIM TRANSCRIPTION FACTOR) (MSIM).//3.00E-24/
5	660aa//26°a/Q61079
	NT2NE20146810
	NT2NE20152750
	NT2NE20155110
o ·	NT2NE20156260
0	NT2NE20157470//COMPLEMENT C2 PRECURSOR (EC 3.4.21.43) (C3/C5 CONVERTASE).//6.60E-138/
	256aa/100^J/P06681
	NT2NE20158600//erythroid ankyrin - Synechocystis sp. (strain PCC 6803).//7.00E-13//160aa//31%//S74626
	NT2NE20159740
	NT2NE20172590
5	NT2NE20174800
	NT2NE20174920
	NT2NE20177520//Guinea pig mRNA for decay-accelerating factor (isoform GDab-SEC), complete cds.//1.70E
	15//?73aa//28*' <sub>~</sub> J/D49421
	NT2NE20181650//Shb=Src homology 2 protein//2.90E-36//115aa//43%//AAB29780
o	NT2NE20183760
	NT2NE20184900//Mus musculus mRNA for transcription factor CA150b, complete cds.//8.60E-29//98aa//55%/
	AB023485
	NT2NE20187390
	NT2RI20C01330//Homo sapiens KE03 protein mRNA, partial cds.//3.40E-103//339aa//57%//AF064604
5	NT2RI20003480//GLYPICAN-2 PRECURSOR (CEREBROGLYCAN) (HSPG M13).//1.80E-261//581aa//82%/
,	
	P51653
	NT2RI20C05750//Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds.//8.90E-139/
	272aa//95° J/AF084464
	NT2RI20C09870//lunatic fringe precursor [Mus musculus]//5.50E-123//237aa//91%//U94351
0	NT2RI20C22600
	NT2RI20C23160
	NT2RI20C23590
	NT2RI20C23910//Homo sapiens TMTSP mRNA for transmembrane molecule with thrombospondin module, com
	plete cds //0/ 480aa//96%//AB044385
5	NT2RI20C25400//Mouse mRNA for P24 protein. complete cds.//9.70E-94//196aa//91%//D83206
	NT2RI20C25640
	NT2RI20C28470
	NT2RI20C36670
	NT2RI20C40930//MITOCHONDRIAL CARRIER PROTEIN YMC2 PRECURSOR.//1.10E-27//194aa//38%/
o ·	P38087
•	NT2RI20040990//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).//2.40E-25/
	368aa//30°J/QC1484
	NT2RI20C41880//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A (CELLULAR MYOSIN HEAVY CHAIN, TYPE
	A) (NMMHC-A) :/8 10E-10//322aa//21%//P35579
5	NT2RI20C46080
	NT2RI20C48340//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2 SUBUNIT (ADENYLATE CYCLA
	SE-INHIB TING G ALPHA PROTEIN).//2.10E-171//316aa//100%//P04899
	NT2RI20C50960//Homo sapiens c53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//5.40E

. 25

164//496aa//61%//AF033120
NT2RI20054050//Drosophila melanogaster Abnormal X segregation (Axs) gene, complete cds.//2.40E-83//487aa//
37%//AF101361
NT2RI20055790
NT2RI20056700//NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL)
(1B426B).//3.40E-237//439aa//97%//Q62609
NT2RI20069730
NT2RI20076290
NT2RI20086220
NT2RI20091730
NT2RI20091940//CORNICHON-LIKE PROTEIN.//9.70E-73//159aa//81%//035089
NT2RI20198260
NT2RI20203900
NT2Ri20207030
NT2RI20216250
NT2RI20240080//SMALL GLUTAMINE-RICH TETRATRICOPEPTIDE REPEAT-CONTAINING PROTEIN.//
1.30E-86//311aa//58%//043765
NT2RI20244600//Homo sapiens mRNA for sphingosine-1-phosphatase (ORF1).//2.60E-50//273aa//36%//
AJ293294
NT2RI20244960
NT2RI20250750 .
NT2Ri20252550
NT2RI20273230//PUTATIVE HELICASE YGR271W.//1.10E-14//152aa//38%//P53327
NT2RP60000770//Homo sapiens mRNA for ZAC zinc finger protein.//5.80E-179//325aa//98%//AJ006354
NT2RP60000850//Bos taurus RPGR-interacting protein-1 (RPGRIP1) mRNA, complete cds.//2.10E-139//751aa//
38%//AF227258
NT2RP70010740
NT2RP70027380//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//7.40E-31//203aa//
36%//P15882
NT2RP70032610//ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEU-
RAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).//4.40E-180//387aa//88%//P06733
NT2RP70036880//Gtpase activating protein for Yptlp; Gyplp [Saccharomyce scerevisiae].//2.00E-66//250aa//
50%//NP_014713
NT2RP70037240//H.sapiens E-MAP-115 mRNA.//1.10E-79//475aa//41%//X73882
NT2RP70043480//ZINC FINGER PROTEIN 93 (ZINC FINGER PROTEIN HTF34) (FRAGMENT) //0//588aa//
91%//P35789
NT2RP70044280//CTD-BINDING SR-LIKE PROTEIN RA4 (FRAGMENT) //1.20E-11//190aa//31%//095104
NT2RP70045590//PUTATIVE ENDONUCLEASE C1F12. 06C (EC 3.1).//3.60E-34//246aa//36%//Q10348
NT2RP70056750
NT2RP70062230//NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NF-H).//
2.50E-29//622aa//29%//P19246 NT2RP70063950//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.90E-13//417aa//26%//P52734
NT2RP70072690
NT2RP70075240 NT2RP70077660
NT2RP70077660 NT2RP70078420//Drosophila melanogaster Centaurin Gamma 1A (ceng1A) mRNA, complete cds.//1.00E-120//
700aa//40%//AF254741
NT2RP70080850
NT2RP70081610//Mus musculus 101F6 protein mRNA, complete cds.//5.20E-52//214aa//50%//AF131206
NT2RP70085440
NT2RP70102350//Mus musculus mRNA for Olig3 bHLH protein, complete cds.//1.90E-134//257aa//98%//
AB038698
NT2RP70105210
NT2RP70110860
NT2RP70111320
NT2RP70122910
NT2RP70125160

X

NT2RP70130020
NT2RP70133740//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.//2.60E-136//267aa//94%//
015127
NT2RP70134990
NT2RP70137290
NT2RP70137640
NT2RP70143480
NT2RP70147210
NT2RP70150800
NT2RP70157890//zinc finger protein 267; zinc finger (C2H2) [Homo sapiens]//1.60E-125//228aa//99%//
NP 003405
NT2RP70159960//Rattus norvegicus p135 SynGAP mRNA, partial cds.//4.80E-60//177aa//69%//AF053938
NT2RP70169110
NT2RP70175670
NT2RP70179710
NT2RP70181970
NT2RP70188020
NT2RP70188710
NT2RP70190640
NT2RP70192730//LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC
3 1 1 13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE) (LIPASE A) (CHOLESTER-
YL ESTERASE).//3.00E-181//323aa//99%//P38571
NT2RP70194450
MT2RP70195430//PUTATIVE NADP-DEPENDENT OXIDOREDUCTASE IN TEHB-RHSE INTERGENIC REGION
(EC 1 · · · ) //1, 10E-57//349aa//38%//P76113
NT2RP70198350//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//2.60E-111//213aa//98%//P51858
NT2RP70203790
NTONG20009770//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITO-
CHONDRIAL CLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP).//1.30E-304//599aa//92%//
P42675
*:TONG20013620//Homo sapiens hydroxysteroid sulfotransferase SULT2B1b (HSST2) mRNA, complete cds.//
4.10E-82/:151aa//100%//U92315
NTONG20015870//KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4).//3.30E-132//489aa//
54" d/ P19013
NTONG20028070//CYR61 PROTEIN PRECURSOR (GIG1 PROTEIN) (INSULIN-LIKE GROWTH FACTOR-
BINDING PROTEIN 10).//1.60E-65//133aa//92%//000622
NTONG20029480//Mus musculus Xin mRNA, complete cds.//7.20E-93//409aa//54%//AF051945
NTONG20029700//Homo sapiens laminin alpha 3b chain mRNA, partial cds.//6.60E-230//425aa//92%//AF005258
NTONG20046140//Homo sapiens mRNA for MNK1, complete cds.//5.70E-89//177aa//98%//AB000409
NTONG20048060
NTONG20049910
NTONG20050620
NIONG20050860
NTONG20051530//KUPFFER CELL RECEPTOR.//6.30E-85//391aa//45%//P70194
NTONG20052650//Gallus gallus Xin mRNA, complete cds.//5.40E-146//768aa//40%//AF051944
NTONG20056570//CORONIN-LIKE PROTEIN P57.//2.20E-121//356aa//62%//Q92176
NTONG20061870
NTONG20063010//Mus musculus EF-9 mRNA, partial cds://1.70E-78//154aa//92%//U72678
NTONG20064400//REPETIN.//2.20E-107//446aa//50%//P97347
NTONG20064840//Mus musculus slpl mRNA for synaptotagmin-like protein 1, complete cds. //2.60E-128//258aa//
90°//AB050741
NTONG20065010
NTONG20066460//Mus musculus Gd mRNA for gasdermin, complete cds.//8.30E-207//446aa//88%//AB033595
NTONG20067090//Mus musculus mRNA for Sh3yl1, complete cds.//2.00E-63//136aa//91%//D85926
NTONG20067830//ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).//1.10E-
24//227aa//34%//P16157
NTONG20070200//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.30E-134//352aa//65%//
P51522

50 .

NTONG20070340//collagen alpha 1(IX) chain//1.50E-43//220aa//45%//S42617 NTONG20075220//Rattus norvegicus SNIP-a mRNA, complete cds://1.80E-121//436aa//41%//AF156981 NTONG20076930//ALPHA-1-INHIBITOR III PRECURSOR.//1.20E-124//513aa//47%//P14046
NTONG20077560
NTONG20083650
NTONG20088620//Homo sapiens genethonin 3 mRNA, partial cds.//4.90E-202//390aa//99%//AF177292
NTONG20090600//SYNAPSIN I (BRAIN PROTEIN 4.1).//2.10E-07//198aa//29%//P17600
NTONG20090680
NTONG20092290
NTONG20092330//BESTROPHIN (VITELLIFORM MACULAR DYSTROPHY PROTEIN) (TU15B).//1.40E-135//
414aa//59%//076090
OCBBF10000540//Mus musculus rjs (rjs) mRNA, complete cds.//4.00E-14//105aa//36%//AF061529
OCBBF10001750//Mus musculus mRNA for sprouty-4, complete cds.//1.50E-159//300aa//92%//AB019280
OCBBF10001850//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.90E-166//605aa//51%//
P51523
OCBBP20005230
OCBBF20006770//TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN).//2.50E-287//693aa//
84%//Q13428
OCBBF20013890
OCBBF20019380//seizure related gene 6//6.00E-170//336aa//90%//NP_067261
OCBBF20019830 .
OCBBF20020150
OCBBF20020830//Homo sapiens Pumilio 1 (PUMH1) mRNA, complete cds.//0//814aa//99%//AF315592
OCBBF20022900//Homo sapiens SCHIP-1 mRNA, complete cds.//2.80E-250//469aa//99%//AF145713
OCBBF20023570
OCBBF20026630
OCBBF20028050//Homo sapiens B2 gene partial cDNA, clone B2E.//7.70E-38//246aa//33%//AJ002220
OCBBF20028650//DOSAGE COMPENSATION REGULATOR (MALE-LESS PROTEIN) (NO ACTION POTEN-
TIAL PROTEIN).//1.40E-50//160aa//47%//P24785
OCBBF20029800
OCBBF20030280//Rattus norvegicus hfb2 mRNA, complete cds.//5.20E-63//175aa//68%//AF031483
OCBBF20030910//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11) (PSA).//2.90E-146//279aa//
98%//P55786
OCBBP20032460
OCBBF20035930//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA).//7.80E-135//264aa//96%//
P81126
OCBBF20037440//ZINC-FINGER PROTEIN HT2A (72 KDA TAT-INTERACTING PROTEIN).//2.10E-08//80aa//
40%//Q13049
OCBBF20039250//Homo sapiens breast cancer metastasis-suppressor 1 (BRMS1) mRNA, complete cds.//2.20E-
55//188aa//56%//AF159141
OCBBF20041680
OCBBF20045330
OCBBF20046120//zinc finger protein 16 (KOX 9)//1.00E-131//350aa//59%//NP_008889
OCBBF20046470//ARFAPTIN 1.//5.80E-114//229aa//97%//P53367
OCBBF20046690//PROBABLE CATION-TRANSPORTING ATPASE WO8D2.5 IN CHROMOSOME IV (EC
3.6.1). //4.20E-105//249aa//39%//Q27533
OCBBF20047570
OCBBF20048660
OCBBF20049300//ZINC FINGER PROTEIN 184 (FRAGMENT).//7.10E-141//566aa//45%//Q99676
OCBBF20049840//Homo sapiens mRNA for neurabin II protein.//4.90E-166//808aa//47%//AJ401189
OCBBF20050770//CARNITINE 0-PALMITOYLTRANSFERASE I, MITOCHONDRIAL LIVER ISOFORM (EC
2.3.1.21) (CPTI) (CPTI-L).//3.10E-211//653aa//56%//P32198
OCBBF20051610
OCBBF20053430//Mus musculus MAST205 protein kinase mRNA, complete cds.//0//498aa//94%//U02313
OCBBF20053490//MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNOSE ISOMERASE)
(PMI) (PHOSPHOHEXOMUTASE).//1.10E-24//52aa//100%//P34949
OCBBF20053730//85 KDA CALCIUM-INDEPENDENT PHOSPHOLIPASE A2 (EC 3.1.1.4) (IPLA2) (CAI- PLA2).//
0//636aa//91%//060733

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OCBBF20054200//DEVELOPMENTAL PROTEIN SEVEN IN ABSENTIA.//1.10E-27//97aa//54%//P21461
OCBBF20054760//SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RE-
CEPTOR INTERACTING PROTEIN).//4.00E-122//230aa//97%//Q13546
OCBBF20059560//Homo sapiens (clone D320) C219-reactive peptide mRNA, partial cds.//6.70E-39//140aa//
62%//L34688
OCBBF20060300
OCBBF20061720
OCBBF20062140
OCBBF20062410
OCBBF20063320
OCBBF20066390//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2),//8.90E-63//173aa//65%//
OCBBF20068490//Mus musculus RW1 protein mRNA, complete cds.//4.60E-40//310aa//37%//AF060565
OCBBF20071210//M-PHASE PHOSPHOPROTEIN 9 (FRAGMENT).//1.80E-96//184aa//100%//Q99550
OCBBF20071840//ZINC FINGER PROTEIN 135.//1.00E-139//416aa//57%//P52742
OCBBF20071960//Coturnix coturnix japonica gMEF2D gene.//6.50E-06//124aa//31%//AJ002238
OCBBF20072240//Homo sapiens candidate tumor suppressor protein DICE1 mRNA, complete cds. //7. 60E-165//
354aa//83%/iAF097645
OCBBF20072320
OCBBF20073540//Homo sapiens p30 DBC mRNA, complete cds.//4.00E-65//146aa//91%//AF293335
OCBBF20074140
OCBBF20076220
OCBBF20078920//Homo sapiens zinc-finger helicase (hZFH) mRNA, complete cds.//3.10E-67//152aa//92%//
U91543
OCBBF20079310
OCBBF20079460
OCBBF20080050//RTOA PROTEIN (RATIO-A).//3.50E-07//191aa//32%//P54681
OCBBF20080410//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//6.90E-145//445aa//51%//P28160
OCBBF20082830//NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1) (REDUCING
AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN
CAP43).//3.10E-190//282aa//99%//Q92597
OCBBF20084660
OCBBF20085200
OCBBF20086400//Mus musculus ADP-ribosylation factor-like membrane-associated protein (Arm1) mRNA, com-
plete cds.//2.10E-114//244aa//87%//AF205936
OCBBF20086910//Mus musculus mSox5L mRNA, complete cds.//9.30E-253//528aa//91%//AB006330
OCBBF20087010
OCBBF20088140
OCBBF20088220
OCBBF20091150
OCBBF20094240
OCBBF20097720
OCBBF20100400
OCBBF20103130
OCBBF20104040
OCBBF20105570
OCBBF20107090//Homo sapiens protocadherin 68 (PCH68) mRNA. complete cds.//2.60E-77//359aa//49%//
AF029343
OCBBF20107920
OCBBF20108190//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//2.90E-151//429aa//61%//P16415
OCBBF20108430//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2 SUBUNIT (ADENYLATE CY-
CLASE-INHIBITING G ALPHA PROTEIN).//2.10E-171//316aa//100%//P04899
OCBBF20108580//APICAL-LIKE PROTEIN (APXL PROTEIN).//1.00E-196//376aa//100%//Q13796
OCBBF20108630//ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 1 (ATP-BINDING CASSETTE TRANS-
PORTER 1) (ATP-BINDING CASSETTE 1).//1.00E-63//268aa//46%//P41233
OCBBF20109310
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OCBBF20111770

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OCBBF20116850//Mus musculus Islr(immunoglobulin superfamily containing leucine-rich repeat) mRNA, com-
plete cds.//2.10E-88//285aa//57%//AB024538
OCBBF20118970
OCBBF20120390//SODIUM-DEPENDENT PROLINE TRANSPORTER (FRAGMENT).//0//636aa//100%//Q99884
OCBBF20121390//RING CANAL PROTEIN (KELCH PROTEIN).//7.80E-28//220aa//31%//Q04652
OCBBF20122620
OCBBF20124360//Homo sapiens mRNA for Misshapen/NIK-related kinase MINK-1, complete cds.//2.70E-98//
185aa//100%//AB035698
OCBBF20125530//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//3.60E-110//281aa//77%//U06944
OCBBF20126780
OCBBF20127040//Drosophila melanogaster woc gene, exons 1-11 //1.10E-09//284aa//24%//AJ276394
OCBBF20127140//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1 (TRANS-
DUCIN BETA CHAIN 1).//5.50E-63//119aa//100%//P04901
OCBBF20127550
OCBBF20128120//Mus musculus mmDNAJA4 mRNA for mmDj4, complete cds.//1.20E-205//397aa//93%//
AB032401
OCBBF20129360//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC
3 1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) //1.00E-130//461aa//36%//P51178
OCBBF20130110
OCBBF20130910
OCBBF20132850//Homo sapiens brain tumor associated protein NAG14 (NAG14) mRNA, complete cds.//3.80E-
24//399aa//27%//AF196976
OCBBF20139260
OCBBF20140640
OCBBF2C140890
OCBBF2C145760//GLYPICAN-1 PRECURSOR.//3.40E-118//222aa//100%//P35052
OCBBF2C148280//Mus musculus mlt 1 gene, complete cds.//1.70E-151//502aa//63%//AB032418
OCBBF2C148730//RING CANAL PROTEIN (KELCH PROTEIN).//2.90E-43//509aa//26%//Q04652
 OCBBF2C149280//Mus musculus WAVE-1 mRNA, complete cds://4.30E-07//210aa//29%//AF290877
 OCBBF20151150
 OCBBF2C153340//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//0//
 701aa//93°J/AF076183
 OCBBF2C153350//G PROTEIN PATHWAY SUPPRESSOR 2 (GPS2 PROTEIN).//1.20E-49//103aa//99%//Q13227
 OCBBF2C155060//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//1.90E-67//
 3074a/37°4/P33450
 OCBBF2C164050
 OCBBF2C164670
 OCBBF2C170690
 OCBBF2C173060
 OCBBF2C173250
 OCBBF2C173980//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//3.70E-211//531aa//
 70% J/AF060219
 OCBBF2C1781501//Plasmodium falciparum ADA2-like protein gene, partial cds.//2.20E-19//322aa//27%//
 AF184590
 OCBBF2C178880//11-CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH).//3.90E-37//101aa//78%//
 O92781
 OCBBF20178990
 OCBBF20180120//Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, com-
 plete cds.i/1.50E-272//320aa//89%//AF154121
  OCBBF20180840
  OCBBF20186870
  OCBBF20188730
  OCBBF20189560
  PANCR10000910//ATP-binding cassette, sub-family A member 8//2.00E-17//230aa//30%//NP_009099
  PEBLM10000240
  PEBLM10000710//leptin receptor//2.10E-29//69aa//91%//U66496
  PEBLM20013120//Homo sapiens rhotekin mRNA, partial cds.//4.10E-25//164aa//36%//AF290512
  PEBLM20024320//zinc resistance protein homolog //3.80E-28//139aa//45%//T27544
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	PEBLM20024550
	PEBLM20040150
	PEBLM20042900
	PEBLM20044520//PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2 (EC 3.1.13.4) (PAB1P-DEPENDENT POLY(A)-NUCLEASE).//2. 40E-54//331aa//39%/P53010
	PEBLM20052820//PROTEIN PHOSPHATASE 2C HOMOLOG 3 (EC 3.1.3.16) (PP2C-3).//7.60E-09//96aa//36%/
	Q09173
	PEBLM20060310
	PEBLM20060360//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946)
0	(FRAGMENT).//5.10E-12//57aa//56%//Q06730
	PEBLM20060490//polymerase (RNA) III (DNA directed) (39kD) [Homo sapiens]//1.50E-72//143aa//100%//
	NP_006457
	PEBLM20071880
	PEBLM20072960
5	PEBLM20074370 .
	PEBLM20075980//Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds.//2.30E-69//
	285aa//52%/AF302046
	PEBLM20078320//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).i/2.00E-184//543aa//59%//
	P51523
0	PEBLM20085760//Homo sapiens mRNA for TOLLIP protein.//1.10E-106//153aa//98%//AJ242972
	PERIC10000250//DNA TOPOISOMERASE III BETA-1 (EC 5.99.1.2).//1.20E-138//271aa//94%//095985
	PERIC20002140
	PERIC20003860
	PERIC20003870//Mus musculus transcriptional activator alpha-NAC (Naca) gene, complete cds.//1.20E-152//
5	956aa//43%//U48363
	PERIC20004220
	PERIC20004780//Rattus norvegicus Jun dimerization protein 1 (jdp-1) gene, complete cds.//2.00E-15//73aa//
	49%//U53450
	PLACE50000660//PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1).//1.60E-12//200aa//27%//
0	Q63009
	PLACE60003480//Rattus norvegicus protein associating with small stress protein PASS1 (Pass1) mRNA, com-
	plete cds.//4.60E-119//255aa//82%//AF168362
	PLACE60004630
	PLACE60060420//60S RIBOSOMAL PROTEIN L44 (L36A).//1.70E-29//58aa//100%//P09896
5	PLACE60079250//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//0//979aa//61%//
	AB029290
	PLACE60086400
	PLACE60119750
	PLACE60121080
0	PLACE60136500
	PLACE60136720
	PLACE60138830
	PLACE60153220
_	PLACE60155130
5	PLACE60161600
	PLACE60169420
	PLACE60177140//PROSTACYCLIN RECEPTOR (PROSTANOID IP RECEPTOR) (PGI RECEPTOR).//9.90E-
	135//257aa//99%//P43119
	PLACE60181070
0 -	PLACE60187690
	PLACE60188340
	PROST10003220//HOMEOBOX PROTEIN HOX-A2.//5.00E-69//139aa//95%//043364
	PROST10004800 -
-	PROST20005050
5	PROST20005670
	PROST20021010
	PROST20024890
	PROST20029270

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PROST20047270
PROST20047390//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.70E-52//427aa//31%//
P51523
PROST20050670
PROST20052280
PROST20057930
PROST20059040
PROST20066880//Mus musculus zinc finger protein 276 C2H2 type (Zfp276) mRNA, complete cds. //9.80E-101//
192aa//94%//AF178935
PROST20079500
PROST20083600//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, com-
plete cds.//1.40E-101//243aa//83%//AF026954
PROST20087700
PROST20097950
PROST20100460//Homo sapiens secretory mucin MUC6 (MUC6) mRNA, partial cds.//3.10E-216//421aa//98%//
PROST20104000//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//1.40E-20//128aa//39%//
Q62203
PROST20107820//Human C3f mRNA, complete cds.//9.90E-140//252aa//100%//U72515
PROST20111050
PROST20112970
PROST20114390
PROST20116600
PROST20120050
PROST20120160
PROST20121900
 PROST20123530
 PROST20127400
 PROST20127800
 PROST20130530
 PROST20132600
 PROST20133270
 PROST20144220
 PROST20146010
 PROST20149160
 PROST20149250
 PROST20151240
 PROST20152460
 PROST20153320
 PROST20159240//Homo sapiens Opa-interacting protein OIP2 mRNA, partial cds.//1.10E-19//46aa//100%//
 PROST20161950//Mus musculus RalGDS-like protein 3 mRNA, complete cds.//8.30E-88//205aa//85%//
 AF237669
 PROST20164440
 PROST20166680
 PROST20168290
 PROST20169800//CYTOCHROME P450 4F2 (EC 1.14.13.30) (CYPIVF2) (LEUKOTRIENE-B4 OMEGA- HY-
 DROXYLASE) (LEUKOTRIENE-B4 20-MONOOXYGENASE) (CYTOCHROME P450- LTB-OMEGA).//6.30E-
  188//507aa//66%//P78329
  PROST20170980
  PROST20171280//hematopoietic zinc finger//2.00E-70//380aa//50%//NP_038894
  PROST20175290
  PROST20176170//Homo sapiens ENIGMA protein mRNA, complete cds.//2.60E-156//270aa//98%//AF265209
  PROST20185830//NITROGEN REGULATORY PROTEIN AREA.//5.50E-07//141aa//28%//013412
  PROST20189770//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-155//459aa//53%//
  P51523
  PROST20191640//Mus musculus UbcM4-interacting protein 4 mRNA, complete cds.//1.50E-91//279aa//57%//
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	AF360998
	PUAEN10000850
	PUAEN20003740
	PUAEN20011880//Mus musculus mRNA for MIWI (piwi), complete cds.//2.70E-190//670aa//51%//AB032604
5	PUAEN20015260//Rattus norvegicus inositol polyphosphate multikinase (Ipmk) mRNA, complete cds.//2.40E-
	111//246aa//85%//AY014898
	PUAEN20015860//Mus musculus PDZ-RGS3 protein mRNA, complete cds.//1.50E-205//469aa//82%//AF350047
	PUAEN20018820//C-ETS-2 PROTEIN.//7.90E-261//469aa//99%//P15036
	PUAEN20025680
0	PUAEN20027580
	PUAEN20030180//CARBONIC ANHYDRASE XII PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE XII)
	(CA-XII) (TUMOR ANTIGEN HOM-RCC-3.1.3).//7.60E-148//259aa//95%//043570
	PUAEN20040670//Mus musculus neuronal protein 4.1 mRNA, complete cds.//0//733aa//93%//AF061283
	PUAEN20044000
5	PUAEN20045110
	PUAEN20045250
	PUAEN20051100//Mus musculus otogelin mRNA, complete cds.//2.60E-89//368aa//43%//U96411
	PUAEN20052470
	PUAEN20055020//Homo sapiens goodpasture antigen-binding protein (COL4A3BP) mRNA, complete cds.//0//
0	624aa//100%//AF136450
•	PUAEN20078980//faciogenital dysplasia homolog//1.00E-19//200aa//39%//NP_032027
	PUAEN20081230
	PUAEN20083140//Homo sapiens SWAP-70 mRNA, complete cds.//2.70E-280//451aa//99%//AF210818
	PUAEN20085150
·5	PUAEN20108240//Drosophila melanogaster ankyrin 2 (Ank2) mRNA, complete cds.//5.00E-22//200aa35%//
_	AF190635
	RECTM10001410
	RECTM20003490
	RECTM20003490 RECTM20005100
10	
	SALGL10001710//Homo sapiens mRNA for C110RF25 gene.//1.80E-88//455aa//41%//AJ300461
	SKMUS20001980//Mus musculus N-RAP mRNA, complete cds.//1.40E-63//141aa//88%//U76618 SKMUS20003610//PUTATIVE MITOCHONDRIAL CARRIER PROTEIN PET8.//7.40E-59//274aa//47%//P38921
	SKMUS20007010//VESTIGIAL PROTEIN.//2.70E-14//209aa//32%//Q26366
) E	SKMUS20007800//PROSTAGLANDIN TRANSPORTER (PGT) (MATRIN F/G).//4.20E-47//274aa//36%//Q00910
35	SKMUS20011640
	SKMUS20012010
	SKMUS20016220//Mus musculus N-RAP mRNA, complete cds.//1.80E-85//352aa//47%//U76618
	SKMUS20018230//Homo sapiens MYPT2 mRNA, complete cds.//8.10E-13//107aa//40%//AB003062
	SKMUS20018500//Homo sapiens t(3;5)(q25.1:p34) fusion gene NPM-MLF1 mRNA, complete cds.//2.30E-131//
10	268aa//94%//L49054
	SKMUS20020840  SKMUS20021530/4 I conicae SBC restain (SBC) mBNA complete add //4 E0E 378//E0620//009/ //AE302154
	SKMUS20021530//Homo sapiens SPG protein (SPG) mRNA, complete cds.//1.50E-278//506aa//99%//AF302154 SKMUS20024750//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.90E-21//203aa//
15	33%//Q15404
13	SKMUS20028210 SKANUS20028400//Atua musaukus VIB1B (Visib) mBNA samplata ada //2 005 52//14/200//749/ //AE217188
	SKMUS20028400//Mus musculus YIP1B (Yiplb) mRNA, complete cds.//2.90E-53//142aa//74%//AF217188
	SKMUS20029200//Homo sapiens ASB-1 protein mRNA, complete cds://1.20E-45//302aa//39%//AF156777
	SKMUS20031680
50	SKMUS20046670
,,,	SKMUS20048970//ACTIN, ALPHA SKELETAL MUSCLE (ALPHA-ACTIN 1).//8.00E-181//263aa//99%//P02568
	SKMUS20049030//H.sapiens mRNA for nebulin.//3.50E-148//286aa//99%//X83957
	SKMUS20077400
	SKMUS20084740
	SKNMC20006220
55	SKNSH20008190//ZINC FINGER PROTEIN 133.//2.80E-165//503aa//56%//P52736
	SKNSH20020540
	SKNSH20028660
	SKNSH20031740

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SKNSH20034660
        SKNSH20051940
        SKNSH20062340
        SKNSH20063040//Homo sapiens tetraspan NET-4 mRNA, complete cds.//1.00E-20//177aa//41%//AF065389
        SKNSH20080430
        SKNSH20087770
        SKNSH20089400//Homo sapiens Rad51-interacting protein mRNA, complete cds.//2.20E-172//292aa//93%//
        AF006259
        SKNSH20091970
10
        SMINT20001760//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.40E-37//138aa//37%//P51522
        SMINT20005410
        SMINT20008240
        SMINT20009840//IG KAPPA CHAIN V-II REGION GM607 PRECURSOR (FRAGMENT).//9.00E-54//117aa//90%//
        P06309
15
        SMINT20011140
        SMINT20011580
        SMINT20011990
        SMINT20013480
        SMINT20014580
20
        SMINT20015590
        SMINT20022020
        SMINT20023280
        SMINT20024570//tektin A1//6. 90E-26//124aa//45%//M97188
        SMINT20026890//SMOOTHELIN.//3.10E-278//611aa//88%//P53814
25
        SMINT20028820//Homo sapiens mRNA for F5-2, complete cds.//2.40E-83//162aa//98%//AB020739
        SMINT20029760
        SMINT20033170
        SMINT20033400
        SMINT20035690
30
        SMINT20040860
        SMINT20042990
        SMINT20047810
         SMINT20049090//Homo sapiens mRNA for partial putative mitogen-activated protein kinase kinase kinase.//
         2.20E-32//69aa//98%//AJ242724
         SMINT20050750//SPARC PRECURSOR (SECRETED PROTEIN ACIDIC AND RICH IN CYSTEINE) (OS-
35
         TEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40).//4.20E-111//259aa//82%//P09486
         SMINT20051610//Mus musculus ES18 mRNA. complete cds.//6.90E-235//485aa//88%//AF083929
         SMINT20053300//Homo sapiens hepatocellular carcinoma-associated antigen 59 mRNA, complete cds.//7.00E-
         20//44aa//100%//AF218421
40
         SMINT20053870
         SMINT20056210
         SMINT20058000
         SMINT20060780
         SMINT20065960
45
         SMINT20068010
         SMINT20071400
         SMINT20073650//IG ALPHA-1 CHAIN C REGION.//7.90E-197//353aa//100%//P01876
         SMINT20076470
         SMINT20080540
50
         SMINT20089170
         SMINT20092330
         SMINT20092720
         SMINT20095050
         SMINT20098320
55
         SMINT20100680
         SMINT20101440//Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds.//
         1.70E-96//182aa//100%//U78556
         SMINT20102780//NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11) (NAPRTASE).//5.30E-05//
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	123aa//33%J/P18133
	SMINT20103690
	SMINT20105000
	SMINT201053000 SMINT20105330//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOS-
=	
,	IDASE) //1.00E-54//138aa//78%//P16278
	SMINT20106290//FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC 3.2.2.23) (FAPY-DNA GLYCOSYLA-
	SE) //7 OOE-07//214aa//32%//050606
	SMINT20106720//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//3.30E-235//477aa//89%//
	Y14737
0	SMINT20108530
	SMINT20109970
	SMINT20110330
	SMINT20110660//Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds.//
	1 20E-33//68aa//100%//AF177145
5	SMIN [20112730]/IG ALPHA-1 CHAIN C REGION.//1.70E-196//353aa//99%J/PO1876
	SMIN120115880//Kruppel associated box (KRAB) zinc finger 1 [Rattus norvegicus]//1.50E-42//211aa//45%//
	NP 062566
	SMINT20121220//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE
	B) (NMMHC-B).//1.00E-18//493aa//24%//P35580
o	SMINT20121950//HYPOTHETICAL 70.2 KDA PROTEIN C22E12.10C IN CHROMOSOME I.//5.70E-16//90aa//
U	
	45°-/-Q10361
	SMINT20122850
	SMINT20122910//Mus musculus StAR-related protein 1-4E mRNA, partial cds.//1.50E-77//170aa//82%//
_	AY007808
5	SMINT20127350//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KDA (U1 SNRNP 70 KDA) (SNRP70).//
	3 50E-14: 185aa//32%//P08621
	SMINT20127930//IG ALPHA-1 CHAIN C REGION.//7.90E-197//353aa//100%//P01876
	SMINT2013C320//Rattus norvegicus MHC class II transactivator type IV (CIITA) mRNA, complete cds.//2.50E-33//
	645aa//26°.√AF251307
0	SMINT20131810
	SMINT20132280
	SMINT20136130//IG LAMBDA CHAIN C REGIONS.//4.00E-51//105aa//95%//P01842
	SMINT20138900//DESMIN.//7.20E-203//425aa//94%//P17661
	SMINT20144430//IG LAMBDA CHAIN V-I REGION BL2 PRECURSOR.//3.80E-55//130aa//83%//P06316
5	SMINT20144800//Human zinc finger protein zfp6 (ZF6) mRNA. partial cds.//1.60E-139//354aa//70%//U71363
	SMINT20144890
	SMINT20152940//Mus musculus ATP-dependent zinc metalloprotease (Afg311) mRNA, complete cds; nuclear
	gene for mitochondrial product.//1.10E-52//75aa//84%//AF329695
	SMINT20153260//EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85).//
0	3 50E-274// <b>476aa//98%//</b> Q16610
	SMINT20153530
	SMINT2015454 CHANNEL PROTEIN P64.//1.10E-135//419aa//68%//P35526
	SMIN I 20155180//Homo sapiens GBAS (GBAS) mRNA. complete cds.//6.70E-115//142aa//97%//AF029786
	SMINT20157450
5	SMINT20158100
	SMINT20161220
	SMINT20162860
	SMINT20163960
	SMINT2016-1-100
0	SMINT20164770
	SMINT20168570//Homo sapiens mRNA for stabilin-1 (stab1 gene).//5.50E-61//128aa//98%//AJ275213
	SMINT20173190
	SMINT20173240
	SMINT20173240 SMINT20174360//RHYTHMICALLY EXPRESSED GENE 2 PROTEIN (DREG-2).//6.90E-24//242aa//28%//
5	094915
. <u>.</u>	SMINT20177360//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLIC-
	ING COMPONENT 35 KDA) (PR264 PROTEIN).//6.40E-37//82aa//92%//P30352
	SMINT20178550

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SMINT20179740//IG MU CHAIN C REGION.//8.50E-248//454aa//99%//P01871
SMINT20183530//GCN20 PROTEIN.//5.50E-118//410aa//52%//P43535
SMINT20190170//IG ALPHA-1 CHAIN C REGION.//8.50E-199//353aa//100%//P01876
SMINT20191420//AMP DEAMINASE 1 (EC 3.5.4.6) (MYOADENYLATE DEAMINASE) (AMP DEAMINASE SO-
FORM M).//5.40E-214//401aa//97%//P23109
SMINT20191530//PUTATIVE ATP-DEPENDENT RNA HELICASE DBP73D.//5.00E-85//547aa//42%//P26802
SMINT20192000
SPLEN10000830
SPLEN20000640
SPLEN20002220
SPLEN20003070
SPLEN20006070//ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).//1.50E-81//
788aa//30%//P16157
SPLEN20008390//Human placenta (Diff48) mRNA, complete cds.//4.60E-108//337aa//60%//U49187
SPLEN20008740//IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (SERINE-RICH RNA
POLYMERASE I SUPPRESSOR PROTEIN).//5.50E-12//490aa//22%//Q02821
SPLEN20008820
SPLEN20011410//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP)
(RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN)
(P50-RHOGAP).//1.50E-21//183aa//34%//Q07960
SPLEN20013540
SPLEN20016260
SPLEN20019450
SPLEN20020070
SPLEN20021660//GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR (EC 2.3.2.2) (GAMMA-GLUTAMYL-
TRANSFERASE) (GGT).//9.00E-23//167aa//33%//P07314
SPLEN20022230
SPLEN20023140
SPLEN20026950//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA).//0//766aa//
81%//P51531
SPLEN20027440//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).//6.10E-25//
368aa//30%//Q01484
SPLEN20029310
SPLEN20031600
SPLEN20032040
SPLEN20032190
SPLEN20033960
SPLEN20039240//HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).//9.80E-112//213aa//
100%//P08107
SPLEN20040600
SPLEN20054290//Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and
vasotocin genes, complete cds.//4.20E-180//448aa//71%//U90880
SPLEN20076530
SPLEN20077500//Mus musculus Niban mRNA, complete cds.//1.30E-39//351aa//31%//AB049355
SPLEN20079260//ZINC FINGER PROTEIN 132.//6.30E-117//320aa//61%//P52740
SPLEN20079510
SPLEN20084600//RING CANAL PROTEIN (KELCH PROTEIN).//5.20E-58//558aa//29%//Q04652
SPLEN20095410//ZINC FINGER PROTEIN 184 (FRAGMENT).//6.50E-83//236aa//58%//Q99676
SPLEN20095550
SPLEN20095810
SPLEN20097330
SPLEN20099700//TAT-BINDING HOMOLOG 7.//1.50E-142//553aa//48%//P54816
SPLEN20103950//40S RIBOSOMAL PROTEIN S17.//7.10E-22//49aa//100%//P06584
SPLEN20106250
SPLEN20117660//Homo sapiens BCL-6 corepressor (BCOR) mRNA, complete cds; alternatively spliced.//1.30E-
38//139aa//61%//AF317391
```

SPLEN20118300//Rattus norvegicus amino acid transport system A3 (Ata3) mRNA, complete cds.//1.70E-20//

210aa//28%//AF295535

	SPLEN20119810 SPLEN20121750//Danio rerio uridine kinase mRNA, complete cds.//1.60E-29//130aa//50%//AF195851
5	SPLEN20126190 SPLEN20128000//Xenopus laevis XMAB21 (Xmab-21) mRNA, complete cds.//6.80E-12//287aa//24%//AF040992 SPLEN20129610
	SPLEN20129810  SPLEN20140800//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-145//586aa//47%// P51523
	SPLEN20141360
0	SPLEN20141990
	SPLEN20142100//Rattus norvegicus alpha D integrin mRNA, complete cds.//7.10E-37//105aa//76%//AF021334 SPLEN20143180//Mus musculus EWS/FLI1 activated transcript 2 (EAT-2) mRNA, complete cds.//2.50E-45//132aa//65%//AF020263
5	SPLEN20144520 SPLEN20145720//Rattus norvegicus nuclear GTPase PIKE mRNA, complete cds.//2.00E-24//120aa//45%//
5	AF280816
	SPLEN20146450//H.sapiens mRNA for plakophilin 2a and b.//1.20E-08//87aa//42%//X97675 SPLEN20146690
	SPLEN20147110//cyclin-E binding protein 1//0//580aa//58%//NP_057407
0	SPLEN20147390//ZINC FINGER PROTEIN 136.//1.40E-105//417aa//49%//P52737
	SPLEN20149110
	SPLEN20149190 .
	SPLEN20149240//Cricetulus longicaudatus arginine N-methyltransferase p82 isoform mRNA, complete cds, alternatively spliced.//3.50E-259//525aa//86%//AF336043
5	SPLEN20150940//Mus musculus histone deacetylase mHDA1 mRNA, complete cds.//4.20E-187//550aa//51%//
	AF006602
	SPLEN20151210//protein tyrosine phosphatase, non-receptor type 13(APO-1/CD95 (Fas)-associated phos-
	phatase)//3.00E-25//250aa//29%//NP_006255
	SPLEN20152610
10	SPLEN20152760
	SPLEN20157300
	SPLEN20157880//Homo sapiens Ig superfamily receptor LNIR precursor, mRNA, complete cds.//1.70E-05//
	137aa//29%/iAF160477
	SPLEN20158900
15	SPLEN20158990
	SPLEN20160450//Homo sapiens mRNA for Hrs, complete cds.//5.60E-28//59aa//100%J/D84064
	SPLEN20160690
	SPLEN20160980
	SPLEN20162680//NUCLEAR PROTEIN SNF7.//4.20E-11//189aa//25%//P39929
10	SPLEN20163560
	SPLEN20165310//Homo sapiens mRNA for immunoglobulin lambda heavy chain. //4.90E-230//477aa//88%//Y14737
	SPLEN20166270
	SPLEN20167200//Mus musculus MPS1 gene and mRNA, 3'end.//1.50E-15//46aa//84%//L20315
15	SPLEN20169220
	SPLEN20169720
	SPLEN20170310//Homo sapiens Asef mRNA for APC-stimulated guanine nucleotide exchange factor, complete
	cds.//8.40E-95//305aa//62%//AB042199
50 ·	SPLEN20171210
, o	SPLEN20171470
	SPLEN20171890
	SPLEN20172120 SPLEN20173510//Xenopus laevis putative N-terminal acetyltransferase mRNA, complete cds.//3.90E-210//
55	413aa//66%//AF247679
,,,	SPLEN20174260
	SPLEN20176200 SPLEN20179180//Homo sapiens EH domain containing 2 (EHD2) mRNA, complete cds.//1.10E-181//340aa//
	94%//AF181263
	0 <del>7</del> /0///N 101200

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SPLEN20179810//Mus musculus pecanex 1 mRNA, complete cds.//3.80E-131//534aa//51%//AF096286 SPLEN20181810//Mus musculus faciogenital dysplasia protein 2 (Fgd2) mRNA, complete cds.//6.60E-68//144aa// 86%//AF017368 SPLEN20186430//PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.//2.20E-163//226aa//96%//P35414 SPLEN20193110 SPLEN20194050//Homo sapiens HOTTL protein mRNA, complete cds.//9.50E-135//264aa//93%//AF078842 SPLEN20198110 SPLEN20204170 SPLEN20211220 SPLEN20211570 SPLEN20211940 SPLEN20212730//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-TRAL PROTEINASE) (CANP) (M-TYPE).//1.70E-137//265aa//98%//P17655 SPLEN20212950 SPLEN20213830 SPLEN20214400 SPLEN20214580//Mus musculus mdg1-1 mRNA. complete cds.//1.40E-16//39aa//94%//AF190624 SPLEN20222270//Mus musculus adaptor protein (Dokl) mRNA. complete cds.//1.10E-42//123aa//61%//AF179242 SPLEN20225220 SPLEN20242320 SPLEN20242730 SPLEN20243830//TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII-135) (TAFII135) (TAFII 130) (TAFII130).//4.70E-38//98aa//87%//000268 SPLEN20245300// ADP-ribosylation factor binding protein GGA1//3.00E-39//120aa//76%//NP\_037497 SPLEN20249560 SPLEN20250170//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//1.40E-51//488aa//27%//P52734 SPLEN20250390//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-TRAL PROTFINASE) (CANP) (MU-TYPE). //3 00E-55//115aa//94%//P07384 SPLEN20252190//ZINC FINGER PROTEIN 135.//6.00E-89//303aa/i52%//P52742 SPLEN2026:440 SPLEN20264110 SPLEN20267650//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.20E-90//410aa//45%//Q99676 SPLEN20273950 SPLEN20279950 SPLEN20280660 SPLEN20283650//Mus musculus ras activator RasGRP (Rasgrp) mRNA, complete cds.//9.80E-54//182aa//57%// SPLEN20284240//Homo sapiens hOBDPF mRNA for osteoblast differentiation promoting factor, complete cds.// 9.80E-93//177aa//98%//AB048363 SPLEN20292950//ATP-binding cassette, sub-family A member 8 //3.30E-211//469aa//64%//NP\_009099 SPLEN20293800 SPLEN20303970 SPLEN20304950//Homo sapiens CAGH32 mRNA. partial cds.//9.60E-44//86aa//98%//U80743 SPLEN20305620//DIHYDROOROTATE DEHYDROGENASE PRECURSOR (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) (FRAGMENT).//3.60E-59//124aa//96%//Q02127 SPLEN20329240 STOMA20001830//IG ALPHA-1 CHAIN C REGION.//2.10E-196//353aa//99%//P01876 STOMA20005390//IG ALPHA-1 CHAIN C REGION.//7.90E-197//353aa//100%//P01876 STOMA20005670//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//1.90E-216//478aa//83%// Y14737 STOMA20006400//Homo sapiens IGHG3 gene for immunoglobulin heavy chain gamma 3 constant region, 4-exon hince isolate Lib-A2.//8.40E-214//377aa//100%//AJ390247 STOMA20005780 STOMA20005860//Homo sapiens TOB3 mRNA, complete cds.//1.80E-74//159aa//97%//AF343078 STOMA20008880//MYOCILIN PRECURSOR (TRABECULAR MESHWORK-INDUCED GLUCOCORTICOID RE-SPONSE PROTEIN) //1 00E-196//405aa//91%//Q99972 STOMA20010250//Homo sapiens RNA-binding protein (RBMS3) mRNA, complete cds.//7.70E-46//116aa//86%//

	AF023259
	STOMA20013890
	STOMA20026880
	STOMA20032890//ZINC FINGER PROTEIN CKR1.//5.80E-30//162aa//38%//P30373
:	STOMA20034770//IG ALPHA-1 CHAIN C REGION.//4.40E-196//353aa//99%//P01876
	STOMA20036460
	STOMA20046680//FOSB PROTEIN (G0/G1 SWITCH REGULATORY PROTEIN 3).//4.10E-14//36aa//100%//
	·
	P53539
	STOMA20048520
9	STOMA20048840
	STOMA20051200
	STOMA20056640//lg lambda chain V region //6.80E-54//150aa//73%//S23626
	STOMA20056670//IG ALPHA-1 CHAIN C REGION.//7.90E-197//353aa//100%//P01876
	STOMA20057820
5	STOMA20062130//IG KAPPA CHAIN V-III REGION HAH PRECURSOR.//3.10E-53//129aa//80%//P18135
	STOMA20062290
	STOMA20063250/TRANSCRIPTION FACTOR COE3 (EARLY B-CELL FACTOR 3) (EBF-3) (OLF-1/EBF-LIKE
	2) (OE-2) (O/E-2).//7.50E-50//105aa//93%//008791
	STOMA20063980
c	STOMA20064470//PLACENTAL RIBONUCLEASE INHIBITOR (RIBONUCLEASE/ANGIOGENIN INHIBITOR)
	(RAI) (RI) //3.60E-14//262aa//30%//P13489
	STOMA20067800 .
	STOMA20069040
	STOMA20072690
4	STOMA20076800
	STOMA20077450//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//2.70E-228//430aa//97%//P22314
	STOMA20080500//ATP-binding cassette, sub-family A, member 7, isoform a//1.00E-297//538aa//94%//
	<del>-</del>
	NP 061985
	STOMA20083610//IG ALPHA-1 CHAIN C REGION.//7.90E-197//353aa//100%//P01876
C	STOMA20085140
	STOMA20088380//IG ALPHA-1 CHAIN C REGION.//2.10E-196//352aa//100%//P01876
	STOMA20092530//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//3.10E-239//477aa//91%//
	Y14737
	STOMA20092560
•	STOMA20092890
	SYNOV20001520//Homo sapiens kappa 1 immunoglobulin light chain mRNA, complete cds.//5.50E-107//236aa//
	66" A AF 113887
	SYNOV20001730//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
	rity-determining regions mRNA, complete cds.//2.60E-226//479aa//86%//M87789
e	SYNOV20002510//Homo sapiens IGHG3 gene for immunoglobulin heavy chain gamma 3 constant region, 4-exon
	tinge solite Kp-25_//6.60E-214//377aa//100%//AJ390254
	SYNOV20002790//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
	r ty-determining regions mRNA, complete cds.//1.30E-238//476aa//91%//M87789
	SYNOV20002970//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
•	r ty-determining regions mRNA, complete cds.//7.00E-226//476aa//86%//M87789
	SYNOV20003970
	SYNOV20004260//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//1.10E-225//477aa//86%//
	Y14737
	SYNOV20007000//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
0 -	rity-determining regions mRNA, complete cds.//4.00E-239//478aa//91%//M87789
	SYNOV20008240//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
	rity-determining regions mRNA, complete cds.//4.10E-237//479aa//90%//M87789
	SYNOV20009230//IG ALPHA-1 CHAIN C REGION.//7.90E-197//353aa//100%//P01876
	SYNOV20010880//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
5	rity-determining regions mRNA, complete cds.//1.60E-233//476aa//89%//M87789
	SYNOV20011110//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
	rity-determining regions mRNA, complete cds.//6.90E-235//476aa//89%//M87789
	Hty-determining regions minima, complete cus.i/o.aoc-233//4/oza//oa///initio//oa
	SYNOV20013000//lg gamma =immunoglobulin heavy chain [rats, humanized lympholytic MoAb CAMPATH-1H,

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mRNA, 1465 nt].//7.70E-220//472aa//86%//S79307 SYNOV20013560//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//1.40E-234//477aa//89%// Y14737 SYNOV20013900//Homo sapiens mRNA for immunoglobulin kappa heavy chain.//3.50E-231//476aa//89%// Y14735 SYNOV20017080 SYNOV30001840 TBAES20000590 TBAES20002550//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMI-NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//2.10E-310//586aa//89%//009175 TBAES20003150//CYTOCHROME P450 4A1 (EC 1.14.15.3) (CYPIVA1) (LAURIC ACID OMEGA- HYDROXYLA-SE) (P450-LA-OMEGA 1) (P452).//1.40E-82//323aa//44%//P08516 TBAES20003770//SPERM-SPECIFIC ANTIGEN 2 (CLEAVAGE SIGNAL-1 PROTEIN) (CS-1).//1.90E-122// 249aa//97%//P28290 TCOLN20001390 TESOP20000900 TESOP20003120 TESOP20004000//CATHEPSIN B PRECURSOR (EC 3.4.22.1) (CATHEPSIN B1) (APP SECRETASE).//3.30E-111//194aa//98%//P07858 TESOP20005270//MONOAMINE-SULFATING PHENOL SULFOTRANSFERASE (EC 2.8.2.1) (SULFOTRANS-FERASE, MONOAMINE-PREFERRING) (M-PST) (THERMOLABILE PHENOL SULFOTRANSFERASE) (TL-PST) (PLACENTAL ESTROGEN SULFOTRANSFERASE) (CATECHOLAMINE-SULFATING PHENOL SUL-FOTRANSFERASE) (HAST3).//3.40E-47//92aa//100%//P50224 TESOP20005690//Mus musculus p53 apoptosis-associated target (Perp) mRNA, complete cds.//2.30E-53// 113aa//91%//AF249870 TESTI10000940 TESTI20001000//FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC 3.2.2.23) (FAPY-DNA GLYCOSYLA-SE) //7. 80E-06//238aa//28%//P74290 TESTI20001170 TESTI20001720 TESTI20002720//TUBULIN--TYROSINE LIGASE (EC 6.3.2.25) (TTL).//1.70E-18//237aa//29%//P38584 TESTI20002780//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLA-SE).//1.90E-11//140aa//36%//P08678 TESTI20004890 TESTI20011200 TESTI20017950 TESTI20018230 TESTI20023510 TESTI20029930 TESTI20030310 TESTI20030890 TESTI20031270//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-TEIN).//7.30E-52//146aa//71%//Q13829 TESTI20031810 TESTI20035960//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.70E-67//329aa/i/40%//Q00808 TESTI20036380//DRA PROTEIN (DOWN-REGULATED IN ADENOMA).//6.40E-46//243aa//35%//P40879 TESTI20037560 TESTI20038270 TESTI20039400//EBNA-1 NUCLEAR PROTEIN.//3.60E-43//298aa//43%//P03211 TESTI20041690/TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN) (KRIP-1).//1.00E-12//341aa//21%//Q62318 TESTI20044230//Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds.//1.70E-94// 291aa//64%//AF042180 TESTI20044310//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.70E-06//118aa// 32%//Q15404 TESTI20046750 TESTI20057750 TESTI20060400//Columba livia mRNA for 5'-nucleotidase.//3.80E-115//328aa//66%//AJ131243

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TESTI20155900

TESTI20061110//Xenopus laevis katanin p60 mRNA, partial cds.//1.80E-170//489aa//66%//AF177942 TESTI20063830//Drosophila melanogaster nuclear fallout (nuf) mRNA, nuf-1 allele, complete cds.//2.10E-34// 371aa//29%//AF045015 TESTI20066670//probable acyl-CoA dehydrogenase //1.90E-72//222aa//60%//D75616 TESTI20066770 TESTI20067200//PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-3 (HOMEOBOX PROTEIN PBX3).// 4.20E-132//352aa//71%//P40426 TESTI20076850 TESTi20082330//helicase II homolog//4.10E-44//775aa//25%//T13889 TESTI20083200//Homo sapiens mitogen-activated protein kinase phosphatase x (MKPX) mRNA, complete cds.// 1.00E-41//131aa//58%//AF165519 TESTI20083940 TESTI20086210 TESTI20087620 TESTI20088220//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.50E-175//633aa// 48%//Q05481 TESTI20094020 TESTI20094120 TESTI20094230//Strongylocentrotus purpuratus tektin A1 mRNA, complete cds//4.50E-64//252aa//50%//M97188 TESTI20094470//ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2).//1.40E-183//318aa//99%// TESTI20098350 TESTI20098530 TESTI20102800 TESTI20105720 TESTI20108720//PROTEIN PHOSPHATASE 2C BETA ISOFORM (EC 3.1.3.16) (PP2C-BETA) (IA) (PROTEIN PHOSPHATASE 1B).//3.30E-49//249aa//46%//P36993 TESTI20110280 TESTI20112940 TESTI20114070 TESTI20116650 TESTI20116830//Homo sapiens liprin-beta2 mRNA, partial cds.//8.20E-17//50aa//92%//AF034803 TESTI20121550//NUCLEOPORIN-LIKE PROTEIN RIP (REV INTERACTING PROTEIN) (REV/REX ACTIVATION DOMAIN-BINDING PROTEIN).//1.60E-152//363aa//85%//P52594 TESTI20122310 TESTI20123080 TESTI20123560 TESTI20127760 TESTI20128350 TESTI20129150 TESTI20129220 TESTI20130010//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.10E-63//173aa//65%//P51523 TESTI20130120 TESTI20135660 TESTI20136100//ZINC/CADMIUM RESISTANCE PROTEIN.//3.70E-12//101aa//35%//P20107 TESTI20136710 TESTI20136990 TESTI20137370 TESTI20137670 TESTI20143240 TESTI20143390//Mus musculus testicular condensing enzyme (AMAC1) mRNA, complete cds.//1.60E-51// 123aa//79%//AF016712 TESTI20143620 TESTI20148000//PROTEIN DISULFIDE ISOMERASE (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (RETINA COGNIN) (R-COGNIN).//2.80E-75//493aa//34%//P09102 TESTI20152460//ML02 PROTEIN.//9.60E-42//170aa//40%//Q09329

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TESTI20156100//KRUPPEL-LIKE FACTOR 4 (EPITHELIAL ZINC-FINGER PROTEIN EZF).//2.30E-32//254aa//
32%//043474
TESTI20157100
TESTI20157520
TESTI20159140
TESTI20161970
TESTI20164100
TESTI20168480//H.sapiens mRNA for titin protein (clone hh1-hh54).//6.30E-48//393aa//31%/X90568
TESTI20168630
TESTI20168960
TESTI20169960
TESTI20170350
TESTI20171020
TESTI20178160
TESTI20179320
TESTI20183370
TESTI20184620//0XYSTEROL-BINDING PROTEIN.//6.20E-27//181aa//28%//P16258
TESTI20185650//Xenopus laevis ubiquitin-like fusion protein mRNA, complete cds.//2.90E-129//543aa//46%//
L08474
TESTI20185810
TESTI20189410//Mus musculus axotrophin mRNA, complete cds.//7.50E-43//142aa//57%//AF155739
TEST120192280
TESTI20192800//Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16 mRNA, complete cds.//
2 40E 23//164aa//41%//AF121775
TESTI20193360
TESTI20194300
TESTI20194810
TESTI20197940
TESTI20199170
TESTI20199750//TRICHOHYALIN.//8.80E-59//547aa//30%//P37709
TESTI20200260
TESTI20200710//Mus musculus epithelial protein lost in neoplasm-a (Eplin) mRNA, complete cds.//4.40E-40//
212an/42°J/AF307844
TEST120202650
TESTI20203440
 TESTI20204450//M.musculus of DNA encoding DNA-binding protein.//1.90E-58//477aa//32%//Z54200
 TESTI20208400//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NU-
 CLEOLAR PROTEIN P120).//1.70E-16//181aa//33%//P46087
 TESTI20208710
 TESTI20209460
 TESTI20209810
 TESTI20209990
 TESTI20211160
 TES1/20211220
 TESTI20211240
 TESTI20213150
 TESTI20213580
 TESTI20214250//MITOCHONDRIAL CARRIER PROTEIN PMT.//1.10E-34//242aa//36%//P32332
 TESTI20215990//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//1.10E-
 39//375aa//28%//AF186273
 TESTI20216370//LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ES-MALE) (ESTERASE-31).//
 1.50E-60//164aa//68%//Q63880
 TESTI20220100
 TESTI20220650
 TESTI20224620
 TESTI20226230//Rattus norvegicus KPL2 (Kpl2) mRNA, complete cds.//8.90E-111//371aa//59%//AF102129
 TESTI20226490
 TESTI20229600//Drosophila melanogaster SP2353 mRNA, complete cds://8.30E-117//607aa//33%//AF239610
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	TESTI20230250
	TESTI20230850//CIRCADIAN LOCOMOTER OUTPUT CYCLES KAPUT PROTEIN (MCLOCK).//1.00E-23//186aa//30%//008785
	TESTI20231920
5	TESTI20231940//Human OB binding protein-2 (OB-BP2) mRNA, complete cds.//4.60E-14//140aa//36%//U71383 TESTI20232140//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC
	3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//2.50E-90//388aa//47%// P10895
	TESTI20234140
0	TESTI20234270
	TESTI20234360//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA-INTERACTING 1 (EC 5.2.1.8).//5.90E-66//128aa//98%//Q13526
	TESTI20237520//poly(A)-specific ribonuclease (deadenylation nuclease)//1.10E-34//311aa//26%/NP_002573
_	TESTI20238000
5	TESTI20238610//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)
	(DAM10).//6.80E-69//268aa//51%//P43366
	TEST120239470
	TESTI20239510//ubiquitin specific protease 6//5.60E-43//182aa//50%//NP_004496
0	TESTI20240090 TESTI20241530
U	
	TESTI20241920 TESTI20242830
	TESTI20242990
	TEST120244190//Homo sapiens IGHG3 gene for immunoglobulin heavy chain gamma 3 constant region, 4-exon
5	hinge, isolate Lib-A2.//8.40E-214//377aa//100%//AJ390247
,	TEST120244760
	TESTI20249990//ATAXIN 7 (SPINOCEREBELLAR ATAXIA TYPE 7 PROTEIN).//7.30E-49//388aa//37%//015265
	TEST120254220
	TESTI20254540//Homo sapiens hepatocellular carcinoma-associated antigen 59 mRNA, complete cds.//1.60E-
0	100//197aa//98%//AF218421
	TESTI20254860//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.//1.20E-35//564aa//28%//P70211
	TESTI20255820
	TESTI20258460//Homo sapiens OSBP-related protein 4 mRNA, complete cds.//8.20E-196//369aa//99%//
	AF323731
15	TESTI20262330
	TESTI20262910
	TESTI20265250
	TESTI20265370
	TESTI20265970
0	TESTI20266740//Homo sapiens topoisomerase-related function protein (TRF4-1) mRNA, partial cds.//2.70E-105/
	278aa//71%//AF089896
	TESTI20269570
	TESTI20271850
	TESTI20272060
15	TESTI20272390
	TESTI20272960//Mus musculus gene for odorant receptor MOR83, complete cds.//3.30E-84//306aa//50%/
	AB030894
	TESTI20275030
	TEST 20275620
50	TEST 20277360
	TESTI20278200
	TESTI20278400//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//2.50E-11//604aa//21%//P25386
	TESTI20280980 TESTI20280540
: =	TESTI20282540
55	TEST/20284880
	TESTI20285830
	TESTI20288110 TESTI20288910//Mus musculus endophilin II mRNA, complete cds.//2.10E-110//225aa//92%//U58885
	TEG 11202009 (OMMIDS HIDSOURGS CHOOPHINIT II THE NAM, COMPRETE COS.II.2. TOC. 110/122000102/07000000

	TEST120289850
	TESTI20291310
	TESTI20291620
	TESTI20291960//RHOMBOID PROTEIN (VEINLET PROTEIN).//2.00E-40//230aa//38%//P20350
5	TEST120294700
,	TEST120297850
	TESTI20301360 TESTI20303220//Rattus norvegicus neural cell adhesion protein BIG-2 precursor (BIG-2) mRNA, complete cds.//
	0//807aa//94%//U35371
10	TESTI20303360
	TESTI20303420
	TESTI20305540//M.musculus mRNA for IB3/5-polypeptide.//1.30E-183//684aa//56%//X79131
	TEST120305560
	TEST120307540
15	TEST120307700
	TESTI20308600
	TESTI20309170//Mucor circinelloides crgA gene for carotenoid regulatory protein.//3.10E-41//198aa//40%//
	AJ250998
	TESTI20310070
20	TESTI20311290
	TESTI20314180//TRYPSIN I-P1 PRECURSOR (EC 3.4.21.4) //2.10E-25//86aa//40%//Q90627
	TESTI20316870//Homo sapiens mRNA for cartilage-associated protein (CASP).//4.90E-106//199aa//99%//
	AJ006470
	TEST 20317600
25	TESTI20318090//ZINC FINGER PROTEIN 135.//2.00E-56//208aa//50%//P52742
	TESTI20319190
	TESTI20320440//THIOREDOXIN.//4.30E-32//103aa//63%//P50413 TESTI20320670//Rattus norvegicus mRNA for type A/B hnRNP protein p40.//2.20E-170//337aa//91%//AJ238854
	TESTI20320670//RATUS norvegicus minia for type A/S fiffally protein p40.7/2.202-1707/33744731767/3230034 TESTI20326810//RAN-SPECIFIC GTPASE-ACTIVATING PROTEIN (RAN BINDING PROTEIN 1) (RANBP1).//
30	2.00E-33//66aa//100%//P34022
	TESTI20327680
	TESTI20327740
	TESTI20328280
0.5	TESTI20330310 TESTI20332420//Mus musculus cell cycle checkpoint control protein Mrad9 gene, complete cds.//5.80E-20//
35	,
	246aa//28%/iAP045662
	TESTI20333000
	TESTI20333950 TESTI20334410//Sus scrofa RNA helicase (RHIV-1) mRNA, complete cds.//4.40E-58//281aa//33%//AF181119
10	TESTI20334410//Sus scrota ANA hericase (HTMV-1) mittA, complete cos.//4.402 06//2014410/Sus scrota ANA hericase (HTMV-1) mittA, complete cos.//4.600 06//2014410/Sus scrota ANA hericase (HTMV-1) mittA, complete cos.//4.600 06//2014410/Sus scrota ANA hericase (HTMV-1) mittA, complete cos.//4.600 06//2014410/Sus scrota ANA hericase (HTMV-1) mittA, complete cos.//4.600 06//2014410/Sus scrota ANA hericase (HTMV-1) mittA, complete cos.//4.600 06//2014410/Sus scrota ANA hericase (HTMV-1) mittA, complete cos.//4.600 06//2014410/Sus scrota ANA hericase (HTMV-1) mittA, complete cos.//4.600 06//2014410/Sus scrota ANA hericase (HTMV-1) mittA, complete cos.//4.600 06//2014410/Sus scrota ANA hericase (HTMV-1) mittA, complete cos.//4.600 06//2014410/Sus scrota ANA hericase (HTMV-1) mittA, complete cos.//4.600 06//2014410/Sus scrota ANA hericase (HTMV-1) mittA, complete cos.//4.600 06//2014410/Sus and complete cos.//4.600 06//2014410/Sus and complete cos.//4.600 06//2014410/Sus and complete cos.//4.600 06//201410/Sus and complete cos.//4.600 06//201410/Sus and complete cos.//4.600 06//201410/Sus
40	99%//AF170724
	TESTI20335200//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//
	8.10E-20//87aa//50%//P13688
	TESTI20336410
45	TESTI20337100
73	TESTI20347400
	TESTI20343070
	TESTI20343570//TRIPEPTIDYL-PEPTIDASE II (EC 3.4.14.10) (TPP II) (TRIPEPTIDYL AMINOPEPTIDASE).//
	2.00E-75//201aa//75%//P29144
50	TESTI20345060
	TESTI20347180//Mus musculus membrane protein TMS-2 mRNA, complete cds.//6.00E-35//186aa//41%//
	AF181685
	TESTI20347300
	TESTI20347740
55	TESTI20347770
	TESTI20351830
	TESTI20352620//PROACTIVATOR POLYPEPTIDE PRECURSOR [CONTAINS: SAPOSIN A (PROTEIN A); SA-
	POSIN B (SPHINGOLIPID ACTIVATOR PROTEIN 1) (SAP-1) (DISPERSIN) (SULFATIDE/GM1 ACTIVATOR); SA-

POSIN C (CO-BETA-GLUCOSIDASE) (A1 ACTIVATOR) (GLUCOSYLCERAMIDASE ACTIVATOR) (SPHINGOL-IPID ACTIVATOR PROTEIN 2) (SAP-2); SAPOSIN D (PROTEIN C) (COMPONENT C)].//1.30E-52//240aa//44%// P07602 TESTI20355020//Drosophila sp. His (hls) mRNA, complete cds.//9.80E-30//416aa//28%//S79915 TESTI20357750 TESTI20357930 TESTI20357960 TESTI20358980//Volvox carteri mRNA for hydroxyproline-rich glycoprotein (HRGP gene).//2.90E-37//155aa// 50%//AJ242540 TFSTI20361140 TESTI20366910//Homo sapiens mRNA for thioredoxin reductase II beta, complete cds.//2.00E-233//442aa//93%// AB019695 TESTI20367360 TESTI20368330//M-PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48).//2.10E-258//473aa//99%//P30307 TESTI20369130 TESTI20369220 TESTI20369650//Homo sapiens mRNA for HsGAK, complete cds.//2.40E-269//493aa//99%//D88435 TESTI20369690 TESTI20370020 TESTI20370550 TESTI20370810//Homo sapiens mRNA for LAK-4p, complete cds.//1.10E-74//385aa//38%//AB002405 TESTI20371030//TIP ELONGATION ABERRANT PROTEIN 1 (CELL POLARITY PROTEIN TEA1).//7.80E-23// 243aa//29%J/P87061 TESTI20371060 TESTI20373820 TESTI20375340//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//4.80E-68//273aa//45%// P10895 TESTI20377230 TESTI20378190//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.30E-114//323aa// 52%//Q05481 TESTI20378450 TESTI20380650 TESTI20381040 TESTI20382750//Homo sapiens hook1 protein (HOOK1) mRNA. complete cds.//2.60E-96//195aa//99%// TESTI20383880//Homo sapiens gamma cysteine string protein mRNA, partial cds.//6.50E-61//109aa//100%// AF368277 TESTI20385960//Homo sapiens mRNA for RET finger protein-like 3.//4.80E-156//288aa//100%//AJ010232 TESTI20386230 TESTI20386440 TESTI20388580 TESTI20390260 TESTI20390410 TESTI20391130 TESTI20391210 TESTI20391770 TESTI20392090 TESTI20392250//Homo sapiens VAV-3 protein mRNA, complete cds.//9.80E-145//268aa//98%//AF067817 TESTI20392270 TESTI20392760//PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT SDS22.//5.70E-22//226aa//31%// P36047 TESTI20393530//MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR (PTP).//9.00E-34// 105aa//68%//P12234

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TESTI20396130

90%//P98195

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TESTI20400940//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//4.70E-16i/669aa//23%//Q02224

TESTI20397760//POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IIB (EC 3.6.1.-).//1.60E-109//221aa//

TESTI20401020//Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete cds.//5.80E-64//234aa//56%//AF004161 TESTI20401280 TESTI20401430 TESTI20404240//INTERFERON-RELATED DEVELOPMENTAL REGULATOR 2 (SKMC15 PROTEIN).//4.60E-36//46aa//93%//Q12894 TESTI20406420 TESTI20408150 TESTI20408970//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PRO-10 TEIN OF 121 KDA) (P145).//4.30E-16//264aa//30%//P52591 TESTI20409440 TESTI20409890//GCD14 PROTEIN.//2.30E-46//263aa//40%//P46959 TESTI20413300 TESTI20415170 15 TESTI20415640 TESTI20416640//CHOLINE/ETHANOLAMINE KINASE [INCLUDES: CHOLINE KINASE (EC 2.7.1.32) (CK); ETH-ANOLAMINE KINASE (EC 2.7.1.82) (EK)].//2.10E-77//139aa//100%//Q9Y259 TESTI20417300//DYNEIN BETA CHAIN, CILIARY.//6.80E-129//552aa//45%//P39057 TESTI20419560 20 TESTI20420620//TRANSCRIPTION INITIATION FACTOR TFIID 70 KDA SUBUNIT (TAFII-70) (TAFII-80) (TAFII80).//0//526aa//99%//P49848 TESTI204214 TESTI20422640 TESTI20423020 25 TESTI20424000 TESTI20424730 TESTI20425070 TESTI20427830 TESTI20428060 30 TESTI20429280 TESTI20429580 TESTI20432750//Mus musculus pantothenate kinase 1 beta (panK1beta mRNA, complete cds.//9.70E-165// 363aa//82%//AF200357 TESTI20432820//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.00E-173//403aa//75%//P28160 35 TEST|20436560//LAMIN C.//9.20E-235//453aa//99%//P02546 TESTI20438570//Homo sapiens nolp mRNA, complete cds.//2.70E-43//146aa//60%//AB017800 TESTI20438660 TESTI20441940//Human K-C1 cotransporter (hKCC1) mRNA, complete cds.//5.50E-139//264aa//99%//U55054 TESTI20442760//Homo sapiens Ig-like membrane protein (IGSF3) mRNA, complete cds.//0//545aa//93%// AF031174 TESTI20443090//DNA REPAIR PROTEIN RAD51 HOMOLOG 4 (R51H3) (TRAD).//2.70E-68//141aa//100%// 075771 TESTI20444130 TESTI20444180 TESTI20447540 TESTI20449200//METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.//9.00E-173//313aa//99%// Q14831 TESTI20451710 50 TESTI20451990 TESTI20455090//KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18) (CK 18).//1.20E-76//199aa// 80%//P05783 TESTI20455620//HEAT SHOCK-RELATED 70 KDA PROTEIN 2 (HEAT SHOCK 70 KDA PROTEIN 2).//4.80E-218//336aa//99%//P54652 TESTI20456110//52 KDA RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//9. 40E-75//382aa//43%//P19474 TESTI20458190 TESTI20463520

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THYMU20118060

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TESTI20463580//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-
RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-
TOUS NUCLEAR PROTEIN HOMOLOG),//1.50E-17//190aa//28%//Q13107
TESTI20465350//2'. 3' -CYCLIC NUCLEOTIDE 3' -PHOSPHODIESTERASE (EC 3.1.4.37) (CNP) (CNPASE).//
2.20E-123//231aa//100%//P09543
TESTI20465520
TESTI20465690//Homo sapiens Borg4 mRNA, complete cds.//2.00E-152//235aa//99%//AB042237
TESTI20467210//Homo sapiens mRNA for HELG protein.//2.00E-166//368aa//83%//AJ277291
TESTI20467320/Mus musculus WAVE-1 mRNA, complete cds.//1.20E-111//233aa//88%//AF290877
TESTI20467970
TESTI20468630
TESTI20471410//PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (EC 3.1.3.16) (PP2C-ALPHA) (IA) (PROTEIN
PHOSPHATASE 1A).//1.30E-210//382aa//99%//P35813
TESTI20471470
TESTI20471530
TESTI20472120
TESTI20473420
TESTI20473830//Columba livia mRNA for 5'-nucleotidase.//2.00E-14//75aa//49%//AJ131243
TESTI20477920
TESTI20478010
TESTI20478180
TESTI20478850
TESTI20479300
THYMU10005360//Human T cell receptor bota chain (TCRB) mRNA, VNDNJC region, 5'end.//1.20E-130//270aa//
91°.//L07294
THYMU10005540//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//1.20E-237//479aa//90%//
Y14737
THYMU20000570
THYMU20011950
THYMU20015210
THYMU20018190
THYMU20023380//Homo sapiens m6A methyltransferase (MT-A70) gene. complete cds.//1.20E-38//86aa//100%//
AF014837
THYMU20027560
THYMU20029100
THYMU20032870
THYMU20039810/MPS1 protein//2.60E-283//646aa//77%//I52603
THYMU20045120
THYMU20058070
THYMU20061700
THYMU20066100
THYMU20070360
THYMU20075320
THYMU20081490//Homo sapiens ICB-1 mRNA, complete cds.//1.50E-23//267aa//33%//AF044896
THYMU20095960
THYMU201004:0
THYMU201016:0
THYMU20101920
THYMU20105190//MYOSIN I ALPHA (MMI-ALPHA).//7.50E-54//282aa//45%//P46735
THYMU20106710//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5).
of the Complete Nucleotide Sequence.//1.20E-54//113aa//98%//AE000660
THYMU20108310//Mouse NCBP-29 mRNA for PW29, complete cds.//7.70E-93//102aa//99%//D49429
THYMU20111180
THYMU20111420
THYMU20111830//protease, serine, 16 (thymus)//1.40E-129//175aa//98%//NP_005856
THYMU20114470
THYMU20115850
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00%//NP_005479 b) (UDP-GLC DEHYDROGENASE) c%//P17008 dG (WASP).//2.60E-12//155aa//32%// ete cds.//5.40E-171//321aa//100%// evy chain.//5.40E-235//477aa//89%// downward complete cds.//1.40E-92// dCLYCERIDE KINASE) (DGK- ZETA) defy/96aa//100%//P31146 TOKINE IK).//2.60E-40//83aa//96%//
c) (UDP-GLC DEHYDROGENASE)  2%//P17008  G (WASP).//2.60E-12//155aa//32%//  ete cds.//5.40E-171//321aa//100%//  avy chain.//5.40E-235//477aa//89%//  0%//P01876 ) mRNA, complete cds.//1.40E-92//  GLYCERIDE KINASE) (DGK- ZETA)  49//96aa//100%//P31146
c) (UDP-GLC DEHYDROGENASE)  2%//P17008  G (WASP).//2.60E-12//155aa//32%//  ete cds.//5.40E-171//321aa//100%//  avy chain.//5.40E-235//477aa//89%//  0%//P01876 ) mRNA, complete cds.//1.40E-92//  GLYCERIDE KINASE) (DGK- ZETA)  49//96aa//100%//P31146
c) (UDP-GLC DEHYDROGENASE)  2%//P17008  G (WASP).//2.60E-12//155aa//32%//  ete cds.//5.40E-171//321aa//100%//  avy chain.//5.40E-235//477aa//89%//  0%//P01876 ) mRNA, complete cds.//1.40E-92//  GLYCERIDE KINASE) (DGK- ZETA)  49//96aa//100%//P31146
%//P17008 G (WASP).//2.60E-12//155aa//32%// ete cds.//5.40E-171//321aa//100%// avy chain.//5.40E-235//477aa//89%// 0%//P01876 ) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA)
ete cds.//5.40E-171//321aa//100%// ete cds.//5.40E-171//321aa//100%// evy chain.//5.40E-235//477aa//89%// 0%//P01876 ) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA)
ete cds.//5.40E-171//321aa//100%// ete cds.//5.40E-171//321aa//100%// evy chain.//5.40E-235//477aa//89%// 0%//P01876 ) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA)
ete cds.//5.40E-171//321aa//100%// ete cds.//5.40E-171//321aa//100%// evy chain.//5.40E-235//477aa//89%// 0%//P01876 ) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA)
ete cds.//5.40E-171//321aa//100%// ete cds.//5.40E-171//321aa//100%// evy chain.//5.40E-235//477aa//89%// 0%//P01876 ) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA)
ete cds.//5.40E-171//321aa//100%// evy chain.//5.40E-235//477aa//89%// 0%//P01876 ) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA)
ete cds.//5.40E-171//321aa//100%// evy chain.//5.40E-235//477aa//89%// 0%//P01876 ) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA)
avy chain.//5.40E-235//477aa//89%// 0%//P01876 ) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA)
avy chain.//5.40E-235//477aa//89%// 0%//P01876 ) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA)
avy chain.//5.40E-235//477aa//89%// 0%//P01876 ) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA)
0%//P01876 ) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA) -49//96aa//100%//P31146
0%//P01876 ) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA) -49//96aa//100%//P31146
) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA) -49//96aa//100%//P31146
) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA) -49//96aa//100%//P31146
) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA) -49//96aa//100%//P31146
) mRNA, complete cds.//1.40E-92// GLYCERIDE KINASE) (DGK- ZETA) -49//96aa//100%//P31146
GLYCERIDE KINASE) (DGK- ZETA) -49//96aa//100%//P31146
.49//96aa//100%//P31146
.49//96aa//100%//P31146
.49//96aa//100%//P31146
FOKINE IK).//2.60E-40//83aa//96%//
TOKINE IK).//2.60E-40//83aa//96%//
HNRNP L).//1.70E-82//157aa//99%//
mRNA, complete cds.//2.90E-122//
, ·
a//99%//035492
a//99%//035492
ad/99%//035 <sub>4</sub> 92
aJ/99%J/035 <sub>4</sub> 92
aJ/99%J/035 <sub>4</sub> 92
al/99%//035 <sub>.</sub> 492
al/99%//035 <sub>.</sub> 492
al/99%//035 <sub>4</sub> 92
al/99%//035 <sub>.</sub> 492
al/99%//035 <sub>.</sub> 492
al/99%//035 <sub>.</sub> 492
ad/99%//035 <sub>.</sub> 492
<b>.</b>
g 2) (UNC-18B).//2.10E-54//112aa//
<b>.</b>
<b>.</b>
G 2) (UNC-18B).//2.10E-54//112aa//
G 2) (UNC-18B).//2.10E-54//112aa//
mRNA, comp

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D83032
THYMU20241850//HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DX BETA CHAIN PRECURSOR.//4.40E-
141//261aa//100%//P05538
THYMU20246840
THYMU20247480//ZINC FINGER PROTEIN 135.//1.20E-97//191aai/90%//P52742
THYMU20250420
THYMU20251890
THYMU20253250
THYMU20255570
THYMU20255720
THYMU20259090
THYMU20265300
THYMU20271250
THYMU20272490
THYMU20277390
THYMU20279750
THYMU20283790
THYMU20284120
THYMU20286290
THYMU20286320
TKIDN10000010//translocase of inner mitochondrial membrane 23 (yeast) homolog//6.30E-67//133aa//98%//
NP_006318
TKIDN20004640//GALACTOKINASE 2 (EC 2.7.1.6).//5.10E-99//200aa//97%//Q01415
TKIDN20005210
TKIDN2003210
TKIDN20030590 TKIDN20030620
TKIDN20030820 TKIDN20047480//MITOGEN-ACTIVATED PROTEIN KINASE 12 (EC 2.7.1) (EXTRACELLULAR SIGNAL-REG-
ULATED KINASE 6) (EC 2.7.1) (ERK6) (ERK5) (STRESS-ACTIVATED PROTEIN KINASE-3) (MITOGEN-ACTI-
VATED PROTEIN KINASE P38 GAMMA) (MAP KINASE P38 GAMMA).//2.20E-52//104aa//100%//P53778
TOVAR20004760
TOVAR20005750 TRACH20002870//CLAUDIN-6.//1.30E-27//175aa//42%//Q9Z262
TRACH20002870//CLAODIN-6.// 1.30E-27/1173aa/1427a/Q92232  TRACH20003590//CYTOCHROME P450 4A4 (EC 1.14.14.1) (CYPIVA4) (PROSTAGLANDIN OMEGA-HYDROX-
YLASE) (P450-P-2).//1.50E-138//493aa//49%//P10611
TRACH20005020 TRACH20005400//Mus musculus GTPase Rab37 (Rab37) mRNA, complete cds.//3.30E-109//223aa//93%//
AF233582 TRACH20007020//TRICHOHYALIN.//5.60E-24//532aa//23%//P37709
TRACH20016210//ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.65) (GALACTOSIDE 3-L-FUCOSYL-
TRANSFERASE) (FUCOSYLTRANSFERASE 6) (FUCT-VI).//5.00E-192//254aa//99%//P51993
TRACH20019960//SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN PRECURSOR (EC
3.6.1.37) (SODIUM PUMP) (NA+/K+ ATPASE).//9.50E-185//410aa//84%//P05023
TRACH20027840 TRACH20028030//Mus musculus mmDNAJA4 mRNA for mmDj4, complete cds.//8.50E-205//397aa//92%//
AB032401
TRACH20029540
TRACH20032720 TRACH20033230//MALTOSE PERMEASE.//1.20E-10//197aa//23%//Q45632
TRACH2003230/MAETOSE FERMEASE.//1.201910//1974420032 TRACH20034840//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//5.90E-14//342aa//
28%//P17437
TRACH20037360 TRACH20041830//Acdcs triseriatus putative disulfide-isomerase mRNA, partial cds.//3.10E-29//134aa//47%//
AF306866 TRACH20042920//Human C3f mRNA, complete cds.//7.80E-195//381aa//89%//U72515
TRACH20042920/Human C3I mRNA, complete cds.//7.802-195//361aa//6978/7072515  TRACH20048450//PROTEIN K4 (PROTEIN K3).//4.70E-57//431aa//32%//P18377
TRACH20048450//PHOTEIN K4 (PHOTEIN K3).//4.70E-57//451826/32/20/F16577  TRACH20050040//PUTATIVE SURFACE GLYCOPROTEIN C210RF1 PRECURSOR (C210RF3).//8.50E-74//
177aa//74%//P53801
TRACH20056980
HIMOHEOUJUJUU

TRACH20057690//RAC-BETA SERINE/THREONINE KINASE (EC 2.7.1.-) (RAC-PK-BETA) (AKT2 KINASE).// 8.80E-22//48aa//100%//P31751 TRACH20060150 TRACH20067620//N-ACETYLLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.150) (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT).//8.20E-76//145aa// 92%//Q06430 TRACH2C063660//Mouse 19.5 mRNA, complete cds.//1.00E-55//263aa//41%//M32486 TRACH20063700//Homo sapiens adaptor protein CIKS mRNA, complete cds.//1.50E-232//572aa//79%// AF272151 TRACH20069180//Homo sapiens IGHG3 gene for immunoglobulin heavy chain gamma 3 constant region, 4-exon hinge. isolate Lib-A2.//1.00E-213//377aa//100%//AJ390247 TRACH20076740//FOLATE-LIKE TRANSPORTER DJ206D15.1 ON CHROMOSOME 1 (FRAGMENT).//1.00E-61//276aa//46%//060779 TRACH20076760 TRACH20077540//DXS8237E PROTEIN (FRAGMENT).//6.00E-96//189aa//95%//P98175 TRACH2C0/9690//ZINC FINGER PROTEIN 136.//1.50E-113//368aa//58%//P52737 TRACH2C084720//METHIONYL-TRNA SYNTHETASE, MITOCHONDRIAL (EC 6.1.1.10) (METHIONINE-- TRNA LIGASE) (METRS) //8.50E-90//525aa//38%//074634 TRACH2C085400//Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds.//1.30E-89// 384aa//47° J/AF302046 TRACH20085830//CYTOCHROME P450 4A8 (EC 1.14.14.1) (CYPIVA8) (P450-KP1) (P450-PP1).//3.70E-247// 508aa//87%J/P24464 . TRACH20091230 TRACH20092680 TRACH2C096610//LAMIN A (70 KDA LAMIN).//1.70E-77//164aa//93%//P02545 TRACH20105870//EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA (EIF-4-GAMMA) (EIF- 4G) (EIF4G) (P220) //9 20E-95//204aa//92%//Q04637 TRACH2C107710 TRACH20109650 TRACH20111130 TRACH2C115740 TRACH20118940 TRACH2C121380//REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) (FRAGMENT).//7.60E-144//308aa// 92%//043566 TRACH2C123110//Rattus norvegicus TM6P1 (TM6P1) mRNA. complete cds.//2.10E-87//187aa//88%//AF186469 TRACH2C128230//Homo sapiens IGHG3 gene for immunoglobulin heavy chain gamma 3 constant region, 4-exon hinge. isolate Lib-A2.//9.60E-213//377aa//99%//AJ390247 TRACH2C134950 TRACH20135520 TRACH20136710//IG LAMBDA CHAIN V-II REGION NIG-84.//2.20E-43//112aa//75%//P04209 TRACH2C139820//SIGNAL RECOGNITION PARTICLE 68 KDA PROTEIN (SRP68).//3.70E-48//107aa//92%// Q00004 TRACH2C140820 TRACH20141240//Mus musculus G21 protein mRNA, complete cds.//6.10E-26//60aa//93%//AF131207 TRACH2C145440 TRACH2C147250 TRACH2C149970//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//2.30E-205//512aa//74%//U16802 TRACH20153810 TRACH2C154860//RETINOIC ACID RECEPTOR ALPHA (RAR-ALPHA).//8.90E-221//443aa//92%//P10276 TRACH2C162860//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B). //1.80E-39//80aa//98%//095298 TRACH20163170//HOMEOBOX PROTEIN MEIS1.//1.50E-131//238aa//100%//000470 TRACH20164980//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.50E-163//488aa//56%//Q99676

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TRACH20167220 TRACH2C168350

	FHACH20169800
	TRACH20180840
	TRACH20183170//Rattus norvegicus Sprague-Dawley SM-20 mRNA, complete cds.//1.60E-75//215aa//61%//
	U06713
5	TRACH20184490//Homo sapiens mRNA for zinc finger protein (ZNF304 gene). //3. 20E-111//477aa//46%//
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	TRACH20187180
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10	TSTOM20001390
	TSTOM20003150
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	TUTER20002830//Homo sapiens transformer-2-beta (SFRS10) gene, alternatively spliced products, complete
	cds.//4.70E-122//253aa//90%//AF057159
15	UMVEN10001560//Anthocidaris crassispina mRNA for outer arm dynein light chain 1, complete cds.//1.90E-24//
, ,	
	119aa//47%//AB010055
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	180aa//33%/iP30337
	UMVEN20000690
20	UMYEN20003540
	UTERU20000740//Human fusion protein mRNA, complete cds.//4.90E-47//97aa//100%//M82829
	UTERU20004240//CGI-96 protein//2.10E-39//108aa//81%//NP_056518
	UTERU20006290
	UTERU2C006960//cndoplasmic reticulum resident protein 58//5.90E-51//150aa//63%//NP_076994
75	UTERU20020010
	UTERU20022940//Human (p23) mRNA, complete cds.//2.80E-80//147aa//99%//L24804
	UTERU2C030570//CHLORIDE CHANNEL PROTEIN CLC-KB (CLC-K2).//3.00E-252//469aa//99%//P51801
	UTERU20040610
	UTFRU2C046640//Mus musculus 1dlBp (LDLB) mRNA, complete cds.//0//839aa//83%//AF109377
30	UTERU2C046980//Mus musculus mRNA for thrombospondin type 1 domain, complete cds.//7.30E-117//232aa//
	€7'/AB016768
	UTERU20050690
	UTERU2C054460
	UTERU20055330
35	UTERU20055480
	UTERU20055930
	UTERU20056010
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	UTERU20061030
10	UTERU20064000
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45	UTERU2C068990
	UTERU20070040
	UTERU2C070810
	UTERU2C076390
	UTERU2C081300
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	UTERU20094350
	UTERU20095380
	UTERU20095400
	UTERU20097760//OVCA2=candidate tumor suppressor [human, fetal brain, Peptide, 120 aa]//6.00E-30//66aa//
55	95%//AAB36422
	UTERU20099720//Homo sapiens mRNA for SPIN protein.//6.50E-72//186aa//79%//Y14946
	UTERU20101240
	UTERU20114100

UTERU20115740//Human PMS2 related (hPMSR3) gene, complete cds.//1.00E-43//84aa//98%//U38979 UTERU20116570//Homo sapiens actin-binding double-zinc-finger protein (abLIM) mRNA, complete cds.//4.80E-163//468aa//71%//AF005654

UTERU20118110

UTERU20118970

UTERU20119060

UTERU20119680

UTERU20120310//Rattus norvegicus rexo70 mRNA, complete cds //1.50E-65//178aa//78%//AF032667

UTERU20124070

UTERU20126880

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UTERU20134910

UTERU20135860

UTERU20143980

UTERU20144640//ACID CERAMIDASE PRECURSOR (EC 3.5.1.23) (ACYLSPHINGOSINE DEACYLASE) (N-ACYLSPHINGOSINE AMIDOHYDROLASE) (AC) (PUTATIVE 32 KDA HEART PROTEIN) (PHP32).//1.90E-166//243aa//100%//Q13510

UTERU20145480//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//4.40E-213//673aa//57%//AB011414

UTERU20146310//DIACYLGLYCEROL KINASE ETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK- ETA) (DAG

KINASE ETA).//4. 50E-242//485aa//92%//Q64398

UTERU20146680

UTERU20150870

UTERU20151980//DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH-5).//5.20E-15//248aa//31%//Q13202

5 UTERU20158300

UTERU20158800//P-SELECTIN GLYCOPROTEIN LIGAND 1 PRECURSOR (PSGL-1) (SELECTIN P LIGAND) (CD162 ANTIGEN).//2.20E-185//384aa//95%//Q14242

UTERU20161570//PROBABLE G PROTEIN-COUPLED RECEPTOR RTA.//2.70E-141//303aa//85%//P23749 UTERU20164260

UTERU20168220//AIG1 PROTEIN.//7.70E-16//145aa//35%//P54120

UTERU20176130//Mus musculus zinc finger protein 289 (Zfp289) mRNA, complete cds.//4.00E-143//297aa// 94%//AF229439

UTERU20176320//DNA REPAIR PROTEIN RAD18.//1.10E-40//333aa//32%//P53692

UTERU20178100

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UTERU20183640//SEMAPHORIN 3B PRECURSOR (SEMAPHORIN V) (SEMA V).//1.20E-69//135aa//100%//Q13214

UTERU20185230//Human androgen-induced prostate proliferative shutoff associated protein (AS3) mRNA, complete cds.//1.90E-255//571aa//80%//U95825

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UTERU20188110//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//4.10E-157//315aa//97%//AF076183

UTERU20188810

#### Claims

- A polynucleotide selected from the group consisting of the following (a) to (g):
  - (a) a polynucleotide comprising a protein-coding region of the nucleotide sequence of any one of SEQ ID NOs:
    - (b) a polynucleotide encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 2444 to 4886:
    - (c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 2444 to 4886, wherein, in said amino acid sequence, one or more amino acids have been substituted, deleted, inserted, and/or added, and wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide comprising the selected amino acid sequence;
    - (d) a polynucleotide hybridizing to a polynucleotide comprising the nucleotide sequence of any one of SEQ

- ID NOs: 1 to 2443, wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide encoded by the selected nucleotide sequence;
- (e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotide according to any one of (a) to (d);
- (f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of any one of SEQ ID NOs: 1 to 2443; and
- (g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of any one of SEQ ID NOs: 1 to 2443.
- 2. A polypeptide encoded by the polynucleotide of claim 1, or a partial peptide thereof.
  - 3. An antibody binding to the polypeptide or the peptide of claim 2.
  - 4. A method for immunologically assaying the polypeptide or the peptide of claim 2, said method comprising the steps of contacting the polypeptide or the peptide of claim 2 with the antibody of claim 3, and observing the binding between the two.
  - 5. A vector comprising the polynucleotide of claim 1.

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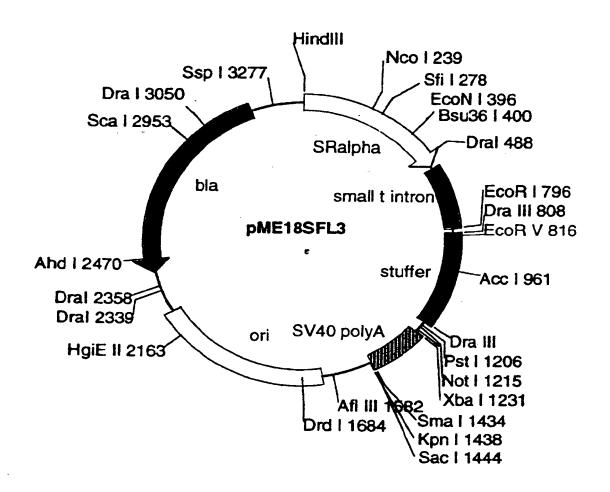
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- 6. A transformant carrying the polynucleotide of claim 1 or the vector of claim 5.
  - 7. A transformant carrying the polynucleotide of claim 1 or the vector of claim 5 in an expressible manner.
  - 8. A method for producing the polypeptide or the peptide of claim 2, said method comprising the steps of culturing the transformant of claim 7 and recovering an expression product.
  - An oligonucleotide comprising at least 15 nucleotides, said oligonucleotide comprising a nucleotide sequence complementary to the nucleotide sequence of any one of SEQ ID NOs: 1 to 2443 or to a complementary strand thereof
  - 10. Use of the oligonucleotide of claim 9 as a primer for synthesizing the polynucleotide of claim 1.
  - 11. Use of the oligonucleotide of claim 9 as a probe for detecting the polynucleotide of claim 1.
  - 12. An antisense polynucleotide against the polynucleotide of claim 1 or a part thereof.
  - 13. A method for detecting the polynucleotide of claim 1, said method comprising the following steps of:
    - a) incubating a target polynucleotide with the oligonucleotide of claim 9 under hybridizable conditions, and
    - b) detecting hybridization of the target polynucleotide with the oligonucleotide of claim 9.
  - 14. A database of polynucleotides and/or polypeptides, said database comprising information on at least one of the nucleotide sequences of SEQ ID NOs: 1 to 2443 and/or on at least one of the amino acid sequences of SEQ ID NOs: 2444 to 4886.

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Figure 1





# **EUROPEAN SEARCH REPORT**

Application Number EP 02 00 8400

Х		sages	to claim	APPLICATION (IntCI.7)
	RYLE (US); HYSEQ IN (US) 26 July 2001 (	RUI HONG ;GOODRICH	1-14	C12N15/00 C07K14/00
×	ID N 1016" Database accession XP002206834 This sequence shows	(2001-07-26) man polynucleotide SEQ no. AAI58813  99.9% identity with nucleotide overlap.	1,14	
x	DATABASE GENESEQ P Derwent26 July 2001 TANG YT: "Human pol 2802" Database accession XP002206835 This sequence shows SEQ ID N 2444 in 54 * the whole documen	(2001-07-26) ypeptide SEQ ID N no. AAM39657 99.4% identity with 3 aa overlap	2,14	TECHNICAL FIELDS SEARCHED (Int.Cl.7) C12N C07K
X .	clone 91-13, mRNA s Database accession XP002206836	98-01-17) man (J. Swensen) cDNA equence" no. AF039235 % identity with SEQ ID lap	1,14	
	The present search report has			
	Place of search MUNICH	19 July 2002	Vi	Examiner (, 0
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# **EUROPEAN SEARCH REPORT**

Application Number EP 02 00 8400

Category	Citation of document with in	dication, where appropriate.		evant	CLASSIFICATE	ON OF THE
Calegory	of relevant pass	ages	to d	aim	APPLICATION	(InLCI.7)
X						
X	DATABASE GENESEQ (Derwent7 November 2: ROSEN CA ET AL.: "Himmune/hematopoietic N 10300" Database accession XP002206837 This sequence shows SEQ ID N 2444 in 52* the whole document	001 (2001-11-07) uman c antigen SEQ ID no. AAM82707  98.5% identity with 7 amino acid overlap	2,14			
X	human protein" Database accession XP002206838	7-01) : "Hypothtical 58.8 kl no. 09BTE6  100% identity with Si overlap			TECHNICAL F SEARCHED	IELOS (Im.Cl.7)
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Α	GILL ROBERT W ET AL to perform assembly Tags (ESTs)." CABIOS, vol. 13, no. 4, 199 XPO01083718 * the whole documen		1   1-14			
	The present search report has	been drawn up for all claims		1		
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	MUNICH	19 July 2002	- 1	· Vix,		
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# **EUROPEAN SEARCH REPORT**

Application Number

	DOCUMENTS CONSID	ERED TO BE RELEVANT		
Category	Citation of document with it of relevant pass	ndication, where appropriate, ages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (InLC).7)
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A	SUZUKI Y ET AL: "C CHARACTERIZATION OF AND A 5'-END-ENRICH GENE, ELSEVIER, AMS vol. 200, no. 1/2, 19 November 1997 (1 149-156, XP00291760 ISSN: 0378-1119 * the whole document	A FULL LENGTH-ENRICHE ED CDNA LIBRARY" TERDAM, NL, 997-11-19), pages 9	1-14	TECHNICAL FIELDS
A	method for cDNA clo FASEB JOURNAL, vol. 13, no. 7, 23 April 1999 (1999 XP001056180 Annual Meeting of t for Experimental Bi and Molecular Biolo California, USA; Ma ISSN: 0892-6638 * the whole documen	-04-23), page A1382 he American Societies ology on Biochemistry gy 99;San Francisco, y 16-20, 1999 t *	1-14	SEARCHED (Int.Cl.7)
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docu	iment of the same category nological background	L: document caed	for other reasons	
O: non-	-written disclosure	& member of the document		

EPO FORM 1503 03 82 (POACO1)



Application Number

EP 02 00 8400

CLAIMS INCURRING FEES
The present European patent application comprised at the time of filing more than ten claims.
Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):
No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.
LACK OF UNITY OF INVENTION
The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:
see sheet B
All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.
As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.
Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:
·
None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:
1-14 (partially)



# LACK OF UNITY OF INVENTION SHEET B

Application Number

EP 02 00 8400

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

1. Claims: Invention 1: claims 1-14 (partially)

Polynucleotide of SEQ ID N 1 and its encoding polypeptide of SEQ ID N 2444

2. Claims: Inventions 2-2442 : claims 1-14 (partially)

Polynucleotides of SEQ ID N 2-2442 and their encoding polypeptides of SEQ ID N 2445-4885

3. Claims: Invention 2443 : claims 1-14 (partially)

Polynucleotide of SEQ ID N 2443 and its encoding polypeptide of SEQ ID N 4886  $\,$ 

## ANNEX TO THE EUROPEAN SEARCH REPORT ON EUROPEAN PATENT APPLICATION NO.

EP 02 00 8400

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report. The members are as contained in the European Patent Office EDP lile on The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

19-07-2002

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